

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 116820

TO: Vanessa L Ford

Location: REM-3B25&3C18

Art Unit: 1645

Thursday, March 18, 2004

Case Serial Number: 09/543407

From: Barb O'Bryen

**Location: Biotech-Chem Library** 

Remsen E01A69

Phone: 571-272-2518

BOB

barbara.obryen@uspto.gov

#### Search Notes

# RUSH



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### STIC-Biotech/ChemLib

Page, Thurman

High

Friday, March 12, 2004 2:35 PM STIC-Biotech/ChemLib Ford, Vanessa FW: In re: 09/543407 sequence search

From:

S nt: To: Cc: Subject:

Importance:

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Thurman K. Pa SPE Art Units Technology Ce	1615 & 1616		
Original Mess	=		
From: Sent:	Ford, Vanessa Friday, March 12, 2004 1:52 PM		
T :	Page, Thurman		
Subject:	FW: In re: 09/543407 sequence search	1	
Christina is out	of the Office today.		
Original Mess	<u>-</u>		
From:	Ford, Vanessa		
Sent: To:	Friday, March 12, 2004 1:50 PM Chan, Christina		
Subject:	In re: 09/543407, sequence search		
Please search:	SEQ ID NOs: 1, 2, 3, 4, 9, 11,	13, 15, 17, 19. please include int	teference searches. Please Rush.
Biotechnology Par Office: REM 3B2! Mailbox: REM 3C: Phone: 571.272.0 Art Unit: 1645	5 18		
Searcher:		TYPE OF SEARCH:	VENDOR/COST (where applic.)
Phone:		NA Sequences:	STN:
Location: Date Picked Up:		AA Sequences: Structures:	DIALOG: Questel/Orbit:
Date Picked Op Date Completed:_		Bibliographic:	DRLink:
Searcher Prep/Rev	riew:	Litigation:	Lexis/Nexis:
Clerical:		Full text:	Sequence Sys.:
Online time:		Patent Family:	WWW/Internet:

Other:\_\_

Other (specify):\_\_\_\_

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                                      3470272 seqs, 21671516995 residues
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

#### Result No. 254.4 254.4 2247.8 2247.8 2247.8 2247.8 2247.9 2217.6 1190.4 1190 446.4 446.4 440.6 331.8 310.4 262.8 256 34.6 34.6 34.4 34.2 Score 36 % Query Match 3 302156 3 168267 3 301214 3 301214 11160 111476 111828 1458 2883 10370 292504 437 19201 1212 1711 10190 306358 327773 230 Length 10346 BB C144908 CSP515700 CSP515700 CFF515701 ECCSGABDG AE000205 D90741 ECCCSGAAA AF27573315 AE005315 AE0053207 SEU53207 SEU53207 AE016981 AF237726 D907257 AE016981 AF237726 D90737726 I44909 SEU43280 STAJ2301 AE008749 AL627269 AE016840 STAGFBA 144908 Sequence 56 AJ515700 Citrobact AJ515701 Citrobact AJ515701 Citrobact AJ515701 Citrobact AJ5015701 Escherichia AE00754 E.coli csgG AE000205 Escherichia AX814811 Sequence L04979 Escherich AE005315 Escherich AE005315 Escherich AE005315 Escherich AE005315 Escherich AE001579 Escherich AE015791 Escherich AP012574 Escherich AJ515702 Enterobac AE015911 Shigella AF237726 Shigella AF237726 Shigella AF237726 Shigella AE016917 Sequence AX814809 Sequence AX814798 Sequence AX814798 Sequence AX814798 Sequence AX814798 Sequence AX814798 Sequence AX814798 Orientia AC016786 Pseudomon AE008209 Pan trog1 AE016786 Pseudomon AE008209 Pan trog1 AE0146009 Pan trog1 AE0146009 Pan trog1 AE015843 Oryza sat BD243118 Hypersens AR403552 Sequence AX34717 Sequence AX34717 Sequence AX34717 Sequence AE016840 Salmonell AJ000514 Salmonell AJ002301 Salmonell AE008749 Salmonell Description Sequence 58 Salmonel

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JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	144909	RESULT 1
Salmonella Patent: US 5635617-A 58 03-JUN-1997;	Methods and compositions comprising the agfA gene for detection of	Doran, J.L., Kay, W.W., Collinson, S. Karen. and Clouthier, S.C.	1 (bases 1 to 456)	Unclassified.	Unknown.	Unknown.		I44909.1 GI:2469622	144909	Sequence 58 from patent US 5635617.	I44909 456 bp DNA linear PAT 07-OCT-1997		
	ion of										CT-1997		

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                                             96146512
                                                                                    Salmonella enteritidis
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Collinson, S.K., Clouthier, S.C., Doran, J.L., Banser, P.A. and
                                                                                                                                                           Doran, J.L., Collinson, S.K., Burian, J., Sarlos, G., Todd, E.C., Munro, C.K., Kay, C.M., Banser, P.A., Peterkin, P.I. and Kay, W.W. DNA-based diagnostic tests for Salmonella species targeting agfa, the structural gene for thin, aggregative fimbriae J.Clin. Microbiol. 31 (9), 2263-2273 (1993)
                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis agfBAC operon: precursor (agfB), thin aggregative fim AgfC (agfC) genes, complete cds.
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456; Conserv
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Submitted (13-DEC-1995) S. Karen Collinson, Microbiology, University of Victoria, P.O. B Victoria, BC V8W 3P6, Canada Location/Qualifiers
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Length

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhimurium
Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  csgA gene; csgB gene; csgC csgG gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhimurium
                                                                                                                                                                                                               Submitted (29-OCT-1997) Romling U.,
Karolinska Institute, MTC, Box 280,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           Romling, U., Bian, Z., Hammar, M., Sierralta, W.D. and Normark, S. Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AJ002301.1 GI:2739232
                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 180 (3),
98117058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
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:8gG, csgF,
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Stockholm,
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S-17177, SWEDEN
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Matches 451; Conservative
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                                                                                                                                                              Salmonella typhimurium LT2
Salmonella typhimurium LT2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriacea; Salmonella.

1 (bases 1 to 22411)
MCClelland,M., Sanderson,K.E., Spieth,J., Clifton,S.W.,
Latreille,P., Courtney,L., Porwollik,S., Ali,J., Dante,M., Du,F.,
Hou,S., Layman,D., Leonard,S., Mguyen,C., Scott,K., Holmes,A.,
Grewal,N., Mulvaney,E., Ryan,E., Sun,H., Florea,L., Miller,W.,
Stoneking,T., Nhan,M., Waterston,R. and Wilson,R.K.
Complete genome sequence of Salmonella enterica serovar Typhimurium
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The Salmonella typhimurium Genome Sequencing Project Direct Submission
Submitted (29-MAR-2001) Genome Sequencing Center, Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421
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AE008749 AE006468
AE0708749.1 GI:16419641
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                                                                                                                                          Nature 413 (6858),
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Salmonella typhimurium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCCGCCAATACGGCGGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT. 4385
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Pred. No. 3.9e-118;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics, Washington University School of Medicine, 4444 Forest
Park Boulevard, St. Louis, MO 63108, USA
COMMENT Supported by NIH grant 5U 01 AI43283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and
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/protein id="AAL20060.1"
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complement(4413. .5099)
/gene="STM1129"
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/product="putative sodium/glucose cotransporter"
/product="putative sodium/glucose cotransporter"
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/translation="MITHSFGIVN"/LAMMLTD"
/translation="MITHSFGIVN"/LAMMLTD"
/translation="MITHSFGIVN"/LAMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(4413..5093)
/gene="STM1129"
/note="similar to E. co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(4083. .4088)
/gene≃"STM1128"
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AIFAAAQSSISSSLNSISSCFNSDIYQRLSKKKRTPENRKKIAKLVILVAGLISSAAS
VMLVMADBSEIMDAFNSLIGLMGGPWTGLFMLGIFFKRANAGSAVLGIIISVITVLGA
RYATDLNFFFYGVIGSLSVVISGVIFAPLFAPAPPLTLDEKPBPKVTL"
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/gene="STM1127"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative inner
/protein_id="AAL20061.1"
/db_xref="GI:16419646"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to E. coli orf, hypothetical
(AAC77266.1); Blastp hit to AAC77266.1 (404
identity in aa 40 - 403"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to E. coli putative cotransporter
(AAC76702.1); Blastp hit to AAC76702.1 (571 aa);
identity in aa 7 - 478"
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/gene="STM1131"
                                                                                                   'gene="STM1131"
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70% identity in aa 1 -
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note="putative

RBS for STM1131; RegulonDB:STMS1H001402"

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ACCESSION
VERSION
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                      complete chromosome; segment AL627269 AL513382 AL627269.1 GI:16502231
                                                                  AL627269 254050 bp
Salmonella enterica serovar Typhi
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                                                                                                                                                                                                                                                      AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 18224
                                                                                                                                                                                     GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCCGTTATGGTAACGGCGCCGAT
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ieklengigfyydasvksggydgeQdkhlsdlyanaielgysynykytunfylqpgfi
fesgedtsiykeylregynfbsgyymagryrydyarktanysddektnredtyigyyf
Delkleynfymdsdqikfdnkktnyehnyalawklnksftpyyeygnyavrnntder
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/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to E. coli putative transport (AAC77235.1); Blastp hit to AAC77235.1 (425 identity in as 25 - 418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="STM1132"
7768. .7773
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7768. .9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="STM1132"
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/protein_id="AAL20062.1"
/db_xref="GI:16419647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="STM1131"
/note="similar to E. coli orf, hypothetical protein
(AAC77267.1); Blastp hit to AAC77267.1 (241 aa), 26%
identity in aa 4 - 239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="STM1132"
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/transl_table=
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98.9%;
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Pred. No. 4
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                                                        DNA linear BCT 04-JUL-20
(Salmonella typhi) strain CT18,
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es 5;
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SOURCE
ORGANISM
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MEDLINE
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                                                                                    misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Details of S. typhi sequencing at the on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhill, J., Dougan, G., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebaihia, M., Baker, S., Basham, D., Brooke, K., Chillingworth, T., Connerton, P., Cronin, A., Davie, P., Davies, R.M., Dowd, L., White, N., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Jagels, K., Whitehead, S. and Barrell, B.G. Complete genome sequence of a multiple drug resistant Salmonella Nature 413 (6658), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkhill,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enterica subsp. enterica serovar Typhi
Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11677608
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                                                                                                                                                 http://www.sanger.ac.uk/Projects/S_typhi/)
Location/Qualifiers
                             family M1, score
                                                                                                     ACLRFLTFGETELANTLVSKQYRDANNMTDALAALSAAVAAQLPCRDTLMQEYDDKWH
QDGLVYDKWFILQSTSPAENVLETVRSLLKHRSFSMSNPNRIRSLIGAFAGSNPAAFH
AQDGSGYQFLVEMLTDLNSRNPQVASRLIEPLIRLKRYDDKRQEKMRAALEQLKGLEN
'gene="STY1078"
                                                                                                 LSGDLYEKITKALA"
                                               note="Pfam match
                                                                gene="STY1078"
                                                                                                                                                                                                                                                                                                                                                                                                         /product="aminopeptidase
/protein_id="CAD08183.1"
/db_xref="GI:16502232"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Orthologue of E.
to AMPN_ECOLI (869 aa);
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="STY1078"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="synonym: pepN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="STY1078"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mol_type="genomic DNA"
strain="CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Salmonella enterica subsp.
Typhi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:90370"
                .1089
                       h to entry PF01433 Peptidase_M1,
245.10, E-value 1.9e-84"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coli pepN (AMPN_ECOLI);
94% identity in 869 aa o
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                                  Peptidase
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/gene="STY1081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MMRIKPDDNWRWYYDEEHDRMMLDLANGMLFRSRFSRKMLTPDA
FCPTGFCVDDAALYFSFEEKCRDFELTKEQRAELVLNALVAIRYLKPQMPKSWHFVAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Orthologue of E. coli YCBW_ECOLI; YCBW ECOLI (192 aa), 90% identity in 180 discrepency in position of translational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="STY1080"
4174. .4719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF01180 DHOdehase,
Dihydroorotate dehydrogenase, score 563.50, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SWISS-PROT:Q827S9"

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KVYAYAGYIA.NISSPNTPGLRTLQVSDALDDLLTAIKNKQNDLQVIHKKYVPVAVKI
APDLCEEELIQVADSLLRHNIDGVIATNTTLDRSLVQGMKNCQQTGGLSGRPLQLKST
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                                                                                                                                                                                                                                                                                                                                                                                          /product="conserved hypothetical protein"
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/db_xref="GI:16502235"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMNDRLKPOVHCHSFSLEOAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEMWTPGTGDAASVWLSDTAEQVNLLVVEPGENAALCLLAQPGVVIAGRTMQLGDAIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="conserved hypothetical protein"
/protein_id="CAD08185.1"
/db_xref="GI:16502234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3874. .3936
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/protein id="CAD08194.1"
/db_xref="GI:16502233"
/db_xref="GOA.982759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to PYRD_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Orthologue of E. coli P75863; Fasta hit (369 aa), 86% identity in 367 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=
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/note="PS00912 Dihydroorotate dehydrogenase
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/note="PS00911 Dihydroorotate dehydrogenase
                                                                                                                                                                                                                                                                                                                                                               db_xref="GOA:Q8Z7S7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="STY1080"
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to PYRD ECOLI (336 aa), 95% identity in 336 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zinc-binding region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="STY1079"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         xref="SPTREMBL:Q8Z7S8"
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Similarity
GTAGGCCAGGGTGCGGATAACAGTACTATTGAACTGACTCAGAATGGTTTCAGAAACAAT 89205
                                                                                                                                                                                                                                                                                              CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                           GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGG 8902
                                                                                                                                                                                                                                                                                                                                                                                                                             GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCGAATAGTTCCGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 8896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAGTCGTAGTTTCTGGCAGTGCTCTGGCT
                                  GTAGGCCAGGGTGCGGATAATAGTACTAITGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                                                                AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
                                                                                                                                                                                                                                                            CCGGATTCCACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
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Rrghrgfsghaphdealwgevvaeagotrarkslerfysshfysgbdafylearhsllastar

Rrghrgfsghaphdealwgevvaeagotrarkslerfysghdsdpaliflaettaskeatva

Rrghrgfsghaphdealwgevvaeagotrarkslebdpblilaettaskeatva

Rofigemnlslesardlegslolradkofkakngeldcvqknyhiaettaskeaptva

Rdyangrefdiiaatusketylgiphklesargkghdflesardkgrykghgelfevesyna

Rlwynltdyldtglflheiriakhgleskgkdflelnlesytgssyhadleskardkgarntt

DMSRTYLEWBERNLELNGLSGRAHRLIQADCLGWLBEANBODLIFIDFTSNSKR

VDMSRTYLEWBERNLELNGLSGRAHRLIQADCLGWLBEANBODLIFIDFTSNSKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Similar to Haemophilus influenzae hypothetical protein hi0116 H10116 SW:YCBY HAEIN (P44524; P43945) fast. scores: E(): 0, 60.3% id in 710 aa Orthologue of E. coli YCBY ECOLI; Fasta hit to YCBY ECOLI (702 aa), 92% identity in 702 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          526 aa overlap
Fasta hit to YUJK_ECOLI (554 aa), 34% identity in 524 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF01170 UPF0020, Uncharacterized protein family UPF0020, scc B-value 3.7e-231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSPDFARNRQIHNCWLIRAA"
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/protein id="CAD08187.1"
/db_xref="GI:1650236"
/db_xref="GOA:082786"
/db_xref="SPTREMBL:Q82786"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Pfam match to entry PF00111 fer2, 2Pe-2S iron-sulfur cluster binding domains, score 55.90,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="STY1083"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="Fasta hit to YBIT_ECOLI (530 aa), 32% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9952
gene="STY1083"
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98.7%;
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Pred. No. 1.5e-117;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deng, W., Liou, S.-R., Plunkett, G. III, Mayhew, G.F., Rose, D.J., Burland, V., Kodoyianni, V., Schwartz, D.C. and Blattner, F.R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deng, W., Liou, S.R., Plunkett III, G., Mayhew, G.F., Rose, D.J., Burland, V., Kodoyianni, V., Schwartz, D.C. and Blattner, F.R. Comparative Genomics of Salmonella enterica Serovar Typhi Strains
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Salmonella enterica subsp. enterica serovar Typhi Ty2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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AE016840.1 GI:29137797
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                                                                                                                        /locus_tag="t1736" complement(844. .1797)
                                                                                                                                                                                                                                  /translation="MGDEKSLAHTRWNCKYHIVFAPKYRRQAFYGEKRRAVGSILRKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /locus_tag="t1735"
/note="corresponds to STY1225 from Accession AL513382:
/Salmonella typhi CT18"
'note=\overline{\ \ }corresponds to STY1223 from Accession AL513382:
                                                                                                                                                                                                                           complement (844. .1797)
                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AA069359.1"
/db_xref="GI:29137798"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="transposase for insertion sequence element
IS200"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus_tag="t1735"
complement(164. .622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sub_species="enterica"
/db_xref="taxon:209261"
complement(164..622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transi_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="tnpA"
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Typhi Ty2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strain="Ty2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _type="genomic DNA"
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AIGSSVAQINNYAKQIANLNDQISRMTGVGAGASENDLLDQRDQLYSELMKIVGVEVS
VQDGGTYNLTWANGYTLVQGSTARQLAAVFSSADPTRTTVAYVDEAAGNIEIPEKLLN
VYSNISMLTTRADGULOQTRYLLQQLALAFADAFNAQHTKGYDADGNKGKDFFSIGSPV
LEIDGLKVTVGTJAKVVDSTKVQATDYKIVFDTHQVTRTADHTTFTATKDADGK
SDNRNGQALLDLQNSVVGGNKTSNDAYATLVSDVGNKTSTLKTSSTTQANVVKQLYK
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COMPLEMENT (3538. .4488)
                     /trānslation="myvfkalagivlalvatlahabrirdlisvogvrensligygly
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OLNGGRITNGAIIERBLPTQFGAGNTINLQLWDBDFTWAQQIIDAINRARGYGSATAL
DARTVQVRVPSGNSSQVRFLADIQNNEVNVTPQDAKVVINSRTGSVNNNREVTLDSCA
vaqgnlsvtvnrqlnvnqpntþfgggqtvvtþqtqidlrqsggslqsvrssanlnsvv
                                                                                                                                                                                                                                                                                     /gene="flg1"
/locus tag="tl739"
/note="corresponds to STY1220 from Accession AL513382:
Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MICDGKLLASAAWDAQSLNELKAKAGQDPAANIRPVARQVEGMF
VQMMLKSMREALPKDGLFSSDQTRLYTSMYDQQIAQQMTAGKGLGLADMMVKQMTGGQ
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LPARLASEQSGVPHHLILAQAALESGWGQRQTLRENGEPSYNVFGVKATASWKGPVTE
ITTTEYENGEAKKVKAKFRVYSSYLEALSDYVALLTRNPRYAAVTTAATAEQGAVALQ
                                                                                                                                                                               /product="flagellar P-ring protein precursor"
/protein_id="AAO69363.1"
/db_xref="G1:29137802"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (4488. .5591)
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/transl_table
                                                                                                                                                                                                                                                                                                                                                                                                                                complement (4488. .5591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="flgI"
/locus_tag="
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Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="flagellar protein FlgJ"
/protein_id="AAO69362.1"
/db_xref="GI:29137801"
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AASQAVULFQAQAQMSQYALARTFATQKVSLEESVLSQVTTALQTAQEKIVYAQMGTL
SDDDRASLATDLOGIRDQLMMLANSTDGMGRYIFAGYKTEAAPEDQATGGYHGGEKSV
TQQVDSARTMVIGHTGAQLFMSITSMAVPEPDGSDSEKULFVMLDTAIAALKTPVEGN
DVEKEKAAAAIDKTMRGLKMSLMNVLTVRAELGTQLSELSTLDSLGSDRALGQKLQMS
NLVDVDMMSUTSYVMQQAALQASYKTFTDMQGMSLFQLMR"
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/protein_id="AAO69361.1"
/db_xref="GI:29137800"
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complement(1812. .3473)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="corresponds to STY1222 from Accession AL513382:
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/protein_id="AAO69360.1"
/db_xref="GI:29137799"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=11
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LYQTIRQPGAQSSEQTTLPSGLQIGTGVRPVATERLHSQGNLSQTNNSKDVAIKGQGF
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QQGQAAPVQVGQLNLTTFMNDTGLESIGENLYIETQSSGAPNESTPGLNGAGLLYQGY
VETSNVNVABELVNNIQVQRAYEINSKAVSTTDQMLQKLTQL"
complement (7146 . .7901)
/gene="flgf"
/locus_tag="t1742"
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                                                                                                                                                                                                                                                                                                                                               /translation="mdhaiytamgaasqtlnqqavtasnlanastpgfraqlnalrav pvdglslatrtutastpgardqqqdlytsreldvalqddmiyvqqaabgabgytrn gniqvgftqultiqdpbytggegpitipabgseitiaadgtisalnpgdppntvapvgr llvkaegnevqrsddclfrltaeaqaergavlaadpsirimsgylegsnvkpvbamtdmixaadpsirimsgylegsnvkpvbamtdmianarrfemqmkvitsvdenegranqllsms"
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SFGFDTVPRYLQGLFGNSRADMEASGGNSFNGKGGANASNTFSGTLTVTVDQVLANGN
LHVVGEKQIAINQGTEFIRFSGVVNPRTISGSNSVPSTQVADARIEYVGNGYINEAQN
                                                                                                                                                                                       /locus_tag="t1743"
/note="corresponds to STY1216 from Accession AL513382:
/salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="corresponds to
Salmonella typhi CT18"
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/gene="flgH"
/locus_tag="t1740"
complement(5597. .6295)
                                                          /trānslation="msfsqavsglnaaatnldvIgnniansatygfksgtasfadmfa
gskvglgvkvagitqdftdgtttntgrgldvaisqngffrlvdsngsvfysrngqfkl
                                                                                                                                                                                                                                                                      complement (7922. .9133)
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complement(7146. .7901)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative flagellar basal-body rod
/protein_id="AAO69366.1"
/db_xref="GI:29137805"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="flagellar basal-body rod protein FlgG"
/protein_id="AAO69365.1"
/db_xref="GI:29137804"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="distal rod protein; corresponds to STY1218 Accession AL513382: Salmonella typhi CT18"
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                                                                                                               (codon start=1
/transT_table=11
product="flagellar hook protein
protein_id="AAO69367.1"
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/protein_id="AAO69364.1"
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/transl_table=11
                                                                                               db_xref="GI:29137806"
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  97.9%;
98.7%;
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  Score 446.4; DB 1;
Pred. No. 1.5e-117;
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                    Length 301983
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                                                                                                                                                                                                                                                2 (bases 1 to 1048)
Sukupplvi,S.S.
Direct Submission
Submitted (14-JUL-1997) Sukupolvi S.S., Medical Biochemistry,
University of Turku, Kiinanmyllynkatu, 20520, FINLAND
                                                                                                                                                                                                                                                                                                                                                                                                                          Normark, S.J. and Rhen, M. Expression of thin aggregative fimbriae Salmonella typhimurium SR-11 with mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       agfA gene; agfB gene.
Salmonella typhimurium
Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Salmonella typhimurium
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                                                                                                                                                                                                                .1048
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agfB and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gordon, J.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agfA genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                            promotes interaction of small intestinal epithe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bian, Z.,
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Pfeifer,J.D.,

epithelial

BCT

26-JAN-1998

360

36951

37011 300 37131 180

37071 240 120

37191

420

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Local Similarity
                                                       Unclassified.

1 (bases 1 to 361)

Doran,J.L., Kay,W.W., Collinson,S.Karen. and Clout Methods and compositions comprising the agfA gene
                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTTTTGGCAACAACGCCACGGCTAACCAGTATTA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATĀĀĊĠĊĊĠĊĠĊŦĠĠŦŦĀĀŦĊĀĠĀĊĊĠĊĀŦĊŦĠĀŦŦĊĊĀĠĊĠŦĀĀŦĠĠŦĠĊĠŦĊĀĠĠŦŦ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
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                            US 5635617-A 56 03-JUN-1997;
                                                                                                                                                                                                                                                                              56 from patent
                                                                                                                                                                                                                                        GI:2469621
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593. .>1048
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                                                                                 Collinson, S. Karen. and Clouthier, S.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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US 5635617.
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Pred. No. 4.9e-116;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                               linear
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                                                                for detection of
                                                                                                                                                                                                                                                                                        PAT 07-OCT-1997
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AUTHORS
TITLE
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ORGANISM
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CSP515700
LOCUS
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ACCESSION
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source
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les 333; Conserv
                                                                                                                                                                                                                                                                                                                       Direct Submission
Direct Submission
Submitted (11-NOV-2002) Romling U.
Center, Karolinska Institute, Box
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301
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                                                                                                                                                                                                                                                                                                                                                                                                                                 20gaj,X., Bokranz,W., Nimtz,M. and Romling,U. Production of Cellulose and Curli Fimbriae by Members of the Fami. Enterobacteriaceae Isolated from the Human Gastrointestinal Tract Infect. Immun. 72 (7), 4151-4158 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 GACTCAACGITGAGCATTIATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Citrobacter sp. Fec2
Citrobacter sp. Fec2
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                              Romling, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Citrobacter sp. Fec2
AJ515700
AJ515700.1 GI:31790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           csgA gene; csgB gene; csgD gene; curlin-csgA protein; component of curlin monomers; regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae; Citrobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACGCCGCGCTGGTTAATCAGACCGCATCTGATTC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCATCGACCAGTGGAAGGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCCAĞĞĞTĞCĞĞATAATAĞTACTATTĞAACTĞACTCAĞAATĞĞTTTCAĞAAATAATĞCÇ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:31790491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Pred. No. 1.2e-84;
D; Mismatches 2
                                                                                                                                 .862)
                                                                                        .862)
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                                           for
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                                      transcription
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                                   of the
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                                 csgBA
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JOURNAL TITLE

Salmonell Patent: U

KEYWORDS SOURCE ORGANISM

Unknown Unknown DEFINITION ACCESSION VERSION

Sequence I44908

I44908

I44908.1

RESULT I44908 LOCUS

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                               GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                               AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                                  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
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GGTTTTGGCAACAACGCCACCGCTAACCAGTACTAA 2571
                                                                                                  CATAACGCCGCACTGGTGAACCAGACTGCGTCCGATTCCAGCGTTCTGGTGCATCAGGTT
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                                                                                                                                                                                                                                                                                                                                                    GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
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/transI_table=11
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/protein_id="CAD56672.1"
/db_xref="G1:31790494"
/db_xref="G1:31790494"
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DQWNGKNSDITVSQYGGHNAALVNQTASDSSVLVHQVGFGNNATANQY"
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2119. .2571
/gene="csgA"
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SISQSNYGNTAMIIQKGSGNKANITQYGTQKTAVVVQRQSQMAIRVIQR"
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/transI_table=11
/product="nucleation component/product="nucleation component/product="CAD56671.1"
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RSLDDISSSCIVLVDMMEADKKLIHYWQDNLSRKNNNLKTLLLLNTPDDYPYRDIENWP
HINGVFYVADDEERVVNGLQGILRGECYFSQKLASYLITHSGNYRYNSSESALLTHRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /genes"cagB"
1623. .2078
/gene="cagB"
/function="nucleator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="CAD56671.:
/db_xref="GI:31790493"
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component of curlin monomers; regulatory protein.
Citrobacter freundii
Citrobacter freundii
Bacteria; Proteobacteria; Gammaproteobacteria; En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (12-NOV-2002) Romling U., Mic
Center, Karolinska Institute, Box 280,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zogaj,X., Bokranz,W., Nimtz,M. and Romling,U.
Production of Cellulose and Curll Fimbriae by Members of the Family
Enterobacteriacese Isolated from the Human Gastrointestinal Tract
Infect. Immun. 72 (7), 4151-4158 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Citrobacter freundii csgB gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="csgD"
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HINGVFYAATEDQRVVSGLOGVLRGECYFSQKLASYLITHSGNYKYNSTESALLTHE
KBILNKLRIGASNIEIARSLFISENTVKTHLYNLFKKIAVKNRTQAVSWANDNLRR"
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                  /translation="MKLLKVAAFAAIVVSGSALAGVVPQWGGNHHGGGSNYGPDSSLS
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2123. .2572
                                                                                                                                                                                                                                                                                     ASIKQGSYGNTAVIIQKGSGNKANITQYGTQKTAVVVQRQSQMAIRVTQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /isolation_source="faeces"
/specific_host="Homo_sapiens"
/db_xref="taxon:546"
                                                                                                                                                                                               gene="csgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="csgB"
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                                                                                                                                                                            function="curli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    function="nucleator"
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80, S-17177 Stockholm, SWEDEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                 Submitted (11-AUG-1995) M. Hammar, Karolinska Institutet, Microbiology and Tumorbiology Center, Box 280, S-171 77 Stockholm, SWEDEN
                                                                                                                                                                                                                                                                                                                                                     Hammar,M., Arnqvist,A., Bian,Z., Olsen,A. and Normark,S. Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   csgA gene; csgB gene; csgD gene; csgE
orfC gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                       Hammar, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X90754.1 GI:1147558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCAACGGTGCGTTGGTTAATCAGACAGCCTCTGACTCCAATGTGCTGATTCAGCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCACTATCGATCAGTGGAATGCAAAAAATGCTGATATTAGCGTGACCCAGTTCGGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTGATGCGCGTAAATCAGATGTCACCATCACACACACGGGCGTGGCAACGGAGCTGTT
                                                                                                                                                                                                                                                                         (bases 1 to 4680)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGACTOTTCACTGAGTATOTACCAATATGGGTCAAACAACTCTGCAAATGCTCTGCAA 2296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTGTTGTTCCGCAATGGGGCGGC-
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                                                                                                                                                                                                                                                                                                                             Microbiol. 18 (4),
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                                                                                                                                                                                                                                        Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 csgG, csgF, csgE,
           organism="Escherichia coli"
                                                                                   /organism="Escherichia coli"
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/strain="K12"
                                                                                                                                                           Location/Qualifiers
                                                  /map="23.15 minutes"
                                                                  db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.6%;
75.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     teria; Gammaproteobacteria; Enterobacteriales; Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 262.8; DB 1;
Pred. No. 1.2e-64;
0; Mismatches 107;
                                                                                                                                                                                                                                                                                                                             661-670 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4680 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cagD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----AATCATCATGGTGGTGGCAGTAATTATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p DNA
csgB, csgA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
and orfC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BCT 07-JUL-2002
genes.
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misc_feature
                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                         /gene="csgD"
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                                                                                                                                                                                                                                        'gene="csgD"
                                                                                                                                                                                                                                                                                                                                                                                                                       production"
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                                                                                                                                                                                                                                                                                                                                                            'db_xref="SWISS-PROT:P52105"
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/db_xref="GI:1147561"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               production'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="assembly /transport component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /insertion_seq="IS2 (partial)"
complement(133..966)
/gene="csqg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
|transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            production"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (133. .966)
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3141. .4680
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:562"
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                                                                                                                                                                                                                                                     .2478)
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ORIGIN
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Best Local Similarity 72.6
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                                                                                                                                                                                                                                                                          CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                              GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGAAACTTTTAAAAAGTAGCAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCTCTGGCA 3788
                                                                                     GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                                                                                                                                            CCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAA
                                                                                                                                                                                                                                                                                                                                                     GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAGTCGTAGTTTCTGGCAGTGCTCTGGCT 60
                                                                                                                                                                                        AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
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3729. .4184
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3140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="GOA:P28307"
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/transI_table=11
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                                                                                                Direct Submission

Direct Submission

AL Submitted (11-0CT-1998) Laboratory of Genetics, University of Submitted (11-0CT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@amber:gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4089
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Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, N. Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
The complete genome sequence of Escherichia coli K-12
Science 277 (5331), 1453-1474 (1997)
Genome Project's World Wide Web site Genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications
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Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/codon_start=1
/product="orf, hypothetical protein"
/product="orf, hyp
                                                                                                                                                                                                                                                      /note="No predicted promoter"
/bound_moiety="DeoR predicted
1337. .1365
                                                                                                                                                                                                                                                                                                                                                                                                                 /note="central position to predicted promoter: -104"
/bound_moiety="DeoR predicted site"
1253, .1280
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                                                                                                               gene="b1030"
                                                                                                                                               note="factor Sigma70; predicted +1
494 .1745
                                                                                                                                                                                                                              gene="ycdU"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/trans[ table=11
/product="orf, hypothetical protein"
/protein_id="AAC74113.1"
/db_xref="01:1787266"
/translation="MEDGVQAMRDYLAGLDIASPEHQVLMNVTAKSEVAPSIIKENLS
LHLTHTVKWTESLDTFLNMPTPVAFLEISNKPYLGNMLNDFAGVDQQRVMHCRKAFSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'function="orf; Unknown"
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/note="0107; This 107 aa ORF is 27 pct identical (0 gaps)
to 58 residues of an approx. 1888 aa protein FAS2_CANAL
SW: P43098"
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389. .1375
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69. .392
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/db_xref="taxon:83333"
complement(<1. .48)
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/mol_type="genomic DNA"
/strain="K12"
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                           Conservative
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/translation="MRINFAQRFSGVSMDIIFYHPTEDTQWMTEALRKAIPQARVRAW KSGDNUSADYALVMHPPVEMLAGRDLKAVFALGAGVDSILSKLQAHPEKLNESVPLFR LEDTGMGEGWGEYAVSGVLHWFRRFDFTGCONSSHWQPLFEXFREDFTIGILGAGVL GSKVAQSLQTMFFPLKGWSRTRKSWFSGVQSERGERLSAFLSQCRVLINLENTPETVGINQCLLEKLPDGAYLLNLARGVHVVEDDLLAALDSGKVKGAMLDVENREPLPPESP LWQHPRVTTTPHVAAITRPAEAVEYISRTIAQLEKGERVCGQVDRARGY"
                                                                                                    /note="factor Sigma70;
3396. .3423
                                                                                                                                                               /gene="ycdW"
/note="factor Sigma70;
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/transT_table=11
/product="putative dehydrogenase"
/protein_id="AAC74117.1"
/db_xref="GI:1787270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SW: P45637"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="putative enzyme; Not classified" /note="0325; This 325 aa ORF is 32 pct identical (2 gaps) to 177 residues of an approx. 312 aa protein YPRA_CORGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="symonym: b1033"
2393. .3370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MCNIRKKSPYFRTSSSLNMAVRGGLTRFARPAGSPLTAFTVCPT
GCRQLSTPGRGFSSPRCVQYTKKKPVLSYELFFKYGGEGGIDSLRSPCGQPAHCVHGL
SNWLSPVVEPRSGLLIPPVCAIYEKKARTFVRALL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ycdW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="factor Sigma70; predicted +1 start at 1097049"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="ycdw"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="factor Sigma70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonym: b1032"
complement(2111, .2198)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="serX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="factor Sigma70; predicted +1 start at 1096980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="anticodon: GGA; CG Site No. 17878"
(function="RNA; tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="tRNA-Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="serX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="putative structure; Not classified"
/note="0137; This 137 aa ORF is 27 pct identical (1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="GI:1787269"
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!513. .1926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Translation="MGGGTRCVQYTKKKPVLSYELFFKYGGEGGIDSLRSPCGQPAHCUGLSNWLSPVVDPRSGLLIPPVCAIHEKKARTFVRALL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="ycdV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="orf, hypothetical
protein_id="AAC74115.1"
db_xref="GI:1787268"
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/function="orf; Unknown"
/note="o83; This 83 aa ORF is 25 pct identical (7 gaps)
to81 residues of an approx. 616 aa protein ALBU_RABIT SW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=]
/transl_table=
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product="orf, h
                               56.1%;
72.6%;
         0,
Score 256; DB 1;
Pred. No. 1.2e-62;
0; Mismatches 125;
                                                                                                                                                          predicted +1 start at 1097992"
                                                                                                                   predicted
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T SW:
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                                                        AUTHORS
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Complete and shotgun sequencing; csgG; csgF; cs csgA; ycdE; cls; nov; mdoG.
Escherichia coli K12
Escherichia coli K12
Bacteria; Proteobacteria; Gammaproteobacteria;
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Direct Submission
Submitted (29-JUL-1996) Hirotada Mori,
and Technology, Res. & Edu. Center for
                                                                                                                                                                             Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoco, K., Irada, T., Isono, K., Isono, S., Itoh, T., Kanai, K., Kashimoto, K., Kim, S., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yamamoto, Y., and Yano, M.
                                                                                                                                                                                                                                                                                                                                                                                                             Oshima,T., Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Ikemoto,K., Inada,T., Itoh,T., Kajihara,M., Kanai,K., Kashimoto,K., Kimura,S., Kitagawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Moti,H., Motomura,K., Nakamura,Y., Nashimoto,H., Nishio,Y., Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamamoto,Y., Yano,M. and Horiuchi,T. Wada,C., Yamamoto,Y., Yano,M. and Horiuchi,T. A 718.4b DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map DNA Res. 3 (3), 137-155 (1996)
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Escherichia coli Kl2 genomic
D90741 AB001340
D90741 1
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  NARA Institute Genetic Info.;
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Collaboration Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Headed by:
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Ikoma, 630-01, Japan
E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Information operator:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Address: National Institute E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name: Hirotada Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name: Takashi Horiuchi
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                           /translation="mypvdlhmhtvasthaystlsdylaqakqkgiklfaitdhgpdm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
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                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:83333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
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                                                                                                                                                                                                        product; ORF_ID:o231#2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product;
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Sgo
                                                                                 complement (5812.
                                                                                   /translation="MKRYLRWIVAAEFLFAAGNLHAVEVEVPGLLTDHTVSSIGHDFY
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s"
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Complement (4117. 4950)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mnefsilcrvlgslyyropodellvplftliregklaanwpleg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="unnamed protein product; ORF_ID:0231#4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Hypothetical protein H11543"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILNVSPRRLLNFLESRGMAPIAEFADL"
2906. .3460
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'transl_table=
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                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                   FEATURES
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ACCESSION
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KEYWORDS
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AX814811
LOCUS
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les 331; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
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Hansa Medical Research Aktiebolag (SE)
Location/Qualifiers
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                                                                                                                    Bjoerck,L., Olsen,A., Wikstroem,M. and Herwald,H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
                                                                                              Patent:
                                                                                                                                                                                                       Escherichia coli
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                         Sequence 15 from Patent AX814811
                                                                                                                 Peptides
                                                                                                                                                                                                                                                             Escherichia coli
                                                                                                                                                                                                                                                                                                                   AX814811.1
                                                                                                                                                                                    Interobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 8168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCÄAČĠGTĠĊTGCAĠŤŤGÁCĊAĠĀĊTĠĆĀŤĊŤAĂCŤĊĊTCĊĠŤĊĀACĠŤĠACŤĊĀĠĠŤŤ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTGÁTGCCCGTAÁCTCTGÁCTTGÁCTÁTTÁCCCAGCATGGCGGCGGTÁATGGTGCAGÁT 7952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAAATTCTGAGCTGAACATTTACCAGTÁCGGTGGCGGTAÁCTCTGCACTTGCTCTGCAA 7892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC 7832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGAAACTTTTAAAAAGTAGCAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCTCTGGCA 7772
                                                                      WO 03064446-A 15 07-AUG-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="csgB"
7217. .7672
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/note="ORF ID:0231#8
similar to SwissProt Accession Number P52106"
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/db_xref="GI:4062613"
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/transl_table=11
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Pred. No. 1.2e-62;
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On Jun 11, 1993 this sequence version replaced gi:145630. Original source text: Escherichia coli (sub_strain W3110, K-12) (library: Kohara) DNA.
                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

1 (bases 1 to 648)

Olsen, A., Arnqvist, A., Hammar, M., Sukupolvi, S. and Normark, S. The RpoS sigma factor relieves H-NS-mediated transcriptional repression of csgA, the subunit gene of fibronectin-binding curli in Escherichia coli Mol. Microbiol. 7 (4), 523-536 (1993)
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Escherichia coli
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ilarity 72.4%;
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/protein_id="CAE3541.1"
/protein_id="CAE3541.1"
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/translation="MKLLKVEAIAAIVFSGSALAGVVPQYGGGGNHGGGGNNSGPNSE
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LNIYQYGGGNSALALQTDARNSDLTITQHGGGNGADVQQGSDDSSIDLTQRGFGNSAT
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/mol type="unassigned DNA"
/db xref="taxon:562"
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GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA
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/db_xref="taxon:562"
/tissue_lib="Kohara"
83. .538
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LNIYQYGGGNSALALQTDARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSAT
LDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQVGFGNNATAHQY"
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/product="curlin subunit"
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/transl_table=11
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/mol_type="genomic DNA"
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Pred. No. 2.9e-62;
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The DNA encodes the Salmonella AgfA protein. The DNA and isolated proteins are used in genetic immunization and vaccine compositions, respectively, to elicit an immune response to Salmonella in animals (e. food producing animals) and humans. (Updated on 25-MAR-2003 to correct field.)

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Query Match
Best Local S
Matches 456
Salmonella; agfA; chromosomal gene replacement;
vaccine; immune response; immunogen; ds.
                                                            Salmonella enteritidis AgfA DNA sequence SEQ
                                                                                                                        26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an isolated agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the antibodies which can be used for assays. The nucleic acid sequence can be used to provide proteins and used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that from virtually all other microbial organisms. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 456 BP; 117 A; 112 C; 122 G; 105 T; 0 U; 0 Other;
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P-PSDB; AAW23570.

    ATGANACTTTTNAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT

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Pred. No. 8.2e-138;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ery Match
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The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA cC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended are: CC directing system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC directing recombination of a recombination of copy of that gene; (3) directing recombination of a recombination of a recombinant gene to back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid polymer incontaining a replacement segment of selection of a coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or containing an immune response in an animal. In a fimbrial presentation the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation containing and the protein the heterologous antigens are presented in high numbers (up to 50,000 copies/cell), the hybrid fimbrin protein possesses both the cimmunogenicity and adhesion properties relevant for an efficient live
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Escherichia coli.
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RESULT 5
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Best Local S
Matches 429
           White AP,
                                                                                                                              05-APR-2000;
                                            (UYVI-) UNIV VICTORIA
                                                                                         05-APR-1999;
                                                                                                                                                                           12-OCT-2000.
                                                                                                                                                                                                                                                                    Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                            WO200060102-A2
                                                                                                                                                                                                                                                           Escherichia
Synthetic.
                                                                                                                                                                                                                                                                                                                                                    Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                    vaccine; immune
                                                                                                                                                                                                                                                                                                                                                                                                   AgfA::PT3#4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC64625 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is giver the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
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    Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence SEQ ID NO:17.
                                                                                                                        2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                  99US-0127888P
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                                                                                                                                                                                                                                                                                                                           response; immunogen;
                                                                                                                                                                                                                                                                                                                   chromosomal gene replacement; fimbrin; epitope; esponse; immunogen; ds.
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    Collison
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94.1%;
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  XS,
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Pred. No. 9.2
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Kay
WW.
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1es 27;
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Sequence 456 BP; 120 A; 110 C; 122

G; 104 T; 0 U; 0 Other;

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Segment of the gene has been replaced by a segment of a foreign DNA CC segment of the gene has been replaced by a segment of a foreign DNA CC (1) use of thin aggregative fimbriae (SEP17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA, homologue fimbriae (SEP17/TAF) nucleation depended CC AgfA, CsgA and AgfA, homologue fimbria subunits, respectively; (2) CC homologues species; (3) directing recombinant gene into the chromosome of the brooking recombinant gene into the chromosome of the CC back into the chromosome of the homologue species, replacing the native CC comprising separating an amino acid polymer comprising a remainal, cc protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or plymer into the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties are resented in high numbers (up to immunogens, which may be important for directing an immune response constitute the inserted epicope, and hybrid fimbrine are usually strong against the inserted epicope, and hybrid fimbrine are easy and the carrier to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 136;
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DB; AAB36349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139pp; English
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밁 Ş DЪ Ś 뫄 δ В Ş Matches Query Match Best Local 421 361 361 301 301 241 241 181 181 121 121 61 425; 61 GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA aaraacécegegerggttaateagecegeatetgattecagegtattectagett AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT ĠĊĊĀĊĊĀŦĊĠĀĊĊĀĠŦĠĠĀĀĊĠĊŦĀĀĀĀĀĊŦĊĊĠĀŦĀŦŦĀĊŦĠŦĊĠĠĊĊĀĀŦĀĊĠĠĊĠĠŦ GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGGGGTTATGGTAACGGCGCCGAT AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCCGAT Similarity ccegacicaacericagearitateaeracegriccecraacecrecericecaa ĠĠĊĠŦĊĠŦŤĊĊĀĊĀĀŤĠĠĠĠĊĠĠĊĠĠĊĠĠŦĀĀŤĊĀŦĀĀĊĠĠĊĠĠĊĠĠĊĀĀŦĀĠŦŤĊĊĠĠĊ GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC argaaactrrraaaagregecagearregeageaaregragrretregeagregere ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT Conservative 89.1%; 93.2%; 0, Score 406.4; DB 3; Pred. No. 1.1e-121; 0; Mismatches 31; Indels Length 0; Gaps 420 420 360 180 300 240 180 240 120 120 60 60 0

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421

GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456

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CC segment of the gene has been replaced by a segment of a foreign DNA CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAR) nucleation depended CC assembly system of strains of Salmonella, Estherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA. CSGA and AgfA. homologue fimbrin subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for S00,000 copies/cell), the hybrid fimbria protein both the carrier imbrial subunit proteins are usually strong immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier imbrial subunit proteins are usually strong CC against the inserted epitope, and hybrid fimbriae are easy and CC inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
 Query Match
Best Local Similarity
Matches 424; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                       Sequence
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DB; AAB36352.
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   Conservative
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                                                                       B₽;
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                88.8%;
93.0%;
                                                                      A; 110 C; 120 G; 107 T; 0 U;
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   <u>,</u>
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Score 404.8; DB 3; Pred. No. 3.7e-121; 0; Mismatches 32;
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                               Length 456;
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\begin{array}{c} \mathsf{CC} \times \mathsf{SS} \times \mathsf{PPT} \\ \mathsf{TPT} \\ \mathsf{CC} \times \mathsf{SS} \\ \mathsf{CC} \\ \mathsf{CC} \end{array}
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AAC64622
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                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                  Salmonella enteritidis.
Escherichia coli.
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                                                                                                                        WPI; 2000-672631/65.
                                                                                                                                                                                                                                                                                                                      Synthetic.
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                                                                                                           P-PSDB; AAB36346.
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                                                                                                                                                                              (UYVI-) UNIV VICTORIA
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                                                                                                                                                  Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence SEQ ID NO:11.
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The present invention describes a recombinant agfA gene (I) where

Disclosure; Page 135; 139pp; English.

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RESULT 8
AAC64629
ID AAC6
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AC AAC6
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Best Local :
                      26-FEB-2001
                                                                    AAC64629;
                                                                                                       AAC64629 standard; DNA; 456
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            (first entry)
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93.0%;
                                                                                                       ВÞ
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Pred. No. 3.7e-121;
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CC The present invention describes a recombinant agfA gene (I) where a CC sequence of the gene has been replaced by a segment of a foreign DNA (CC (I) use of thin aggregative fimbriae (SEF17/TAP) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CA AgfA, CsgA and AgfA-homologue fimbriae (SEF17/TAP) nucleation depended CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively, (2) cc homologous species; (3) directing recombination of a recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising sequence of the homologous species, replacing the native comprising sequence of the homologous species, replacing the native comprising sequence or sequences of the homologous species in an animal. CC protein containing a replacement segment or segments of foreign amino CC protein containing a replacement segment or segments of foreign amino CC sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the cC useful for the expression of recombinant AgfA protein which is useful for CC system the heterologous antigens are presented in high numbers (u) is CC ploymer into the animal in conjunction with a carrier or diluent. (I) is CC eliciting an immune response in an animal. In a fimbrial presentation CC immunogenicity and adhesion properties relevant for an efficient live computed the terminance of the hybrid fimbria protein segments both the carrier fimbrial subunit proteins are usually strong component the inserted epitope, and hybrid fimbriae are easy and consequence is given in the examplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 456 BP; 114 A; 108 C; 123 G; 111 T; 0 U;
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P-PSDB; AAB36353.
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Escherichia coli
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121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
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Pred. No. 3.7e-121;
0; Mismatches 32;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAR) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunite, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of the chromosome of the back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, agfA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella; agfa; chromosomal gene replacement; vaccine; immune response; immunogen; ds.
                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Escherichia coli.
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DB; AAB36347.
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Matches 424
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                                                                                                               Salmonella; agfA;
vaccine; immune re
                                                                              Salmonella enteritidis.
                                                                                                                                                                AgfA::PT3#3
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                                                                                                                 chromosomal gene replacement; fimbrin;
esponse; immunogen; ds.
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93.0%;
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WO200060102-A2 Synthetic Escherichia

coli

12-OCT-2000

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CC Regment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA-homologue fimbriae comprising recombinant CC homologous species; (2) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E coli or coli and CC eliciting an immune response in an animal. For the expression of recombinant gene comprising separating an amino acid polymer comprising the native comprising separating an amino acid polymer comprising a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E coli or collinate the containing a replacement segment or segments of foreign amino CC eliciting an immune response in an animal for collinate and introducing the ccuseful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to companion), the hybrid fimbrian protein possesses both the vaccine, the carrier fimbrial subunit proteins are usually strong capainst the inserted epitope, and hybrid fimbriae are easy and colination of the present invention.
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Best Local
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                                                                                                                                                                                                                                                                       Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
vaccine; immune response; immunogen; ds.
                                                                                                                                                                                                                                                                                             AgfA::PT3#9
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                                                                                                                                                                                  Doran JL,
                                                                                                                                                                                                                                                                                           DNA sequence SEQ
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                                                                                                                                                                                                         99US-0127888P
                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                  Collison
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                                                                                                                                                                                  SK,
                                                                                                                                                                                 Kay
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 138; 139pp; English.

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CC Segment of the gene has been replaced by a segment of a foreign DNA CC (1) use of thin aggregative fimbriae (SEP17/TAF) nucleation described are: CC assembly system of strains of Salmonella, Escherichia coli and CC (1) use of thin aggregative fimbriae (SEP17/TAF) nucleation depended CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC directing recombination of a recombinant gene into the chromosome of the copy of that gene; and (4) eliciting an immune response in an animal, CC protein containing a replacement segment or segments of foreign amino CC Enterobacteriaceae host cell, from the host cell and introducing the cuseful for the expression of recombinant AgfA colymer into the animal in conjunction with a carrier or diluent. (1) is CC eliciting an immune response in an interface cuseful for the expression of recombinant AgfA protein which is useful for copies/cell), the hybrid fimbrin protein possesses both the CC vaccine, the carrier fimbrial subunit proteins are usually strong cimmunogenicity and adhesion properties relevant for an efficient live cimmunogenic, which may be important for direction as usually strong. proteins are usually r directing an immune

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RESULT 12
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Best Local S
Matches 422
 WPI; 2000-672631/65
                                                                                                                                                                                                                                                                              Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                    Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC64627 standard; DNA; 456
                                    White AP,
                                                                                                            05-APR-1999;
                                                                                                                                             05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                      12-OCT-2000
                                                                                                                                                                                                                       WO200060102-A2
                                                                                                                                                                                                                                                                                                                                    vaccine;
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                                                                       (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                  immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
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                                  Doran JL,
                                                                                                                                                                                                                                                                                                                                                    agfA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                            99US-0127888P
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                                                                                                                                                                                                                                                                                                                                                    chromosomal gene replacement; fimbrin; epitope
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92.5%;
                                    Collison SK,
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Pred. No. 4.1e-120;
0; Mismatches 34;
                                    Kay WW;
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Best Local :
                   421
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P-PSDB; AAB36351

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 137; 139pp; English.

CC Agfa, CsgA and Agfa-homologue finbrin subunits, respectively, (2)

CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene combinant gene into the chromosome of the homologous species, (3) directing recombination of a recombinant gene coback into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, and comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino caid sequence or sequences grown on a Salmonella, E. coli or conjumer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation conjunction with a carrier or diluent. (I) is cusful for the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response capainst the inserted epitope, and hybrid fimbriae are easy and conversed to purify in large amount. The present sequence is given in the exemplification of the present invention The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Escheriaceae for the production of fimbriae comprising recombinant

Sequence 456 BP; 112 A; 113 C; 125 G; 106 T; 0 U; 0 Other;

Length 456;

Matches 422; 361 301 301 241 241 181 121 421 361 181 121 61 61 μ. μ AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC 120 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAGTGGTAGTTTCTGGCAGTGCTCTGGCT ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGG GCACATGCAGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT GTAGGCCAGGGTGCGGATAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC Conservative 88.1%; ,. Score 401.6; DB 3; Pred. No. 4.1e-120; 0; Mismatches 34; 456 Indels 0 Gaps 420 360 300 120 420 240 180 60

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ARCSULT 13
AAC64631
ID AAC64
XX AAC64
XX AAC64
XX Salmo
X
                                                                                                                                                                                                                                                                               CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
CC directing recombination of a recombinant gene into the chromosome of the chromosome of the chromosome of the corp.
CC back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, cc copy of that gene; and (4) eliciting an immune response in an animal, cc comprising separating an amino acid polymer comprising a recombinant AgfA acid sequence or sequences grown on a Salmonella, E. coli or polymer into the animal in conjunction with a carrier or diluent. (I) is cc polymer into the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong capainst the inserted epitope, and hybrid fimbriae are easy and consensive to purify in large amount. The present sequence is given in the exemplification of the present invention.
                                                                                           Query Match
Best Local Similarity
Matches 420; Conserv
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 138; 139pp; English.
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Escherichia coli.
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                                                                                                                                                                                                                                                                        exemplification of the present invention
          ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                                                                                                                                                                                                                456
                                                                                                                                                                                                    BP; 113 A; 110 C; 124 G; 109 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence SEQ
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                                                                                                                          87.4%;
92.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogen;
                                                                                 Score 398.4; DB 3;
Pred. No. 4.5e~119;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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                                                                                                                                           Length
                                                                                 Indels
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                                                                       Gaps
                60
                                                                          0
RESULT 14
AAQ73066
ID AAQ73
AC AAQ73
AC AAQ73
AC 27-AW
DT 25-MA
DT 25-MA
DT 25-MA
DT 25-MA
DT 26-JU

XX Salmo
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26-APR-1993;
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25-MAR-2003
26-JUN-1995
                            26-APR-1994;
                                                         10-NOV-1994
                                                                                   WO9425598-A2
                                                                                                                                          misc_feature
                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                          Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                                                            Salmonella; AgfA; vaccine; genetic immunization; ds
                                                                                                                                                                                                                                                                                                                                                                                                                   AgfA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ73066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ73066 standard; DNA; 361 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ĠĠĊĠŦĊĠŦŤĊĊŔĊŔŔŦĠĠĠĠĠĠĠĠĠĠĠĠĠĠŦŔŔŦĊŔŦŔŔĊĠĠĊĠĠĊŔŔŢŔĠŦŤĊĊĠĠĊ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
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93US-00054452
                         94WO-IB000207.
                                                                                                                                                                       /*tag= e
                                                                                                                                                                                                                                                                         /note=
37. .60
                                                                                                                                         complement (292.
                                                                                                                                                  /note= "TAF6 primer (pair
                                                                                                                                                                                                                                52. .69
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                    'note= "TAF3
                                                                                                                                                                                                                                       /*tag= d
/note= "TAF5 primer (pair with
                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                       . 60
                                                                                                       "TAF4 primer (pair with TAF3)
                                                                                                                                                                                                                                                                                  a
"AgfA"
                                                                                                                                                                                  primer (
03. .129)
                                                                                                                                         .402)
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                                                                                                                                                                                             with
                                                                                                                                                   with TAF5)
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360

240 240 180

120

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RESULT 15
AAT74141
ID AAT74
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Best Local Similarity
Matches 333; Conserv
                                                        primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (KING/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The DNA encodes the Salmonella enteritis27655-3b TnphoA mutant strain agfA gene cloned into pUC19. The DNA and isolated proteins are used in genetic immunization and vaccine compositions, respectively, to elicit an immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Хау
                                                                                                                                                                                                                           Salmonella enteritidis.
                                                                                                                                                                                                                                                                           Enteropathogenic bacteria;
                                                                                                                                                                                                                                                                                                                              Salmonella
                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
30-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT74141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT74141 standard; DNA; 361 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 361 BP; 94 A; 93 C; 94 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 7A; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-358275/44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTTGCGCTTGCTCTGCAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR62761.
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                                                                                                                                                                                                                                                                                                                           enteritidis 27655-3b TnphoA mutant agfA gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                   (revised)
/label= agfA_gene_fragment
16. .60
/*tag= b
/label= Primer_TAF5
                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.8%;
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                                                                                                                                                                                                                                                                           enterobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 331.8; DB 2;
Pred. No. 1.9e-97;
0; Mismatches 2;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents an isolated agfA gene fragment derived from Salmonella enteritidis 27655-3b TnphoA mutant strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 361 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Col 107-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
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               AACGCCGCGCTGGTTAATCAGACCGCATCTGATTC 398
                                                                             ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAAT 363
                                                                                                        GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC
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/label= Primer_TAF4
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99.4%;
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completed: March 15,

2004, 17:51:39

Job time : 254.684 secs

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Maximum DB
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Maximum Match 100%
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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3 US-09-103-840A-2
3 US-09-103-840A-1
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US-09-252-991A-10818
US-09-252-991A-7641
US-09-252-991A-7641
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US-09-252-991A-12269
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# ALIGNMENTS

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ZIP: 98104-7092

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C2
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
FEATURE:
NAME/KEY:
LOCATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
NUMBER OF SEQUENCES: 61
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                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           TELEPHONE: (206) 622-49-00
TELEFAX: (206) 682-6031
TELEX: 3723036 SEEDANBERRY
TELEX: 3723036 TR NO. 58:
                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                         linear
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Query Match 100.0%; Score 456; DB 1; Best Local Similarity 100.0%; Pred. No. 3e-149; Matches 456; Conservative 0; Mismatches 0;

Length 456; Indels

0

Gaps

В Ś 뮍

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PATENT NO. 5532.

GENERAL INFORMATION:

APPLICANT: Doran, James L.

APPLICANT: Kay, William W.

APPLICANT: Collinson, Karen S.

APPLICANT: Clouthier, Sharon C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry

ADDRESSEE: Seed and Berry

CONTROL OF Columbia Center, 701 Fifth Avenue
                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT IMPORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 920043.403C2
REFERENCE/DOCKET NUMBER: 920043.403C2
TELECOMOUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: 372336 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENUTH: 31, baco.
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US-08-233-788A-56
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GENERAL INFORMATION:
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STATE: Was...
COUNTRY: U.S.A.
7TP: 98104-7092
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: BC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,927
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/055,108
FILING DATE: 06-ANG-1977
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 30603/1581
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-120-927-1/c
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Patent No. 6262018
GENERAL INFORMATION:
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Best Local Similarity
Matches 333; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: P.O. Box 1051, Clinton Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kim, Jihyun Francis
APPLICANT: Beer, Steven V.
TITLE OF INVENTION: HYPERRENSITIVE RESPONSE ELICITOR FROM
TITLE OF INVENTION: ERWINIA AMYLOVORA AND ITS USE
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: P.O. Box
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
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밁 Ś 밁 Ş 멍 Ś В Ś B Ś

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TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
FEATURE: CDS
LOCATION: 1..357
                                                                                                                                                                             121 GATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGCGATGTA
                                                                                                                                                                                                 184 GATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCCGATGTA
                                                                                                                                                                                                                                                         124 GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC 183
AACGCCGCGCTGGTTAATCAGACCGCATCTGATTC 398
                                                                         ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCGATACGGCGGTAAT 363
                                                            ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACT
                                                                                                                 ĠĠĊĊĀĠĠĠſĠĠĠĠŔŦĸĀŦŔĠŦĀĊŦŔŦŦĠĀĀĊŦĠĀĊŦĊĀĠĀĀŦĠĠŦŦŦĊĀĠĀĨĀŦĸĀŦĠĊĊ
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                                                                                                                                                                                                                                       GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC
                                                                                                                                                                                                                                                                                                   GTCGTACCÁCÁGTGGGGGGGGGGGGGTÁÁTCÁTAÁCGGCGGCGGCÁÁTÁGTTCCGGGCCCG
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                                                                                                                                                                                                                                                                                                                                                                                    72.8%;
                                                                                                                                                                                                                                                                                                                                                                Score 331.8; DB 1
Pred. No. 6e-106;
0; Mismatches 2
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APPLICANT: Wei, Zhong-Min

APPLICANT: Schading, Richard L.

TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS

TITLE OF INVENTION: RESISTANCE

FILE REFERENCE: 21829/41 (EBC-003)

CURRENT APPLICATION NUMBER: US/09/431,614

CURRENT APPLICATION NUMBER: 60/107,243

EARLIER APPLICATION NUMBER: 60/107,243

EARLIER APPLICATION NUMBER: 60/107,243

EARLIER FILING DATE: 1998-11-05

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PSECONS: 18

SOFTWARE: PSECONS: 18

SOFTWARE: 1344

TYDER: NAM
                                                                                                   RESULT 5
US-09-125-619-3
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; ORGANISM: Erwinia amylovora
US-09-431-614-5
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Sequence 3, Application US/09125619
Patent No. 6437116
GENERAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 7.5%;
Best Local Similarity 54.9%;
Matches 67; Conservative
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Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                 172 GC 173
                                                                                                                                                                                                                                                             149 AATTGAGCCATTTGCTCAATGGTTTGCCGATCGATGGGTTGTTGCCCCAACGCAGAATTT
                                                                                                                                                                                                                                                                                          112 AGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTT 171
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                                                                                                                                                                                  68
                                                                                                                                                                                                                                                                                                                                                                       52 GCTCTGGCTGGCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAAT 111
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ilarity 54.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    ;; Score 34; DB 4;; Pred. No. 0.12; 0; Mismatches
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APPLICANT: HARDHAM, JOHN M.

APPLICANT: BARBOUR, ALAN G.

APPLICANT: WEINSTOCK, GEORGE M.

TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA

FILE REFERENCE: UTSH:234

CURRENT APPLICATION UMBER: US/09/125,619

CURRENT FILING DATE: 1999-01-27

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 3

LENGTH: 7766

TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FA66473-3/c

Fatent No. 5486473

APPLICANT: FUKITA, HIROYUKI; YOSHIDA, IW.

MANABE, SADAO; FUKAI, KONOSUKE

TITLE OF INVENTION: A DNA CODING FOR A

NUMBER OF SEQUENCES: 16

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                           SEQ ID NO:3:
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.3%;
Best Local Similarity 47.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: modified_base
LOCATION: (127)
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/194,049
FILING DATE: 09-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 809,255
FILING DATE: 18-DEC-1991
APPLICATION NUMBER: 279,685
                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                  FILING DATE: 05-DEC-1988
APPLICATION NUMBER: 932,419
                                                                                                                                                                                                                                                          LENGTH: 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4612 TTTGCTGTGAAGAGTAATGATGGTGAGAAAG 4642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217
                                   238 GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT 297
                                                                             204 CAAGTCACTGACCGAAGCTAAGGTAACAGTAACTGCGCACATCTGCGAGGTTGGCTGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157 GCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAG 216
144 CATGTTCATCATTTTGACATCAATGGTTGGCTTGTCTTTTGACATTATGGTCACAACT
                                                                                                                                                                         6.8%;
Similarity 50.0%;
                                                                                                                    CAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTGCTGCTATTGGGAAGGGTAATGAGGATGGTGCGGATTTTGGTAAGGATGAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTACGGCTGCGGCTGCTGGTGAGCAGGATGGAGAGAGCCTGCAGAGGCTACAAATCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTACTGTCGGCCAATACGGCGGTAATAACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGAT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTG 276
                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                  19-NOV-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIROYUKI; YOSHIDA, IWAO; TAKAGI, MITSUO;
                                                                                                                                                      Score 31.2; DB 6; Length 1491; Pred. No. 1.2; 0; Mismatches 78; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33.4; DB 4; Length 7766; Pred. No. 0.51;
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298 AATGCCACCATCGACCAGTGGAACGCTAAAAACTCC 333

ATCGCCTTCCAGTACCAGATCAACCCATGTAGCTCC 49

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FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte template ID No. 6632636 31

PUBLICATION INFORMATION:
US-09-596-002-31
                                                                                                                                                                                                                                                                                                                                                                                                  US-09-596-002-31/c
Sequence 31, Application US/09596002
Patent No. 6632636
GENERAL INFORMATION:
                                                        Query Match 6.8%;
Best Local Similarity 53.7%;
Matches 88; Conservative
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SEQ ID NO 31
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                                                                                                                                                                                                                                                                                              PILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 492, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAFFILE REFERENCE: 2709.2005-001
CURRENT SPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                       ORGANISM: M. catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                          LENGTH: 65792
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 492
LENGTH: 2436
TYPE: DNA
ORGANISM: M. Catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-540-236-492/c
209 TTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1391 ACTGTCACCTCÁTGÁCCATCAACCAÁAACTTCGGTTGCÁTTGCC 1348
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                                                                                                                                                                                                                                                                                                                                                           Patterson, Chandra
Berg, Kim, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAÁCTTCATAÁTCCÁAAÁTÓCCTTCÁTAÁÁTÁÁAÓCCÁGTÁTCGCCCTCTGCÁCAAGAÁ 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGA---ACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTĀĆĊĠĀCĀTTCAŤCĀŤAAŤCTTAAAĠGĆAĀGTŤCĠĠGĆĀTĠĠŤĠĆTĠĀŤTGAĀTŤĀĆGC 1452
                                                                                                                                                                                                                                              PERL Program
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                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCES
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                                                   Score 31.2; DB Pred. No. 9.7; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 31.2; DB 4;
Pred. No. 1.6;
0; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                  OF MORAXELLA CATARRHALIS GENOME
                                                                       DB 4; Length 65792;
                                                 73;
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                                                   Indels
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ORGANISM:
FEATURE:
NAME/KEY:
LOCATION:
US-08-508-761B-1
                                             Query Match
Best Local Similarity 50.,
53; Conservative
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US-08-508-761B-1
                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (202) 638-
TELEFAX: (202) 393-53
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Дb
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                                                                                                                                                                                                     HYPOTHETICAL: NAME OF SENSE NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Applice Patent No. 602792
                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 2547 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                               NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 31-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/09652
FILING DATE: 29-JUL-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 400 Seventu CCITY: Washington D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: System for Protein Expression and TITLE OF INVENTION: Secretion Especially in Corynebacteria NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Joliff, Gwennael APPLICANT: Guyonvarch, Armel
                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
280 CAGAATGGTITCAGAAATAATGCCACCATCGACCAGTGGAAGGCTAAAAACTCCGATATT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Jacobson, Price, STREET: 400 Seventh St. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6699 ACTGTCACCTCATGACCATCAACCAAAACTTCGGTTGCATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6759 TGAĀCTTCATAĀTCĊĀAĀĀTGCCTTCĀTĀĀĀTĀĀĀĀĀĀĢČCĀGTĀTĊĞCCČTCTĞCĀCAAGAĀ 6700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6819 TTACCCACATTCATCATAATCTTAAAGGCAAGTTCGGGCATGGTGCTGATTGAATTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 AAAACTCCGATATTACTGTCGGCCAATACGGCGGGTAATAACGCC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 TTGA---ACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                     SOURCE:
                                                                                                                                     CDS
420..2390
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                                                                                                                                                                           Corynebacterium Melassecola
                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                393-5350
                                                                         58.9%;
                                                                                                                                                                                                                                                                                                                                                                638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FR 91/09870
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                                                    ; Score 30.8; DB; Pred. No. 2.2; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           P58525NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holman & Stern, PLLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
                                                                                DB 3;
                                                  37; Indels
                                                                                Length 2547;
                                                  0;
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6760
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KEY: misc_feature	INFORMATION: n	OTHER
: (1084830) . (1084830)	CON: (191995) (191995)	NAN
OTHER INFORMATION: n equals a, t, c, or s	INFORMATION: n equals a. t. c. or q	LOCAT
Ö	INFORMATION equals a, t, c, or g	OTHER
: misc feature : (855539)(855539)	Ó	NAM
<u> «</u>	NAME/KEY: misc feature	MAN
: (7794 FORMATI	ture (103998)	E CAM
<u>S</u> .		OCI
OTHER INFORMATION: n equats a, C, C, OT NAME/KEY: misc feature LOCATION: (741584) (741584)	equals a, t, c, or g	N O TO
, ~ , ,	misc feature (10076)	NAM
: (6824 FORMATI	ture . (98239)	 LOC
g	INF(	; LOCATI
<pre>EY: misc_feature ON: (674435)(674435)</pre>	INFORMATION: n equals a, t, c, or g  KEY: misc feature	OTHER NAME/
LOCATION: (657203) (657203) OTHER INFORMATION: n equals a. t. c. or o	NAME/KEY: misc feature LOCATION: (98120)	NAM
OTHER INFORMATION: n equals a, t, c, or on the control of the cont	ION: (84812)  TARDEMATION: Demails of Corrections	LOCATI
misc_feature (657081)(657081)	n equals a, t, c, or g	NAN
T	NAME/KEY: misc_fecture   COCATTON: (84808)   C	NAM
. Ä.	(84773)	
🔀	UCCATION: (2825)(28258) OTHER INFORMATION: n equals a, t, c, or g NAME/KEY. misc fearure	OTHER
CEY: m18C feature ION: (559241)(559241)	misc featu	NAM
Z	ature (28222)	NAM
OTHER INFORMATION: n equals a, t, c, or on the control of the cont	ORGANISM: Methanococcus jannaschii FEATURE:	; ORGANIS
·		LENGTH:
EY: misc feature ON: (312993)(312993)	RE: PatentIn version 3.1	SOFTWARE:
: (3128 FORMATI	LICATION NUMBER: US 60/024,428 ING DATE: 1996-08-22 ;	; PRIOR ; PRIOR
OTHER INFORMATION: n equals a, t, c, or on the control of the cont	APPLICATION NUMBER: US/08/916,421B FILING DATE: 1997-08-22	CURRENT
č	TITLE OF INVENTION: jannaschii	FILE :
ture (309398)	Complete Genome Sequence of the Methanogenic Archaeon, Methanococ	TITLE
Ä	INFO 6	; Patent
: (2342 FORMATI : misc	RESULT 10  US-08-916-421B-1  ; Sequence 1, Application US/08916421B  ;	RESULT 10 US-08-916-4 ; Sequence
LOCATION: (234187)(234187) OTHER:INFORMATION: n equals a, t, c, or ; NAME/KEY: misc_feature	936 GTTGTGCTCCCAATCGGTGGCGAGAGCTCC 965	Db
	ACTGTCGGCCAATACGGCGTAATAACGCC	8
NAME/KEY: misc feature	876 CAGAGTGGTTGGACCATTGAGACCAACATTGAGCAGTACTACGCCGATAAGAACGCCATT 935	ğ

OTHER INFORMATION: n equals a, LOCATION: (1119881) .. (1119881)

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OCATION: (1096846) . (1096846)

INFORMATION: n equals a,

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RESULT 11
US-09-103-840A-2/c
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
     FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                        APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (1602912)...(1602912)
DTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (1470091)...(1470091)
OTHER INFORMATION: n equals a,
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LOCATION: (1349473) ... (1349473)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1569020)...(1569020)
DTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (1313224)..(1313224)
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LOCATION: (1130881)..(1130881)
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RESULT 13 US-09-252-991A-10904

Sequence 10904, Application US/09252991A Patent No. 6551795

GENERAL INFORMATION:

APPLICANT:

Marc J. Rubenfield et al.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FRASER, CLAIR M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2
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LENGTH: 4403765
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OTHER INFORMATION: H37Rv
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APPLICANT: WHITE, Owen R.
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1357630 CCCGGACGTGCTG 1357618
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                                                                                                            1357690 AMACACCGCATGCCGTAACGAGCCCACGATAAGGTGTGGCCATGTCGTATCTGGTGGCGC
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10818
LENGTH: 1077
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1990-US-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10904
ENGTH: 1008
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US-09-252-991A-10865
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US-09-252-991A-10818/c
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US-09-252-991A-10904
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
PILE REFERENCE: 107196.136
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No. 3;
0; Mismatches 52;
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 10865
LENGTH: 1521
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                                                                                                                                                                                                                                  ; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-10865
                                                                                                                                                          Matches
                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                             6.5%;
Local Similarity 54.0%;
tes 61; Conservative
                                                                            230
                                                                                                                 41 TTTCTGGCAGTGCTCTGGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACG 100
                                  GCGGCGCAATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGT 153
GCGGGGAGGAGAGCCGGACCCGGTCGCGGCGTTGCGCTTGATCAAGCACGAT 282
                                                                                                                                                          0
                                                                                                                                                      Score 29.8; DB 4;
Pred. No. 3.7;
0; Mismatches 52;
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                                                                                                                                                                                           Length 1521;
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Search completed: March 16, 2004, 04:36:14 Job time: 70.6647 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                           Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

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14: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10E_PUB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10E_PUB.seq:*

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SUMMARIES
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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
c 1	34.2	7.5	616	12	US-10-424-599-88945	Sequence 88945,
ი 2	34	7.5	1344	ø	US-09-835-684-6	Sequence 6, A
ი ა	34	7.5	1344	9	US-09-880-371-6	Sequence 6, A
c 4	34	7.5	1344	ø	US-09-879-248-5	Sequence 5, Appli
ი წ	34	7.5	1344	14	US-10-010-390-6	Sequence 6, Appl
6	34	7.5	1344	15	US-10-441-736-5	Sequence 5, Appl
7	34	7.5	2886	9	US-09-801-368-131	
8	33.4	7.3	7766	12	US-10-222-566-3	Sequence 3,
9	33.4	7.3	7766	14	US-10-222-162-3	Sequence 3, Appl:
10	33.4	7.3	7766	14	US-10-143-024-3	Sequence 3, Appli
c 11	33.2	7.3	1662	14	US-10-156-761-3483	Sequence 3483, Ap
12	33.2	7.3	9025608	_	1 US-10-156-761-1	Sequence 1, App
13	32.8	7.2	1059	9	9 US-09-738-626-482	Sequence 482,
c 14	32.8	7.2	1113	ဖ	9 US-09-738-626-481	Sequence 481,
c 15	32.8	7.2	3309400	,		

				6.6	30.2	45
	US-10-282-		w	6. 6	•	44
Sequence 28546	2 US-10-425-114-28546		654	6.6	•	43
	US-10-424-	379 12		6.6	•	42
Sequence 364,	1 US-09-984-429-364		25	6.7	•	41
	2 US-10-425-114-31747	92 12	992	6.7	٠	40
Sequence 25231	2 US-10-282-122A-25231	392 12		6.7	•	39
641	4 US-10-080-170-646	16 14	75216	6.7		38
904:	US-09-815-242-9042		2301	6.7	30.6	37
484	US-09-815-242-4844	9		6.7	•	36
			1668	6.7	•	35
13	2 US-10-282-122A-13500			6.7	•	34
	US-10-			6.8	•	33
				6.8		32
				6.8	30.8	31
Sequence 3563	Sn		2751	6.8	31	30
	US-09			6.8	31	29
Sequence 26837	Sn			6.8		28
				6.8	٠	27
Sequence 9, Appli		03 13		6.9	31.6	26
	.4 US-10-132-134-1		52101	7.0		25
				7.0		24
	-SD			7.0		23
Sequence 24480,				7.0		22
æ	.2 US-10-282-122A-20335			7.0	٠	21
	US-09-815-242-6028	930 9		7.0		20
	.2 US-10-282-122A-27869		4830	7.1		19
	US-10	83 15		7.1		18
4	.4 US-10-333-631-4	972 1		7.1		17
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## ALIGNMENTS

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496	161	556	101	at cal	; OTHER INFORMATION: Clone ID: PAT_MRT3847_51326C.1 US-10-424-599-88945	FEATURE:	LOCATION: (1)(616) OTHER INFORMATION: unsure at all n locations	NAME/KEY:	CKGANISM: GIYCINE max FEATURE:	TYPE: DNA	LENGTH:	SEQ ID NO 88945	NUMBER OF SEQ ID NOS	CURRENT APPLICATION NUMBER: US/10/424,599	FILE REFERENCE: 38-21(53223)B	TITLE OF INVENTION: Plants and Uses	TITLE OF INVENTION: Soy Nucleic	APPLICANT:	APPLICANT:	APPLICANT:	GENERAL INFORMATION:	Sequence 88945, Application US/10424599	RESULT 1 US-10-424-599-88945/c	
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ATGA	4.50.50 4.50.50	CTGA	- GGG 	Score Pred. ; Mis	I MA		ם							0/42		Uses	Acid					4245		
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66CA	TGA.	TCCA	CATT	12; 78;												P1a	nd C							
CCGA	ACGA	TGTG	TATC	Length 616; Indels 0												int I	ther							
AGGA	CCAT	TGGA	AGTA	18												ord m								
ATGATGGTGATGATGAGGATGATGAGGCATGGGAGGTGGCACCGAAGGATAGTAACCGGG	ACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCG	GGCCCACAAGGGTAACGCCCCTGAATCCACGCCGGGTCCATGTGTGGATGATGATGATGTTG	GCGGCGGCAATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTA	16;												Thereof for Plant Improvement	Molecules and Other Molecules							
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; SOFTWARE: PatentIn Ver. 2.1; SEQ ID NO 6; LENGTH: 1344; TYPE: DNA; ORGANISM: Erwinia amylovora US-09-880-371-6
                                                                                                                                                                                                                                                                                                                   RESULT 3
US-09-880-371-6/c

Sequence 6, Application US/09880371

Parent No. US20020059658A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 1344
TYPE: DNA
ORGANISM: Erwinia amylovora
US-09-835-684-6
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          Query Match 7.5%;
Best Local Similarity 54.9%;
Matches 67; Conservative
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APPLICANT: Wei, Zhong-Min
APPLICANT: DEROCher, Jay
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Matches 67; Conservative
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                                                                                                                                                                  APPLICANT: DEROCHE, Jay

TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC

TITLE OF INVENTION: PLANTS

FILE REFERENCE: 21829/91

CURRENT APPLICATION NUMBER: US/09/880,371

CURRENT FILING DATE: 2001-06-13

PRIOR APPLICATION NUMBER: 60/211,585

PRIOR APPLICATION NUMBER: 60/211,585

NUMBER OF SEQ ID NOS: 16

SOFTWARE OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Qiu Deven
APPLICANT: Remick, Dean
TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE
TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR
FILE REFERENCE: 21829/71
CURRENT APPLICATION NUMBER: US/09/835,684
CURRENT FILING DATE: 2001-04-16
PRIOR APPLICATION NUMBER: 60/198,359
PRIOR APPLICATION NUMBER: 60/198,359
NUMBER OF SEQ ID NOS: 12
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09835684
Patent No. US20020019337A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wei, Zhong-Min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 AATTGAGCCATTTGCTCAATGGTTTGCCGATCGATGGGTTGTTGCCCCAACGCAGAATTT
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          0;
 Score 34; DB 9; Length 1344;
Pred: No. 0.81;
0; Mismatches 55; Indels
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0; Mismatches 55; Indels
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Best Local
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APPLICANT: Wei, Zhong-Min
APPLICANT: Leon, Ernesto
APPLICANT: Leon, Ernesto
APPLICANT: Oviedo, Agustin
TITLE OF INVENTION: METHODS OF INHIBITING DESICCATION OF CUTTINGS REMOVED
FILE REFERENCE: 21829/111
CURRENT APPLICATION INUBER: US/10/010,390
CURRENT APPLICATION INUBER: US/10/010,390
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: 60/248,169
PRIOR APPLICATION NUMBER: 60/248,169
PRIOR FILING DATE: 2000-11-13
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/10010390
Publication No. US20030104979A1
GENERAL INFORMATION:
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TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE
FILE REFERENCE: 21829/81
CURRENT PILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/212,211
PRIOR FILING DATE: 2000-06-16
INUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 5
IERCTIN 12.4
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Patent No. US20020062500A1
GENERAL INFORMATION:
ORGANISM: Erwinia amylovora
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ORGANISM: Erwinia amylovora
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Pred. No. 0.81;
0; Mismatches 55; Indels
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APPLICANT: Well Zhong-Min
APPLICANT: Well Zhong-Min
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
TITLE OF INVENTION: RESISTANCE
FILE REFERENCE: 21829/203 (EBC-003)
CURRENT APPLICATION NUMBER: US/10/441,736
CURRENT FILING DATE: 2003-05-20
PRIOR APPLICATION NUMBER: 60/107,243
PRIOR FILING DATE: 1998-11-05
PRIOR PILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
NUMBER OP SEQ ID NOS: 18
SOPTWARE: Patentin Ver. 2.1
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US-10-441-736-5/c
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                                                                                                                                                                                                                                   RESULT 7
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/ ORGANISM: Erwinia amylovora
US-10-441-736-5
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                                                   APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Keyin
                                                                                                                                                   Sequence 131, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.5%;
Best Local Similarity 54.9%;
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                       APPLICANT:
     APPLICANT
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Maxon, Mary
Milne, Todd
No. US20020128250Alman, Thea
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Pred. No. 0.81;
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Pred. No. 0.81;
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APPLICANT: NORRIS, STEVEN J.
APPLICANT: NORRIS, STEVEN J.
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: WEINSTOCK, GEORGE M.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234USD3
CURRENT APPLICATION NUMBER: US/10/222,566
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 7766
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Best Local Similarity
Marches 82; Conserva
                                                                                                                                                  ; OTHER INFORMATION: R = A OR US-10-222-566-3
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SEQ ID NO 131
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                                                                 Matches
                                                                                  Query Match
Best Local Similarity
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR PRIOR PRIOR DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
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                                                                                                                                                                                       NAME/KEY: modified_base LOCATION: (127)
                                                                                                                                                                                                                                                  ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                   FEATURE:
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157 GCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205 ACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGT 264
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Silva, Jeff
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llarity 47.4%;
Conservative
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                                                          Score 33.4; DB 12; Pred. No. 3.3; 0; Mismatches 111;
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Pred. No. 1.2;
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RESULT 10
US-10-143-024-3
            Sequence 3, Application US/10143024
Publication No. US20030092903A1
GENERAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Publication No. US20030060618A1
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CURRENT FILLING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BARBOUR, ALAN G.
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TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234USD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: R = A OR
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ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified_base
LOCATION: (127)
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Similarity 47.4%;
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Pred. No. 3.3;
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Query Match
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US-10-156-761-3483
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; LOCHIN: (127)
; OTHER INFORMATION: R = A OR US-10-143-024-3
                                                                                                                                                       PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILLING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILLING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3483
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                        APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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APPLICANT:
APPLICANT:
                               LENGTH: 1662
TYPE: DNA
ORGANISM: Streptomyces avermitilis
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1662)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: UTSH:234USD1
CURRENT APPLICATION NUMBER: US/10/143,024
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
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APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Borrelia burgdorferi FEATURE:
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HORIKAWA, HIROSHI
SHIBA, TADAYOSHI
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Pred. No. 3.3;
0; Mismatches 111;
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                                                      Sequence 482, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
PILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OMURA, SATOSHI APPLICANT: IKEDA, HARUO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptomyces avermitilis FEATURE:
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LOCATION: (4187715)
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                                                                                                                                                                                                                                                                                                             110 ATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGC 169
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HORIKAWA, HIROSHI
  MIZOGUCHI, HIROSHI
ANDO, SEIKO
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Pred. No. 1.3e+02;
0; Mismatches 68;
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 90/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PATENTIN VET: 3.0
SEQ ID NO 482
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Corynebacterium glutamicum
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                                         AACGCCGCGCTGGTTAATCAGACCGCATCTGA 395
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YOKOI, HARUHIKO
TATEISHI, NAOKO
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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03 US-09-738-626-481/c Sequence 481, Application US/09738626 Publication No. US20020197605A1 APPLICANT: APPLICANT: PRIOR FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7059 APPLICANT: APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSHI PPLICANT: OF INVENTION: NOVEL POLYNUCLEOTIDES REFERENCE: 249-125 INFORMATION HAYASHI, MIKIRO OCHIAI, KEIKO YOKOI, HARUHIKO IKEDA, MASATO OZAKI, AKIO SENOH, AKIHIRO TATEISHI, NAOKO SEIKO

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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
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TYPE: DNA
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US-09-738-626-481
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Best Local Similarity 47.2%;
Matches 100; Conservative
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LENGTH: 3309400
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Publication No. US20020197605A1
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
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TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
TORRENT APPLICATION NUMBER: US/09/738,626
TORRENT FILING DATE: 2000-12-18
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                                                             451760 GCCGGTGAAAAAGTAACCATCACCGTCTACACCTCTGAGCCTGAGGAAAAAGGTCGATGAG 451701
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APPLICATION NUMBER: JP 99/377484
FILING DATE: 1999-12-16
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304 ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAAT 363
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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A180	AL809250	9 0	505	7.3	. ω	
CF4:	CF437982	14	712	7.4	·w	
вJ3:	вJ336964	12	653	7.4	w	
BJ3	BJ335653	12	594	7.4	ω.	
AL1	CNS02GQP	29	1098	7.4	ω.	
CG1	CG178280	29	941	7.4	w	
BU7	U7651	L :	559	• .	·	
CD37	7442	14	55.8	• •	·	
AA74	746477	9	365	•	ω	
BZ4	469		811	•		
Þ	A71147		500	•	34	
. 885	B58198		234	•		
BG6	G67154	12	1036	7.5	34.2	
2	B.T1346		523	٠.	4	
AV05	AVOSAGIO	9 F	296	•	. A	
502	,		1	J.	,	П

# ALIGNMENTS

BJ618688 NIEB Mochii normalized Xenopus early gastrula library
Xenopus laevis cDNA clone XL186b22 5', mRNA sequence.

ON BJ618688 I GI:37256713
SEST.
Xenopus laevis (African clawed frog)
Xenopus laevis entry
Xe

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COMMENT
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AV430994/c
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Best Local
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Contact: Erika Asamizu
The First Laboratory for Plant
Kazusa DNA Research Institute
                                                               Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
                                                                                                                                                                                                                                                   AV430994 484 bp
AV430994 Porphyra yezoensis TU-1
PL027e10 r 5', mRNA sequence.
AV430994
                                                                                                                            Nikaido, I., Asamizu, E., Nakajima, M., Nakamura, Y.,
                                                                                                                                                                      Eukaryota; Rhodophyta; Bangiophyceae; Bangiales;
                                                                                                                                                                                             Porphyra yezoensis
Porphyra yezoensis
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                                                  10907854
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Location/Qualifiers
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/dev_stage="stage 10.5"
/clone_lib="NIBB Mochii normalized Xenopus early gastrula
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/mol_type="mRNA"
/db_xref="taxon:8355"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Other GSSs: CH230-390D21.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321 CGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGTTAA 380
                                                                                                                                                                                       Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 390 row: D column: 21
                                                                                                                                                                     Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Riggs, F., de Jong, P. and Fraser, C.M. Rat BAC End Sequences from Library CHORI-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68;
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Email: asami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCGAAAGCTGGTGTATCCAAAGTACTGGTGCAGGGTGCGGGAAAGGGCGTCGCCGGCA
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                                                /mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
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/clone="CH230-390D21"
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/mol_type="genomic DNA"
cell_type="Brain"
clone_lib="CHORI-230
                                   sex="Female"
                                                                                                                                                   Location/Qualifiers
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/clone="PL027e10 r"
/clone lib="Porphyra yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Porphyra
/mol_type="mRNA"
/strain="TU-1"
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Rodentia;
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Pred. No. 9.5;
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Segment 2"
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URL:http://www.kazusa.or.jp/en/plant/.
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Russell, D.,
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   Query Match 7.6%;
Best Local Similarity 46.5%;
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute Clemson University
100 Jordan Hall, Clemson, SC 29634, US
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GA Ea0014A14f Gossypium arboreum 7-10 dpa fiber library
arboreum cDNA clone GA Ea0014A14f, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
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Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T.,
Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
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                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
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h quality sequence stop: 696.
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                                                                                                                                                /db_xref="taxon:29729"
/clone="GA_Ea0014A14f"
/tissue_type="Fibers isolated from dpa"
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                                                                                                                                                                                                                                         /organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
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Score 34.6; DB 12;
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Pred. No. 51;
O; Mismatches
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Gossypium arboreum
Gossypium arboreum
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Gossypium.
rosids; eurosids_I; Malvales; Malvaceae; Malvoideae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
High quality sequence stop: 804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A. An integrated analysis of the genetics, development, and evolution of the cotton fiber
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GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
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                                      NACAATGACGGGAATGCGAATGGGAATGTTGGCAGCACAGACAATCAGAGCAACACCCAAT
                                                                           AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
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oreum cDNA clone GA__Ea0023M14f, mRNA sequence.
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                                                                                                                    Conservative
                                                                                                                                                                                                             /clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: BcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                         tissue_type="Fibers isolated from
                                                                                                                                                                                                                                                                                                             /db_xref="taxon:29729"
/clone="GA__Ea0023M14f"
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                                                                                                                                                                                                                                                                                                                                                                       strain="AKA"
                                                                                                                                                                                                                                                                                                                                                                                       organism="Gossypium arboreum"
|mol_type="mRNA"
                                                                                                                                                                                                                                                      .ab_host="E. coli"
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Pred. No. 81;
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                         13
                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T., Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Nitsuma, H., Oda, H., Owa, C., Sato, K., Shibata, Y., Shigamoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muranatsu, M., Okazaki, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tal: 81-298-36-9145 Fax: 81-298-36-9098
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GTÓGAGACCACAGTTTTTTCTAGGTCACCAAGGCTGGGTAAAGAAAAGAAGCATCAACTG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN Mouse ESTs
Unpublished (1999)
Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 bp mRNA linear EST 23-JUN-1999
AV058630 Mus musculus pancreas C57BL/6J adult Mus musculus cDNA
Clone 1810054H02, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV058630.1 GI:5158377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CÁGGÁĆGGGAAGAATGCCÁCTĆÁGÁGTAACAČTGÁCAACÁATGAÁÁATGTGGGTCÁGAAT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCACCATCGACAGTGGAACGCTAAAAACTCCCGATATTACTGTCGGCCAATACGGCGGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAÁATGCTGCACÁGAGCÁÁCÁCCÁÁCÁÁCAATGÁAÁACÁATAACAATGÁÁAÁTGCGGGT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACAATGTAAATGCAAATGAAGATGTTACTCAAAAGGAAAACAACGATTCAAGTTCAAAT 304
                                                                                               Conservative
                                                                                                                                                                            /tissue_type="pancreas"
/dev_stage="adult"
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/mol_type="mRNA"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                         clone="1810054H02"
                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                          sex="male"
                                                                                                                7.5%;
                                                                                       Score 34.2; DE
Pred. No. 63;
0; Mismatches
                                                                                                                               BB
                                                                                     63;
                                                                                                                           9
                                                                                  Indels
                                                                                0,
                                                                            Gaps
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REFERENCE
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ORGANISM
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VERSION
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BG671547
                                                                                                                       KEYWORDS
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ORGANISM
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AUTHORS
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VERSION
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BJ334624
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                              298 AAIGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACT 342
                                                                                                                                                                                                                                                                                                                       398 GATGAAGATGATGAATTGGAGAATAGATATTTGGAATCAATAGAAATGANGACAATAAT 457
                                                                                                                                                                                                                                                                                                                                                      238 GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT 297
        1 (bases 1 to 1036)
Xiao, H.S., Huang, Q.H.,
                                           Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                    DRNBUBO5 Rat DRG Library Rattus mRNA sequence.
EG671547
                                         Rattus
                                                                                                                       EST
                                                                                                                                 BG671547.1 GI:13893646
                                                                                                                                                                                                  BG671547
                                                                                                                                                                                                                                                                                                                                                                                                       60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 ACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGGGGTAATAACGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center For Genetic Resource Information Mational Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                AATAACAACAACAACAATAATAATAAAAATAANAATATTAAT 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium (bases 1 to 523)
Urushihara, H., Tanaka, Y., Kohara, Y., and Shin-i, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BJ334624 Dictyostelium discoideum cDNA linear EST 05-MAR-20 discoideum cDNA library, AF Dictyostelium discoideum cRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BJ334624.1 GI:19164754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGATGCCAAAATAGA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCTGGTTAATCAGA 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TĊĊĀĠĪĠAĀĢĊĀĊĀĀĀĀĀTGĀĀĠĀĀGĀĀĀĀĀĠĀTTĀĊĊCĀĀĀĀĠTTĠĠĀĀTĪĀĀĠĠTĀĠ 132
                                                                                                                                                                                                                                                                                                                                                                                                7.5%;
ilarity 57.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
length cDNA of Dictyostelium discoideum at the aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="Aggregation stage"
/clone_lib="Dictyostelium discoideum cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:44689"
/clone="dda47006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Dictyostelium discoideum"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="mat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                             Score 34.2; D
Pred. No. 82;
0; Mismatches
      Zhang, F.X.,
                                                                                                                                                                                          1036 bp
                                                                                                                                                                   mRNA linear EST 30-APR-
norvegicus cDNA clone DRNBUB05
   Bao, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
                                                                                                                                                                                                                                                                                                                                                                                             45;
Lu, Y.J., Guo, C.,
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 523;
                                                                                                                                                                                  EST 30-APR-2001
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                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                                        RESULT 9
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MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 CGTTGAGCATTTATCAGTACGGTTCCGCTTAACGCTTGCGCTTGCTCTGCAAAGCGAIGCCC 190
                                                                                                                                                                                                                                                                                                                                                                                      348
                                                                                                                                                                                                                                                                                                                                                                                                                           191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
1 (Dases 1 to 234)
Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T.,
Carninci,P., Hanagaki,T., Hayatsu,N., Hiraoka,T., Hiroz
Hodoyama,Y., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., K
                                                                                                                                                                                                                                BB581987 234 bp mRNA lines BB581987 RIKEN full-length enriched, adult male CDNA clone 9030005005 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang, L., Huang, W.J., Fu, G., Xu, S.H., Cheng, X.P., Yan, Q., Zhang, X., Chen, Z., Han, Z.G. and Zhang, X.
Identification of gene expression profile of dorsal root in the rat peripheral axotomy model of neuropathic pain proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome
This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
Pax: 86-21-64713446
                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: T3 POLYA=No.
                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                                           BB581987.1 GI:11478531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACKWARD: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR PRimers
FORWARD: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Zhang Xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGAAAGATACATGAGTGACAGTGTCCGTGATTGCAGACATTGCTGTATGATGCGTCCTGT 227
                                                                                                                                                                                                                                                                                                                                                                                                                              GTA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTAGGAGTCCTCGCTGGTAACGATGCCGAGAGTGCACATCGATATCGGTGGGCGGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACAATGGGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGCCCGGACTCAA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATCTGAAGTGGAAGAGGTGGCTCTTTCGAACTCTGACTTTGATCTGTCAAGGGACGCTT 347
                                                                                                                                                                                                                                                                                                                                                                                      GTA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                   Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat_DRG_Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="DRNBUB05"
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49.2%;
                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34.2; DB 12;
Pred. No. 1.1e+02;
0; Mismatches 93;
                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                        colon Mus musculus
                      Hirozane, T.,
                                                                                                                                                                                                                                                                              EST 30-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ganglion
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200

TCGTAGTTTCTGGCAGTGCTCGGCTGGCGTCCACAATGGGGCGGCGGCGGCGGTAATC 94

Matches

0;

Mismatches

0

Gaps

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JOURNAL COMMENT
                                                                                             ORIGIN
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                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover.A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA, Proc. Natl. Acad. Sci. U.S.A. 95 (2), S20-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
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RIKEN Mouse ESTS (Aizawa,K. et al. 2000)

Unpublished (2000)

Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              further details.
   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                       /Clone lib="RIKEN full-length enriched, adult male colon" note="Site 1: Sall; Site 2: BamHI; CDNA library was prepared and sequenced in Mouse Genome Encylopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue_type="colon"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="9030005005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db xref="taxon:10090"
Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yokohama, Kanagawa 230-0045, Japan
                                10;
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ACCESSION
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SOURCE
ORGANISM
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BZ469000/c
                                                                                                                                                DEFINITION
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AUTHORS
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CA711477/c
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                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                       214
                                                                                                                                                                                                                                                                                                 274
GSS.
Brassica oleracea
Brassica oleracea
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                  75 ATGGGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCGGAC 126
                                                                                                                                                                                                                                                                                                                           15
                                                                                                                BOOAO58TF BO 1.6_2_KB_tot genomic survey sequence.
BZ469000
                                                                                             BZ469000.1 GI:26764546
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                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E. I. DuPont de Nemours and Company
I Innovation Way, P.O. Box 6104, Newark,
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott V. Tingey@USA.dupont.com
                                                                                                                                                                                                                       TGTGGGAGGCGGTGGGCATGACCATGGCGGCGGCGGCGGCGGTGGCCNCCAC 163
                                                                                                                                                                                                                                                                               AGNTÉNTÉCÁGTCGCÁGCCNCCGGTCTCCCCGGCCGTNTCGAACCCGGCGGAGCTCCCCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tingey,S.V., Powell,W., Wolters,P., Miao,G., Caraher,N. and Hanafey,M.K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crop Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                          AGTGGCAGÇATTÇGÇAGÇAATÇGTAGTTTÇTGGÇAGTGCTCTGGÇTGGÇGTÇĞTTÇÇAÇA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA711477 500 bp mRNA linear EST 26-NOV-2002 wdk2c.pk014.o3 wdk2c Triticum aestivum cDNA clone wdk2c.pk014.o3 5'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGAACGCCGGGTGCTTTATAGCCTTGTTCAAAATATGGTAGCCCATTTACCACCACCTTT
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                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wdk2c.pkcl1.03"
/tissue_type="kernel"
/clone_Tib="wdk2c"
                                                                                                                                                                                                                                                                                                                                                                                                           /note="vector: pBluescript SK+; Site 1: EcoRI; Site 2: xhoI; Wheat (Triticum aestivum L.) developing kernel, days after anthesis."
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Pred. No. 91;
0; Mismatches
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                                                                                                                                     Brassica
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                                                                                                                                  DNA linear oleracea genomic
                                                                                                                                                     DNA
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                                                                                                                                                                                                                                                                                                                                                                          Length 500;
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                                                                                                                               GSS 13-DEC-2002 clone BOOAO58,
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AA746477/c
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 CCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAA 295
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D.,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares,
Bonaldo, Ph.D.
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 365)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 TGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCG 235
                                                                                                                                                                                                                                                                                                     AA746477

M62602.sl NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1251194 3'
similar to TR:000555 000555 NEURONAL CALCIUM CHANNEL ALPHA 1A
SUBUNIT ISOFORM A-1. ;contains element TAR1 repetitive element ;,
                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                               AA746477.1 GI:2786463
                                                                                                                                                                                                                                                                                       mRNA sequence.
AA746477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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1 (bases 1 to 811)

Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)

Other_GSSs: BOOAO58TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATPATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATACG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: TF
Class: sheared ends.
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DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Tel: 301-838-3523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Chris Town
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="BOOAO58"
/clone lib="BO 1.6 2 KB tot"
/clone lib="BO 1.6 2 KB tot"
/note="Vector: pHOS1; Site 1:
total DNA inserted into pHOS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Brassica ole:
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
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Pred. No. 1.1e+02;
0; Mismatches 95;
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              Soares,
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                                                                                                                                                                       Hominidae;
                                          Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 811;
          Ph.D.,
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                                        David Allman,
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          M. Fatima
                                                                                                                                                                                        Euteleostomi;
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CD374421/c
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                                                                                                                            Unpublished (2003)
Contact: Thomas B. Nutman
Laboratory of Parasitic Diseases
                                                                                                                                                                             Toward the characterization of the Wuchereria bancrofti microfilarial transcriptome with comparisons to those o malayi and Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                     CD374421

TNWbmfC2H3T3 Wuchereria bancrofti microfilaria cDNA (SAW95SjL Wuchereria bancrofti cDNA clone TNWbmfC2H3 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                            Wuchereria bancrofti
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/inage/inage.html
Insert Length: 661 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 292.
                                                                                                                                                                                                                                       Ndi, J
                                                                                                                                                                                                                                                                     Onchocercidae; Wuchereria.
                                                                                                                                                                                                                                                                                                                    Wuchereria bancrofti
                                                                                                                                                                                                                                                                                                                                                      CD374421.1 GI:31229939
                                                                                                  Building 4 Room 126,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGGGCGGCGGTAATCATAACGGCGGCGAATAGTTCCGGCCCG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCGGCCCTCGGAGGTACCCAGGCCCGCACGGCCGACGCTACTGGCCGG
                                               il: tnutman@niaid.nih.gov
| primer: pBluescript T3.
| Location/Qualifiers
                                                                                                                                                                                                                                  (bases 1 to 558)
,J.S., Ribeiro,J.M. and Nutman,T.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop: 292.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mxNA"
/db_xref="taxon:9606"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.4%;
56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type="mRNA"
                                                                                                  Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33.8; DB 9;
Pred. No. 91;
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                                                                                                  MD 20892-0425, USA
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                                                                                                                                                                                                  those of Brugia
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(SAW95SjL-WbMf)
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RESULT 14
BU765156/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76
                                                                                                                                                                                                                                                                                                                                                                                                     Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65;
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BU765156

Gm-c1080 Glycine max CDNA Clone SOYBEAN CLONE ID: Gm-c1080-4869 5' similar to SW-D100 ARATH Q00874

DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR ;, mRNA
                                                                                                                                                This clone is available through: ResGen, Invitrogen Corp. South Memorial Parkway Huntsville, AL 35801 For further in call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycine max (soybean)
Glycine max
                                                                                                                                                                                                                                                     Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BU765156.1
                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shoemaker
                                                                                                                       www.resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACATTTANCCAAGANCGGTGGCGGNANCTCTGCNCTTGCTCTGNAA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCGGACTCAACGTTG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGCGCGGTGGCGGTAACCNCGGTGGTGGCGGTAATAATAAGCGGCCCAAATTCTANGCT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 559)
                                                                                                  primer: -40RP from Gibco
                                                                         quality sequence stop: 448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome@smith.edu.
/organism="Glycine max"
                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="Wuchereria bancrofti microfilaria cDNA
(SAW95\(\overline{S}\)jL-WbMf)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="microfilaria"
/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:6293"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:23733884
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Pred. No. 1.1e+02;
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REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                    RESULT 15
CG178280
                                                                                                                                                                                                                                                     DEFINITION
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                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                            136 AGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGT 192
                                                                                                                                                                                                              PUJDF79TD ZM 0.6_1.0 KB Zea mays genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
                            1 (bases 1 to 941)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                           Zea таув
                                                                                                                                                                                                CG178280.1 GI:34069341
               Bennetzen, J
                                                                                                                                                              Zea mays
                                                                                                                                                                                                                                                                                                                                                             AAGATGCCCAAGTAGGGTTCGATCAGGGCAGCTTTGAAGGCCAAGAGTGCTGCCCGT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGGTCGCAGGCGACGCCATACCAGCTCCGGCAACAGTACAGTGCCCGACCATGTGTTG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGGCGGCGGTAATCATAACGGCGGCGCCAATAGTTCCGGCCCGGACTCAACGTTG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Roots of 8 mutant NTS382 seedlings" /dev_stage="8 days old" /lab_host="DH10B" /lab_host="Theor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-Tvector: pBluescript II SK+; Site_1: EcoRI; Site_2: /note-Tvector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from roots of 8 day old 'Bragg' supernodulating mutant NTS382 seedlings that were infected with Bradyhizobium japonicum, strain USBA 110, 72 hours prior to harvest. Dr. Gary Stacey generously donated the tissue. The roots were flash-frozen in liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="SOYBEAN CLONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.4%;
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_type="Roots of 8 day old 'Bragg' supernodulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.8; DB 13;
Pred. No. 1.1e+02;
0; Mismatches 52;
                                                                                                                                                                                                                                                                      941 bp
                                                                                                                                                                                                                                                    DNA linear GSS 21-AU genomic clone ZMMBTa0641N14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13;
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Best Local Similarity
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                                                                                                                                   236 TIGCAGTCTACACATCAGTGGTCGTATATGCCACAGTTCCTGCACCGGCCTTTCCGCCGC
 356 CTTCTTCTCGCCACCGCTCAACGGCGACGACTCTGGC 392
                                137 GCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGC 173
                                                                                                                                                                       17
                                                                                                                                                                                                          80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9712 Medical Center Drive, Rockville, Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2003)
Other_GSSs: PUJDF79TB
Contact: Cathy Whitelaw
                                                                                                    GGGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGCCCGGACTCAACGTTGA 136
                                                                                                                                                                   regeagearreecaecaareeraerreereecaecaecereereecereereecaecareereecaecar 76
                                                                     GGAGTACCCTCCGTCGCCACCACGACCGCCGGTCTTCGACTTGCCGGGACTGTACCCCGA
                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                             /clone="ZMMBTa0641N14"
/clone="Ibh="ZM_0.6_1.0 KB"
/clone="Vector: pCR4_TOPO; Site_1:
/note="Vector: pCR4_TOPO; Site_1:
COT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                   /organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                            51.0%;
                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                            Score 33.8; DB 29;
Pred. No. 1.4e+02;
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Search completed: March 16, Job time : 2240.91 secs 2004, 04:28:29

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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1: gb_ba:*
2: gb_htg:
3: gb_in:*
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10077.856 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

. 4.4.4. 2.6.4.4.0	C 40		c 28 c 29 c 31 c 32 33	00 0 022222 02222	c 200	Result No. 1 2 3 3
36.6 36.6 6	5.5.5	,	37.8 37.8	2 4 4 4 9	71231112222462	52. 51.
						% Query Match 100.0 99.3 99.3 98.9 98.9
9638 3005 5449 2393	237	209 4250 4230	168457 178934 193553 295500 298406 174732 191567	6578110	10325 10325	Length 2067 5103 22411 254050 301983
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AC113159 AC108229 AC119520 AC109520 AP003194	AE014841 BX537249 AC095863_06	AX655393 AL591911 AC063967 CBRG01B5	1142 2796 1241 0595 7588 3616	AE016786 AE008209 AE009405 AC116971 I66494 BX640594	00151 00151 00160 00151 00151	ID SEU43280 SETAJ2301 AE008749 AL627269 AE016840
	14841 37249 tinuat	55711	11425 R 27966 R 124196 05954 B 033514 C 33514 C 36702 H	16786 Pseudom 08209 Agrobac 09405 Agrobac 16971 Trypanc 40594 Sequence 40594 Psetrafi	000514 Salmonel 515700 Citrobac 015131 Shigella 015131 Shigella 000205 Escheric 000205 Escherich 016981 Shigella 016753 Escheric 016753 Escheric 005315 Escheric 005315 Escheric 515702 Enteroba 515702 Enteroba 131756 Escheric 015532 Shewanel	Description U43280 Salmonella AJ002301 Salmonell AE008749 Salmonell AL627269 Salmonell AE016840 Salmonell

## ALIGNMENTS

RESULT 1

SEU43280	
LOCUS	SEU43280 2067 bp DNA linear BCT 14-FEB-1996
DEFINITION	Salmonella enteritidis agfBAC operon: fimbrin-like protein
	precursor (agfB), thin aggregative fimbriae precursor (agfA), and
	AgfC (agfC) genes, complete cds.
ACCESSION	U43280
VERSION	U43280.1 GI:1184712
KEYWORDS	•
SOURCE	Salmonella enteritidis
ORGANISM	Salmonella enteritidis
	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
	Enterobacteriaceae; Salmonella.
REFERENCE	1 (bases 1 to 2067)
AUTHORS	Doran, J.L., Collinson, S.K., Burian, J., Sarlos, G., Todd, E.C.,

FEATURES

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Gaps

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815

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CDS gene TITLE JOURNAL

TITLE

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REFERENCE
AUTHORS
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(Collinson, S.K., Doran, J.L., Banser, P.A. and Kay, Direct Submission
Submitted (13-DEC-1995) S. Karen Collinson, Bion University of Victoria, P.O. Box
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Collinson, S.K., Clouthier, S.C., Doran, J.L., Banser, P.A.
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8104955
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J. Clin. Microbiol. 31 (9), 2263-2273 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriol. 178 (3),
                                          1352. 1645
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subunit of thin aggregative fimbriae"
1667. 1696
1710. 2036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="agfB"
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/protein id="AAC43598.1"
/therealstill 1184713"
                                                                                                                                                                                                                                                                                                                                                                                  /note="putative signal sequence of fimbrin-like protein"
                                                                                                                                                                                                                                                                                                                                 /gene="agfA"
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696. .752
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="agfB"
753. .1148
                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="agfB"
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96. .1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="between putA and pyrc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Salmonella enteritidis"
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Box 3055 Petch Bldg.,
                                                                        major fimbrial
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AUTHORS
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TITLE
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ORGANISM
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Best Local ;
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Romling, U.
                                                                 Romling, U., Bian, Z., Hammar, M., Sierralta, W.D. and Normark, S. Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and
                                                                                                                                                       Salmonella typhimurium
Salmonella typhimurium
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           936 AAAGTCGACCAGGCAGGGAATTATAACTTTGCGTATATTGAGCAAACGGGCAATGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301
                                            98117058
                                                                                                                                                                                                     csgA gene; csgB gene; csgG gene;
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                                                       Bacteriol.
           (bases 1 to 5103)
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56; Conservative
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                                                      180
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100.0%; Pr
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Pred. No. 3.8e-123;
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csgF,
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BCT 15-NOV-2000 csgA,

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Submitted (29-OCT-1997) Romling U.,
Karolinska Institute, MTC, Box 280,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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              Salmonella typhimurium LT2
Salmonella typhimurium LT2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Salmonella.
1 (bases 1 to 22411)
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AE008749.1 GI:16419641
                                                                                                                           Salmonella typhimurium
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99.6%;
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Pred. No. 3.4e-122;
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complement(1414.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one m13 subclone.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GIIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McClelland,M., Sanderson,K.E., Spieth,J., Clifton,S.W.,
Latreille,P., Courtney,L., Porwollik,S., Ali,J., Dante,M., Du,F.,
HOU,S., Layman,D., Leonard,S., Nguyen,C., Scott,K., Holmes,A.,
Grewal,N., Mulvaney,E., Ryan,E., Sun,H., Florea,L., Miller,W.,
Stoneking,T., Nhan,M., Waterston,R. and Wilson,R.K.
Complete genome sequence of Salmonella enterica serovar Typhimurium
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/protein id="AAL20057.1"
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GEAGGCKTWISAAKAAEALIHKDVERIIVTRPVLQADEDLGFLPGDIAEKEAPYFRPY
LTRLGENVTVIVAGDITQCDLPRGVRSGLSDALERFEEDEMVGIVHENKDDCVRSALC
                                                                                                                                                                                                                                                                                                                                                                                                           /notee "similar to E. coli PhoB-dependent, ATP-binding regulon component; may be helicase; induced by p starvation (AAC74105.1); Blastp hit to AAC74105.1 (354 abs), 92% identity in aa 71 - 354"
                                                                                                                                                                                                                                                                                  component"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="phoH"
/note="putative
454. .1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="synonym: 434. .439
                                                                                                                                                                                                                                                                                                 /product="PhoB-dependent ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="phoH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Salmonella typhimurium LT2"
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/db_xref="ATCC:700720"
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/gene="STM1129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LISVMCIIYTMMGGIBGVIWTDVIQGLLLSGSAILIFIVICLKVQGGIDEIFTVTQQA
DKFFPATQFHHSMTESTVPULMIGFLFANIQQFTASQDVVQRXIVTDSIBETKCTLLT
NAKLVAVIPVFFFAIGSALFVYYQQHPQLLPAGFNTGGILFVVTEMPVGIAGLI
AIFAAAQSIESSLANSISSCTENSIVQRLSHKKRTPEBRRMKIAKLVILVAGLISSAAS
VMLVMADESEIWDAFNSLIGLMGGPMTGLFMLGIFFKRANAGSAVLGIIISVITVLGA
RYATTLLNFFFYGVIGSLSVVLGGVIFAPLFAPAPPLTLDEKPEPKVTL"
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/gene="STM1127"
/note="putative RBS for STM1127; RegulonDB:STMS1H001399"
                                                                                                                    /gene="STM1130"
5599. .6759
                                                                                                                                                                                                                                                     /tränslation="MSLLARLEQS VHENGGLIVSCQPVPGSPMDKPEIVAAMAQAAAS
AGAVAAVRIEGIENLRTVRPHLSVPIIGIIKRDLTGSPVRITPYLOVDALAQAGADIGI
AFDAASFRSRPVDIIGSLITRIRLHGLLAMADCGSTVNEGISCHQKGIEFIGTTLGGYTGI
AFDAASFRSRPVDIIGSLITRIRLHGLLAMADCGSTVNEGISCHQKGIEFIGTTLGGYTGI
ITPVEPDLAMVTQLSHAGCRVIIAEGRYNTPALIAANAIEHGAWAVTVGSAITRIEHICQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to E. coli putative enzyme (AAC76255.1);
Blastp hit to AAC76255.1 (229 aa), 70% identity in aa 1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (4413. .5093)
/gene="STM1129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MITHSFGIVNYLVLFGYLLAMMLVGVYFSRRQKTADDYFRGGGR
VPGWAAGVSVFATTLSSITFMSIPAKAFTSDWTFIIGQYLAIAILPLVFYFYIPFFRK
LKVTSAYEYLEARFDVRCRLFASMSFWLFHIGRIAIITFLTVLALRPFIAIDPVILVL
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/note="putative RBS for STM1129; RegulonDB:STMS1H001401"
5599. .6759
                                                                                                                                                                                                                  complement (5094.
                                                                                                                                                                                                                                                                                                                                     /transT_table=11
/product="putative inner membrane protein"
/protein ide""AAL20060.1"
/db_xreff="GI:16419445"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative sodium/glucose cotransporter"
/protein_id="AAL20059.1"
/db_xref="GI:16419644"
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/gene="STM1128"
                                                                                              5599. .6759
/gene="STM1130"
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(AAC76702.1); Blastp hit to AAC76702.1 (571 aa),
identity in aa 7 - 478"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
/product="putative transcriptional regulator"
/protein id="AAL20058.1"
/db_xref="GI:16419643"
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                                    dentity in aa 40 -
                                                     note="similar to E. coli orf, hypothetical protein (AAC77266.1); Blastp hit to AAC77266.1 (404 aa), 41%
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="STM1127"
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Matches 454;
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GGAAATAAGGCCAATATTACCCAGTACGGTACGCAGAAAACAGCAGTTGTAGTGCAGAAA 420
                                                                                     GATGCCAGTATATCGCAAAAGCGCTTACGGTAATAGTGCAGCTATTATCCAGAAAAGGTTCT
                                                                                                                                                                                                                                                                                                                              CGCCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGAAGGAGGAAATAATCGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGACAAATTATGATCTGGCTCGTTCAGAATATAATTTTTGCGGTAAATGAATTAAGCAAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGAAAAACAAATTGTTATTTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACC 60
                                                       GATGCCAGTATATCGCAAAGCGCTTACGGTAATAGTGCGGCTATTATCCAGAAAGGTTCT 17631
                                                                                                                                                                           AAAGTCGACCAGGCAGGGAATTATAACTTTGCGTATATTGAGCAAACGGGCAATGCCAAC
                                                                                                                                                                                                             AAAGTCGACCAGGCAGGGAATTATAACTTTGCGTATATTGAGCAAACGGGCAATGCCAAC
                                                                                                                                                                                                                                                                                             CGCCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGAAGGAGGAAATAATCGGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGACAAATTATGATCTGGCTCGTTCAGAGTATAATTTTGCGGTAAATGAATTAAGCAAG
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6793. .6798
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AIDNNGVIYVGLGTAGTSWYKIDLKKQHKWALTCFSVAITTSGYATTLPDIPBPLKNGTG
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BHIFDKYFIDIAAAADESEKNKVIYNYFNKADYFFNKIVFIYNAKENTWKNAGEL
FGAGTAGSSSVMGVLLVGGGANPFQAKQNYTNGKFYKHBGINKKWRDEVGLINGH
QQEGLAGAFSGYSHGVLLVGGGANFPQAKQNYTNGKFYKHBGINKKWRDEVGLINGH
QQEGLAGAFSGYSHGVLLVGGGANFAGKFYNGKFYKHGGINKKWRDEDEVGLINGH
WQYMGKMKQPLGYGVSVSYGDEVFLIGGENAKGKPVSSVTSFTMRDGNLLIK"
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/gene="STM1132"
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ieklpngigfyvdasvksggvdgeqdkhlsdlvanaielgvsynykvtdnfvlqpgfi
fesgfdtsiykfylrgqynfdsgvymagryrydyarktanysddektnrfdtyigyvf
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/protein_id="AAL20061.1"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="similar to E. coli putative transport protein (AAC77235.1); Blastp hit to AAC77235.1 (425 aa), 57% identity in aa 25 - 418"
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/protein_id="AAL20062.1"
/db_xref="Gi:16419647"
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AAC77267.1); Blastp hit to
dentity in aa 4 - 239"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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JOURNAL
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AL627269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-OCT-2001) sequencing team, Sanger Hinxton, Cambridge CB10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Details of S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 254050)
Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkhill, Dugan, G., James, K.D., Thomson, N.R., Pickard, D., Walin, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Scbaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, J., Feltwell, T., Hanlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Ouall, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Complete genome sequence of a multiple drug resistant Salmonella Nature 413 (6858), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella enterica subsp. enterica serovar Typhi Salmonella enterica subsp. enterica serovar Typhi Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
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Salmonella enterica serovar Typhi
complete chromosome; segment 5/20.
AL627269 AL513382
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GCBNYNG TONDETWDGT CENERAL NAMED CLEVERDGTSSDL
ARTDTATDKOYLDIERVIGHESPHMWTGNRVTCRDWFQLSUKEGLTVFRDQEFSSDL
GCBNYNG TONDETWDGT CENERAL NAMED CONTROLLEY C
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         transl
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Orthologue of E.
to AMPN_ECOLI (869 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                              'codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:90370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="STY1078"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="synonym: pepN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="STY1078"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain="CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Salmonella enterica subsp. enterica serovar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                typhi sequencing at the Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                         table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted on behalf of the Salmonalla Centre, Wellcome Trust Genome Campus, 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                    coli pepN (AMPN_ECOLI); Fasta hit 94% identity in 869 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA linear BCT 04-J
(Salmonella typhi) strain
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) strain CT18,
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                                                                       Complement (4716 . .5825)
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Complement (4716 . .5825)
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(369 aa), 86% identity in 367 aa overlap"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               discrepency in position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Orthologue of
YCBW_ECOLI (192 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3238. .3297
/gene="STY1079"
                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="STY1080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="PS00912 Dihydroorotate dehydrogenase signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="PS00911 Dihydroorotate dehydrogenase signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Pfam match to entry PF01180 DHOdehase,
Dihydroorotate dehydrogenase, score 563.50, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="STY1080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="STY1079"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "gene="STY1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Orthologue of E. coli pyrD (PYRD_ECOLI); Fasta hit
to PYRD_ECOLI (336 aa), 95% identity in 336 aa overlap"
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLLGEENFOKGMOLYFERHDGSAATCDDFVQAMEDASNVDLSHFRRWYSQSGTPIVTV KDDYNPETEQYTLTISQRTPATADQAEKQPLHLPFAIELYNNEGNVLFLQKGGHPVNA LVLVVTQAEQTFTFDNVYFQPVPALLCEFSAPVKLEYKWSDQOLTFLMRHARNDFSRWD AAQSLLATYI KLNVARHQQGQLSLFVHVADAFRAVLLDEKIDPALAAEILTLFSANE AAQSLLATYI KLNVARHACQGQDLSLFVHVADAFRAVLLDEKIDPALAAEILTLFSANE ACLRFYTDFIAIAQVREALTRTLAAELADEFLAIYVANHLDEYRVDHGDIGKRTLRN ODGLVNDKWFLLQSTEBAENVLETVRSLLKHRSFSMSNPNRLRSLIGAFAAGSNPAAFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aqdgsgyqflvemltdlnsrnpqvasrlieplirlkryddkrqekmraaleqlkglen
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                                                                                                                                                    .5825)
                                                                                                                                                                                                                                                                                                                                                                                                                           of E. coli YCBW_ECOLT; Fasta hit to
a), 90% identity in 180 aa overlap. N
sition of translational start site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E-value
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codon\_start=1

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Query Match
Best Local
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                                                                                                                                                                      Similarity
                            ATGAAAAACAAATTGTTATTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACC 60
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
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/db_xref="GOA:Q8Z756"
/db_xref="SpTREMBI:Q8Z756"
/db_xref="SpTREMBI:Q8Z756"
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/db_xref="SpTREMBI:Q8Z756"
/db_xref="SpTREMBI:Q8Z756"
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/responsering="massipagragstering"
/responsering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagragstering="massipagrags
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/db_xref="GI:1650235"
/db_xref="GI:1650235"
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/db_xref="GOA:Q827S7"
/db_xref="GOA:Q827S7"
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/fTAROFPOMYRFTSSPHDGLHLTTAPDGSSALVRFTDETPQDAPTEVWGNHFTARVA
PTAINOWLSGFFSRDVQLCWVGPQLTRRVKRHNAVPLGFADGYPYLLTNEASLRDLQQ
RCPAGVQMEQPRENLVVSGVAAMEEDSWKVLRIGDVIFDVKRPCSRCIFTTVSPEKGO
KHPSGEPLATIQAFRTAQDNGDVDFQONLIARNSGVIRVGDEVEILATAPAKAYGATT
LDDSVTPEKHPDGSVTLDWQGQTFCGNNQQVLLEQLENQGIRIFYSCRAGICGCCRIR
LLEGEVSPLKKSAMGDDGTILSCSCVPKTALRLEN"
                                                                                                                                                                                                                                                                                                                                                                                                     /gene="STY1083"
8045. .9952
/gene="STY1083"
                                                                                                                                                                                                                                                                                           /note="Fasta hit to YBIT_ECOLI (530 aa), 32% identity in 526 aa overlap Fasta hit to YJJK_ECOLI (554 aa), 34% identity in 524 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Uncharacterized protein E-value 3.7e-231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Similar to Haemophilus influenzae hypothetical protein hi0116 H10116 SW:YCBY HAEIN (P44524; P43945) Bcores: E(): 0, 60.3% id in 710 aa Orthologue of E. coli YCBY ECOLI; Fasta hit to YCBY E(702 aa), 92% identity in 702 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(4737. .4955)
/gene="STY1081"
/note="Pfam match to entry PF00111 fer2, 2Fe-2S
iron-sulfur cluster binding domains, score 55.90,
8.5e-13"
                                                                                                                                                                                                                                                                     overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        signature"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="STY1082"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Pfam match to entry PF01170 UPF0020, ncharacterized protein family UPF0020, sco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="STY1082"
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                                                                                                                               Score 451.2; DB 1;
Pred. No. 1.2e-121;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella enterica subsp. enterica serovar Typ Salmonella enterica subsp. enterica serovar Typ Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                          Submitted (25-SEP-2002) Laboratory of Genetics, Wisconsin - Madison, 445 Henry Mall, Madison, W
                                                                                                                                                                                                                                                                                                                                                                                                         Deng, W., Liou, S.-R., Plunkett, G. III, Mayhew, G.F., Rose, D.J., Burland, V., Kodoyianni, V., Schwartz, D.C. and Blattner, F.R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deng, W., Liou, S.R., Plunkett III, G., Mayhew, G.F., Rose, D
Burland, V., Kodoyianni, V., Schwartz, D.C. and Blattner, F.
Comparative Genomics of Salmonella enterica Serovar Typh
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Salmonella enterica subsp.
16 of the complete genome.
AE016840 AE014613
AE016840.1 GI:29137797
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                                                                                                                                                /db_xref="taxon:209261"
complement(164. .622)
/note="corresponds to STY1225 from Accession AL513382:
Salmonella typhi CT18"
                                                                                  /locus_tag="t1735"
complement(164. .622)
                                                                                                                                                                                                                                                                                 Typhi Ty2"
                                                                  'gene="tnpA"
                                                                                                                                                                                          /sub_species="enterica"
                                                                                                                                                                                                                                                                                                  'organism="Salmonella enterica subsp. enterica serovar
                                          locus_tag="t1735"
                                                                                                                                                                                                                                         strain="Ty2"
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                                                                                      / CTAINS LATE OF "MISDIGKLIASAAWDAQSINELKAKAGQDPAANIRPVARQVEGMF
/ CTAINS LATE ON "WISDIGKLIASAAWDAQSINELKAKAGQDPAANIRPVARQVEGMF
VQMMLKSMREALPKDGLESSDQTRLYTSMYDQQIAQQMTAGKGLGLANMVIKQMTGGQ
TWPADDAPQVPLKFSLETVNS YQNQALTQLVRKAIPKTPDSSDAPLSGDSKDFLARLS
LPARLASEQSGVPHHLILAQAALESGWGQRQILRENGEPSYNVFGVKATASWKGPVTE
ITTTEYENGEAKKVKAKFRVYSSYLEALSDYVALLTENPRVAAVTTAATAEQGAVALQ
NAGYATDPNYAKKLASWIQQLKAMSEKVSKTYSANLDNLF"
complement (4488. .5591)
                                                            complement (4488. .5591)
/gene="flgI"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /locus_tag="t1738"
/note="corresponds to STY1221 from Accession AL513382:
Salmonella tphi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / CHARLE TO THE WASEL NAMED PARLATVESNI INNYNVAGYTROTTI LAQA NSTLGARGWIGNGYVYSGYOREYDAFI INQLRGAQNQSSGLITRY EQWSKLINLLADK NSTLGARGWIGNGYVYSGYOREYDAFI INQLRGAQNQSSGLITRY EQWSKLINLLADK NSSLAGGLUQSFFTSLQTLVSNAED PARRQALI GEAEGLVNQFKTTDQYLFADDDKQNI LESSVAQINNYAKQI ANLIDQI SEMTGYGAGAS FUNDLDQRDQLV SELNKU VGVEVS ALGSSVAQINNYAKQI ANLIDQI SEMTGYGAGAS FUNDLDQRDQLV SELNKU VGVEVS YOLGGITYNLTMANGYTLIVQGSTARQLAAVPS SAD PTRTTAVDEARAGNI EL PEKLLN VSNSNALKTVSLTAKVDGSTKVQATDYKI VFDGTDWQVTRTADNTTFFS IGSPV LEI DGLKVTVGTGAQKNDS FLLKEVSNAL I UMNVKTUNEARI AMASESKLD PDVDTGD SDNRNGQALLDLQNSNYGGINTENDAYATI VFDGTDVGNKTSTLKSTTQANVVKQLYK SDNRNGQALLDLQNSNYGGINTENDAYATI VFDKTSTLKSTTQANVVKQLYK SDNRNGQALLDLQNSNYGGINTENDAYATI VFDKTSTLKSTTQANVVKQLYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(3538. .4488)
/gene≈"flgJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQQSVSGVNLDEEYGNLQRYQQYYLANAQVLQTANALFDALLNIR"
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Salmonella typhi CT18"
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/producte if lagellar hook-associated protein 3"
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Salmonella typhi CT18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (7146. .7901)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="flgF"
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SFGFDTVFRYLQGLFCNSRADMEASGGNSFNGKGGANASNTFSGTLTVTVDQVLANGN
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Accession AL513382: Salmonella typhi CT18"
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Salmonella typhi CT18"
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complement (5597. .6295)
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DARTVQVRVPSGNSSQVRFLADIQMCENVTPQDAKVVINSRTGSVVMNRRVTLDSCA
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/transT_table=
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Salmonella typhi CT18"
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/transl_table=11
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N AJ000514

N AJ000514.1 GI:2275119

agfA gene; agfB gene.
Salmonella typhimurium

ISM Salmonella typhimurium

Bacteria; Proteobacteria; Gammaproteobacteria; Ent
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2 (bases 1 to 1048)
Sukupolvi,S.S.
Direct Submission
                                                                                                              Sukupolvi,S., Lorenz,R.G., Gordon,J.I., Bian,Z., Normark,S.J. and Rhen,M.
Expression of thin aggregative fimbriae promotes salmonella typhimurium SR-11 with mouse small int
                                                                                  Infect. Immun.
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/note="corresponds to STY1216 from
Salmonella typhi CT18"
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/transl_table=11
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Pred. No. 1.2e-121;
0; Mismatches 3;
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                                                  GTTGTAGTGCAGAAACAGTCGCATATGGCTATTCGCGTCA
                                                                                                                                                                                                                                                                                                                          CGCCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGA---AGGAGGAAATAATCGG
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                              GTTGTAGTGCAGAAACAGTCGCATATGGCTATTCAGGCCA
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                                                                                                                     ATCCAGAAAGGTTCTGGAAATAAGGCCAATATTTACCCAGTACGGTACGCAGAAAACAGCA
                                                                                                                                                                    AACGATGCCAGTATATCGCAAAGCGCTTACGGTAATAGTGCGGCTATTAGTGCGGCTATT
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593. .>1048
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sisqsaygnsaaisaaiiqkgsgnkanitqygtqktavvvqkqshmaiqanitqygtq
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14. .553
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Pred. No. 1.3e-101;
0; Mismatches 7;
                              470
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Submitted (11-NOV-2002) Romling U., Microbiology and Tumorbiology Center, Karolinska Institute, Box 280, S-17177 Stockholm, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZOGAJ,X., Bokranz,W., Nimtz,M. and Romling,U.
Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract
Infect. Immun. 72 (7), 4151-4158 (2003)
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Citrobacter sp. Fec2
Citrobacter sp. Fec2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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AJ515700
AJ515700.1 GI:31790491
/translation="mkilqvaafaaivvsgsalagsvpqwggggggggggsssgpestl
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/transT table=11
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/db_xref="GI:31790493"
                                                                                                                                                                          function="curli subunit"
                                                                                                                                                                                                  'gene="csgA"
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RSLDDISSSCIYLVDMMEADKKLIHYWQDNLSRKNNNLKTLLLNTPDDYPYRDIENWP
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KEILNKLRIGASNIEIARSLFISENTVKTHLYNLFKKIAVKNRTQAVSWANDNLRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="csgB"
/function="nucleator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative regulatory protein"
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complement(212. .862)
/gene="csgD"
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2 (bases 1 to 10370)
Jin,Q., Shen,Y., Wang,J.H., Liu,H., Yang,J., Yang,F., Zhang,X.B.
Zhang,J.Y., Yang,G.W., Wu,H.T., Dong,J., Sun,L.L., Xue,Y.,
Zhao,A.L., Gao,Y.S., Zhu,J.P., Chen,S.X., Yao,Z.J., Wang,Y.,
Lu,W.C., Qiang,B.Q., Wen,Y.M. and Hou,Y.D.
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of Public Health,
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                                                                                                                                                                                                                    Jin,Q., Yuan,Z.H., Xu,J.G., Wang,Y., Shen,Y., Lu,W.C., Wang,J.H., Liu,H., Yang,J., Yang,F., Qu,D., Zhang,X.B., Zhang,J.Y., Yang,G.W., Wu,H.T., Dong,J., Sun,L.L., Xue,Y., Zhao,A.L., Gao,Y.S., Zhu,J.P., Qiang,B.Q., Wen,Y.M., Hou,Y.D., and Yu,J., Ma,D.L., Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coliman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                    Nucleic Acids Res. 30 (20), 4432-4441 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                 genome.
AE015131 AE005674
AE015131.1 GI:24051313
                                                                                                                                                                                                                                                                                                                                                               Shigella flexneri 2a str. 301
Shigella flexneri 2a str. 301
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE015131
Shigella flexneri 2a str.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGAAAAACAAATTGTTATTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGTCGCATATGGCTATTCGCGTCACCCAACGCTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGĀĀĀTĀĀAGCAĀĀTĀTTĀCTCĀGTĀTGGTĀCGCĀĀĀĀĀĀĀČĀGCĀGTTGTĀGTGCĀGĀGĀ 2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAAATAAGGCCAATATTACCCAGTACGGTACGCAGAAAACAGCAGTTGTAGTGCAGAAA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGCCAGTATATCGCAAAGTAATTACGGTAATACTGCGATGATTATCCAGAAAGGTTCT 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATGCCAGTATATCGCAAAGCGCTTACGGTAATAGTGCAGCTATTATCCAGAAAGGTTCT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGTTGACCAATGAGGAGCTTATAATTTTGCGTATATTGCTCAGTCGGGTCATTCCAAT 1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAGTCGACCAGGCAGGGAATTATAACTTTGCGTATATTGAGCAAACGGGCAATGCCAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGAAGGAGGAAATAATCGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retreatriaateaggeageeatriatriggicaaggeaggeaggatagatagtagtgeaaggig 1802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ĆĠĊĊĀĠĠĀĠĠĠĊŤĊŦĀĀĀĊŤŦŤŦĠŦĊĠĠŤĀĠŤŦŤĊĀĊĀĀĠĀĀĠĠŦĠĠĀĀĠŤĀĀĊĊĠĠĠĊC 1862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTTCATTTAATCAGGCGGCCATTATTGGTCAAGTCGGCACGGATAATAGTGCCAGAGTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĠĊAĀĊĀĀĢĪTĀĪĠĀĪTĪĀĠĊĠĊĀTĪĊĊĠĀĀTĀĪĀĀĊĪTĪĠĊĠĠŢĀĀĀĪĠĀĀĪTĀĀĠTĀĀĠ 1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGACAAATTATGATCTGGCTCGTTCAGAATATAATTTTGCGGTAAATGAATTAAGCAAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                angaaaaacaaarigitattiaigargitaacagtactgggigcgcctggaaattgcttcc
1. .10370
/organism="Shigella
                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                    (08-MAY-2001) Microbial Genome Center of Chinese Ministry
Health, 100 YingXin Jie, XuanWu Qu, Beijing 100052, p.R.
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85.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10370 k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 348.8; DB : 
Pred. No. 1.4e-91
0; Mismatches 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp DNA 1
1 section 94 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear BCT 18-UC1-, f 412 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2889;
                                                                                                                                                                                                                                                                                                    Yang, G.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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flexneri

2a

. CDS	0		CDS	gene	CDS	gene	CDS	gene	trna
2811. 3350 /gene="ycd2" /locus tag="SF1030" /note="Residues 1 to 179 of 179 are 98 pct identical to residues 1 to 179 of a 179 as protein from Escherichia coli K12 ref: NP 415554.1" /codon_start=1 /transI_table=11 /product="orf, conserved hypothetical protein" /protein_id="AAN42654.1"	(D II	/ Jenes your / Jones /	/gente="your" /locus tag="SF1029" /2032757	/db_xref="GI:24051314" /trans1ation="myrvdlhmitvasthaystlsdyiaqakqkgiklfaitdhigddm /trans1ation="myrvdlhmitvasthaystlsdyiaqakqkgiklfaitdhigddm Edaphhmhfinmrimpravvdgwgillrgieanikavvdgeidcsgkmfdsldliiagfhe PVFAPHDKATMTQAMISTIASGNVHIISHPGNPKYEIDVKAVAEAAAKHQVALEINNS SFLHSRKGSEDNCRAVAAVRDAGGWVALGSDSHTAFTMGEFEECLKILDAVDFPLER ILNVSPRRLLNFLESRGMAPIAEFADL" 22032757 /gene="vcdY"	1442. 72179  /gene="ycdX" /locus tagg="SF1028" /note="Residues 1 to 245 of 245 are 99 pct identical to residues 1 to 245 of a 245 as protein from Escherichia coli 0157:H7 EDL933 ref: NP_287168.1" /codon start=1 /transT_table=11 /product="orf, conserved hypothetical protein" /protein id="ANM42652.1"	/pseudo /codon_start=1 /transT_table=11 14422179 /gene="ycdX" /locus_tag="SF1028"	/pseudo 4101387 4101387 /gene="ycdw" /locus_tag="SF1027" /locus_tag="SF1027" /note="similar to Escherichia coli K12 putative /note=msimilar to Escherichia coli K12 putative dehydrogenase gi: 1787270 (326 aa). BLAST with identity of 99% in 326 aa. This CDS contains an in-frame stop codon. The sequence has been checked and is believed to be correct."	/note="anticodon: GGA" 4101387 /gene="ycdW" /locus_tag="SF1027"	/mol_type="genomic DNA" /strain="301" /serotype="2a" /db_xref="taxon:198214" complement(127214) /product="tRNA-Ser"
	CDS	gene	Ç	gene		gene CDS		CDS	gene

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DAGFKVPWYKSVEKLGWYWLSRVRGKVQYADLGAENWKPISNLHDMSSSHSKTLGYKR
LTKSNMPISCOILLYKSRSKGRKONGRSTRTHCHHPSPKIYSASAKEPWILATNLPVEIR
TPKQLVNIYSKEMQIEETFRDLKSPAYGLGLRHSRTSSSERFDIMLLIALMLQLTCWL
AGVHAQKQGWDKHFQANTVRNRNVLSTVRLGMEVLRHSGYTITREDSLVAATLLTQNL
FTHGYVLGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (4454. . .5662)
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/codon_start=1
/transl_table=11
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/notes_similar to Escherichia coli K12 curli production
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(278 aa). BLAST with identity of 97% in 257 aa. This CDS
contains an in-frame stop codon. The sequence has been
checked and is believed to be correct."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MCSISFMAAFSAIMRGMNILLSIAITTGILSGIWGWVAVSLGLL
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IVAFLWCIQAKQLLLSFVPGTFIGACATFAGQGDWKLVLPSLALGLVFGYAMKNSGLW
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/locus tag="SF1033"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
complement(4454.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3414. .4189)
/gene="csgG"
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RAFSDKWESDYTGNLTINERPSARWGSWITITVNQDVIFQTFLFPLKRDSEKTVVFAL
IQTEEALNRRQINQALLSTDDLAHDEF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /locus_tag="SF1033"
complement(5995. .6384)
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                                                                                                /product="curli production assembly-transport component, 2nd curli operon" (protein ide"AAN42656.1" /db_xref="GI:24051318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (5995. .6384)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /locus_tag="SF1032"
                                                                                                                                                                                                                                      transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="csgE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="transposase of Tn10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="csg8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 locus_tag="SF1031"
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/locus tag="sp1034"
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complement (6389. .7069)

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/transl\_table=1
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/db xref="Gi:24051319"
/translation="MRSIKKWGFIMFNEVHSIHGHTLLLITKPSLQATALLQHLKQSL

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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GATGCCAGTATATCGCAAAGCGCTTACGGTAATAGTGCAGCTATTATCCAGAAAGGTTCT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7853
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                                                                                                          Escherichia coli
Escherichia coli
Bacteria, Proteobacteria,
                                              Hammar,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                          Enterobacteriaceae;
                                                                                                                                                                                     csgA gene; csgB gene; orfC gene.
                                                                                                                                                                                                                                      X90754.1 GI:1147558
                                                                                                                                                                                                                                                                       E.coli csgG, csgF, csgE,
X90754
                                                                                                                                                                                                                                                                                                                   ECCSGABDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTCGCAAATGGCAATTCGCGTGACACAACGTTAA 8248
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGTCGCATATGGCTATTCGCGTCACCCCAACGCTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTÄÄTÄÄAGCAÄÄTÄTTÄCACÄGTÄTGGTÄCTCÄAÄÄÄÄCGGCÄGTTGTÄGTGCÄGÄGÄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAAATAAGGCCAATATTACCCAGTACGGTACGCAGAAAACAGCAGTTGTAGTGCAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GÄTĠĊĊĀĠŦĀŦŦŤĊĠĊĀĀĠĠŦĠĊŦŦĀŦĠĠŦĀĀŦĀĊŤĠĊĠAŦĠĀŦŤĀŤĊĊĀĠĀĀĀĠĠŦŤĊŦ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGATTGÁCCÁGACÁGGAGÁTTATÁÁCCTTGCATÁTÁTTGÁTCÁGGCGGGGGÁGTGCCGÁC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGTCGACCAGGCAGGGAATTATAACTTTTGCGTATATTGAGCAAACGGGCAAACGCCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTTCATTTĀĀTCĀGGCAĢGCCĀTAĀTTGGTCĀĀGCTGGGĀCTAĀTĀĀTĀĠTĠCTCAGTTĀ. 7972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTTCATTTAATCAGGCGGCCATTATTGGTCGAGTCGGCACGGATAATAGTGCCAGAGTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĠĊAĠĊŔĠĠŦŦŔŦĠŔŦŦŦŖĠĊŦŖŖŢŦĊŔĠŔŔŦŔŦŔŔĊŦŦĊĠĊĠĠŦŔŔŔŦĠĸŔŦŦĠŖĠŦŔŔĠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAAAAACAAATTGTTATTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGĀĀĀĀĀČĀĀĀTĪĠĪTĀĪTĪĀTGĀTGTTAĀČĀĀTĀČTGGĠĪTĠĊĠĊĊTĠĠĠĀTTĠĊĀGĊĊ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                         Arnqvist,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="g1:24051320"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus tag="SF1035"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="minor curlin subunit precursor, similar ro/protein_id="AAN42658.1"
/db_xref="G1:2405.1320"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1/transl_table=11
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YPYRDIENWPHINGVFYAMEDDERVVNGLOGVLRGECYFTOKLASYLITHSGNYRYNS
TESALLTHEEKEILNKLRIGASNNEIARSLFISENTVKTHLYNLFKKIAVKNRTQAVS
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/locus_tag="SF1035"
/766. .8248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.3%;
83.3%;
                                                                                  Escherichia.
                                                                                                                                                                                                         csgD
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                                 Bian, Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 334.4; DB 1;
Pred. No. 2.6e-87;
0; Mismatches 76;
                                                                                                                                                                                                                                                                            4680 b<sub>l</sub>
                                                                                                  Gammaproteobacteria;
                                                                                                                                                                                            gene; csgE gene; csgF
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                                                                                                                                                                                                                                                                          cegB,
                                 Olsen,A.
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B, csgA,
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and orfC
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                                                                                             Enterobacteriales;
                                                                                                                                                                                            gene; csgG
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Submitted (11-AUG-1995) M. Hammar, Karolinska Institutet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expression of two csg operons is required for production fibronectin- and congo red-binding curli polymers in Esch Mol. Microbiol. 18 (4), 661-670 (1995)
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Hammar, M.
                                                                                                                                                                                  /Protein_id="CAA62278.1"
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AQAQNSYKDESYNDDEGIETPSALDNFTQAIOSQILGGLLSNINTGKPGRMVTNDYIV
COMPLEMENT (1434. .1823)
                                              production"
                                                        /codon_start=1
/transl_table=11
/product="assembly /transport
                                                                                                                                         complement (1434.
/gene="csgE"
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db_xref="GI:1147561"
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/db xref="GI:1147559"

/db xref="GS:PS2103"

/db xref="GMISS-PROT:P52103"

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IGADTQYQLDQIAVHLRVANVSTGEIISSVNTSKTILSYEVQAGVERFIDYQRLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (993. .1409)
/gene="csgf"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=
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/transl_table=11
/product="assembly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strain="W3110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA
/strain="MC4100"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA'
/strain="K12"
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                         Similarity
  73.0%;
ilarity 83.1%;
Conservative
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/protein_id="CAA62281.1"
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Complement (2626)
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LDQWNGKNSEMTVKQFGGNGAAVDQTASNSSVNVTQVGFGNNATAHQY"
3729. .3788
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4243. .4575
                                                                                                                                                                                                                                                                                                                                                        /gene="csgA"
4243. .4575
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/transT table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="csgA"
3729. .4184
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      0;
    Score 332.8; DB 1;
Pred. No. 7.5e-87;
0; Mismatches 77;
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      Indels
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                                           4680;
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                                                                                                                                                                                                                                        Direct Submission
Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 10346)
Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, 1 Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
Plunkett,G. III.
Direct Submission
Submitted (13-OCT-1998) Laboratory of Genetics,
                                                                                                   Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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                                                                                 Email: ecoli@genetics.wisc.edu
608-263-7459
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                                                                                                                                                                                                                               608-263-7459
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Escherichia coli K12
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ĀE000205.1 GI:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
University of Wisconsin-Madison (Frederick R. Blattner, director).
Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently frames were determined using GeneMark Software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta GA, have been correlated with genetic loci are being annotated with CG Stock Center (CGSC) database at Yale University, kindly supplied by (http://cgsc.biology.yale.edu). Annotation of the genome is an by correlated. Updated information will be available at the E coli Genetic by correlating it with other data. Comments to the authors are fenome project's World Wide Web site hose anotations are periodically updated; this is version M54. No anotation updates: updated gene identifications Riley; added promoters, protein binding sites, and repeated beginning with a lowercase 'b' assigned to each gene (protein-or names. This should allow them to be searched for in Entrez as gene
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/note="0328; This 328 aa ORF is 19 pct identical (4 gaps)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="orf; Unknown"
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SW: P43098"
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                                                                                                                                                                                                                                               note="synonym: b1029"
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69. .392
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|strain="K12"
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SW: P45637"
                                                                              /note="synonym: b1033"
2393. .3370
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                                                                                                                                                                                                                                                                             note="
                                                                                                                                                                                                                                                                                                           complement (2111. .2198)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl table=11
/product="putative ribosomal protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="serx"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="orf; Unknown"
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/note="o83; This 83 aa ORF is 25 pct identical (7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1/
transl_table=
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bound_moiety="DeoR predicted site"
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/translation-"MIDDYLTFIREQDKRNLLYIYAIGLILIGEYWKNAGFTEPSEDI GVVSGILALVLYNFIFDLKAYWAYKCVTKNIDFSWEKKKQNHKIELFLTQELVAGFLG LIMLSAMSWGLYQLLESGLYALFLISLLGEDLVIFLERMIRTGYVKQVAISVAKVKVK KELFYVLLSVCISTVVMLLTISPLRNSDSFYTEGGONLTFKSIIALLILCGVVLAINLE FLRESKRYAFLGELLFLGEIDLFESSENALSTEFAKPLMLRLEILLVIEVMRITLVSVLAILLEGTLVUEVMRITLVSVLAINLE ATLVERNIWEFAYFLLCYVPCLIYYFFYCRFLWHNDFMMACDMYFRWGHFNK" /db\_xref="GI:1787267"

="factor Sigma70; predicted +1 start at 1096049" .1745

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/product="orf, hypothetical protein"
/protein id="AAC74115.1"
/db\_xref="GI:1787268"
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VHGLSNWLSPVUDPRSGLLIPPVCAIHEKKARTFVRALL"

function="putative structure; Not classified" /note="0137; This 137 as ORF is 27 pct identical (1 gap) to47 residues of an approx. 80 as protein R337\_YEAST SW:

/translation="MCNIRKKSPYFRTSSSLAMAVRGGLTRFARPAGSPLTAFTVCPTGCRQLSTPCRGFSPRCYQYTKKKPVLSYELFFKYGGEGGIDSLRSPCGQPAHCVHGLSNWLSPVVEBRSGLLIPFVCAIYEKKARTFVRALL"

/note="factor Sigma70; predicted +1 start at 1097067" actor Sigma70; predicted +1 start at 1097049" actor Sigma70; predicted +1 start at 1096980

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REFERENCE
AUTHORS
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ORGANISM
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N Escherichia coli K12 genomic DNA. (
D90741 AB001340

1 D90741.1 GI:1651509

Complete and shotgun sequencing; csc
csgA; ycdE; cls; nov; mdoG.
Escherichia coli K12

M Escherichia coli K12
Bacraria nov;
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Oshima, T., Aiba, H., Baba, T., Fujita, K., Hayashi, K., Ho Ikemoto, K., Inada, T., Itoh, T., Kajihara, M., Kanai, K., Kimura, S., Kitagawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashi Nishio, Y., Saito, N., Sampei, G., Seki, Y., Tagami, H., Ta
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                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                  Enterobacteriaceae; Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGACAAATTATGATCTGGCTCGTTCAGAATATAATTTTTGCGGTAAATGAATTAAGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                     CAGTCGCAAATGGCTATTCGCGTGACACAACGTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAG
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3383. .3410
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83.1%;
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Pred. No. 7.7e-87;
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 Nashimoto,H.,
H., Takemoto,K.,
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                                                       Honjo, A.,
., Kashimoto, K.,
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PUBMED
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codon_start=1
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S 밁 श् 밁 ঠ 밁 ঠ 밁 ર્ В ঠ 밁 . 8 용

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ALUGA, H., BADA, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, S., Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yamamoto, Y. and Yano, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Members: 1995.4 - 1996.3)
Alba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A.,
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Yamamoto, Y. and Yano, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-JUL-1996) Hirotada Mori, and Technology, Res. & Edu. Center for Takayama, Ikoma, Nara 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wada, C., Yamamoto, Y., Yano, M. and Horiuchi, T. A 718-kb DNA sequence of the Escherichia coli K-12 corresponding to the 12.7-28.0 min region on the li DNA Res. 3 (3), 137-155 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (E-mail:hmori@gtc.aist-nara.ac.jp, Fax:81-7437-2-5669)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collaboration Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The systematic sequencing of the Escherichia coli genome in Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name: Hirotada Mori
Address: NARA Institute of Science
Ikoma, 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Information operator:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Address: National Institute
E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name: Takashi Horiuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Japan E.coli genome DNA sequencing group
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hmori@gtc.aist-nara.ac.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
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                        assembly/transport component
                                                                                                                                                                                                                                                                                                                                                                    assembly/transport component
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                                                GGTĀĀTĀĀAGCAĀĀTĀTTĀCĀCĀGTĀTGGTĀCTCĀĀĀĀĀĀCGGCĀĀTTGTĀGTGCĀGĀGĀ
                                                                              GGAAATAAGGCCAATATTACCCAGTACGGTACGCAGAAAACAGCAGTTGTAGTGCAGAAA 420
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RSLDDISSGSIILLDMMEADKKLIHYWQDTLSRKNNNIKILLLNTEEDYFYRDIENWP
HINGVFYSMEDQERVVNGLQGVLRGECYFTQKLASYLITHSGNYRYNSTESALLTHRE
KEILNKLRIGASNNEIARSLFISENTVKTHLYNLFKKIAVKNRTQAVSWANDNLRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="csgB"
7217. .7672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ORF_ID:0231#8 similar to SwissProt Accession Number P52106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="csgD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="BAA35830.1"
db_xref="GI:4062613"
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/transl_table=
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Kafsdkwesdytgnltinerpsarwgswititvnqdvifqtflfflkrdfektvvfal
IQTeealnrrqinqallstgdlahdef"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
/product="Curli production assembly/transport component CsgE precursor."
CsgE precursor."
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similar to SwissProt Accession Number
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complement(5.
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complement (5418. .5807)
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|db_xref="GI:4062612"
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Pred. No. 7.8e-87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wei,J., Goldberg,M.B., Burland,V., Venkatesan,M.M., Deng,W., Fournier,G., Mayhew,G.F., Plunkett,G. III, Rose,D.J., Darli Mau,B., Perna,N.T., Payne,S.M., Runyen-Janecky,L.J., Zhou,S. Schwartz,D.C. and Blattner,F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shigella flexneri 2a str. 2457T
Shigella flexneri 2a str. 2457T
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.

1 (bases 1 to 292504)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete Genome Sequence and Comparative Genomics of Shigella flexneri Serotype 2a Strain 2457T Infect. Immun. 71 (5), 2775-2786 (2003)
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Shigella flexneri 2a
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                                                                                                                                                                                                                                                                                                                                                            /product="protein chain initiation factor IF-1" /protein id="AAP16348.1" /db/xref="GI:30040617" /translation="MAKEDNIEWQGTVLETLPNTMFRVELENGHVVTAHISGKWRKNY IRILTGDKVTVELTPYDLSKGRIVFRSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="S0884"
complement(223. .441)
/gene="infA"
                                                                                                                                                                                            modification"
                                                                                                                                                                                                                                                                                                                                              complement (726. .1430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="residues 1 to 72 of 72 are 100.00 pct identical to residues 1 to 72 of 72 from Escherichia coli K-12 : B0884
                    /transT_table=11
/product="leucyl, phenylalanyl-tRNA-protein
/protein_ide="AAP16349.1"
/db_xref="GI:30040618"
                                                                                                                                                                                                                                                                               complement (726. .1430)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                             gene="aat"
locus_tag="$0885"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="2457T"
translation="MRLVQLSRHSIAFPSPEGALREPNGLLALGGDLSPARLLMAYQR
                                                                                                                                                  note="residues 1 to 234 of 234 are 100.00 pct identical coresidues 1 to 234 of 234 from Escherichia coli K-12 :
                                                                                                                                                                                                              function="enzyme; Aminoacyl tRNA synthetases, tRNA
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function="factor; Proteins - translation and
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                                                                                                                                                                                                                                     ocus_tag="S0885"
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section 4 of 16 of the complete
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SIWAAALIILIGTAPLI PLFMALVGMGAADANRRNFLALARLSGHFLDRLRGMETLRI F
GRGEAEI ESI IKSASBDFRQRTMEVLRLAFLSGGILEFFTSLS IAVAVFGFS YLGEL
DFGHYDTGVTLAAGFLAL ILAPEFFQDLRDLGTFYHAXAQAVGAADSLUFFMSTPLAH
PQRGEAELALTDPLT IEAEDLF ITS PEGKTLAGPLNFTLPAGQRAVLVGRSGSGKSSL
LNALSGFLSYQGSLRINGI ELRDLSFESWRKHLSWVGQNPQLFAKLLBNVLLARPDA
SEQELQAALDNAWVSEFLFDLFQGVDTPVGDQAARLSVGQAQRVAVARALLNPCSLLL
LDEPAASLDAHSEQRVMEALMAASLRQTTLMVTHQLEDLADWDVI WVMQDGR I IEQGR
YAELSVAGGFFATLAHRQEEI "
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/db xref="GI:30040620"
/db xref="GI:30040620"
/translation="maksROKELTRWLKQQSVISQRWLNISRLLGFVSGILIIAQAWF
/translation="maksROKELTRWLKQQSVISQRWLNISRLLGFVSGILIIAQAWF
MARILQHMIMENIPREALLLPFTLLVLTGIDDMLDYXARYLDQWALAVSVPLLIVVAIFP
LDRLQQAGPAWIQGKRAGSWATLVLEQIDDMLDYXARYLDQWALAVSVPLLIVVAIFP
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QQGEILLNDSPIASLNEAALRQTISVVPQRVHLFSATLRDNLLLASPGSSDEALSEIL
RRVGLEKLLEDAGLNSWLGEGGRQLSGGELRRLAIARTLLHDAPLVLLDEPTEGLDAT
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TLAFTIGSVNILTILFIMPPLEYRAGKSTGQNLTHLRGQYRQQLTAWLQGQAELTIFGA
SDRYRTQLBNTEIQWLEAQDRQSELTALSQALMILLIGALAVILMLMAMASGGVGGANQ
GALIALFVFCALAAFEALAFVTGAFQHLGQVIASAVRISDLTDQKPEVTFPDTQTRVA
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ASDREEGTWITRGVVEAYHRLHELGHAHSIEVWREDELVGGMYGVAQGTLFCGESMFS
RMENASKTALLVFCEBFIGHGGKLIDCQVLNDHTASLGACEIPRRDYLNYLNQWRLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="S0887"
/function="transport; Not classified"
/note="residues 1 to 588 of 588 are 92.85 pct identical to residues 1 to 588 of 588 from Escherichia coli K-12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (3194. .4960)
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/db_xref="GI:30040619"
/translation="MRALLPYLALYKRHKWMLSLGIVLAIVTLLASIGLLTLSGWFLS
ASAVAGVAGLYSFNYMLPAAGVRGAAITRTAGRYFERLVSHDAFFRVLOHLRIYTFSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="transport; Transport of small molecules: Other" /note="residues 1 to 573 of 573 are 97.03 pct identical to residues 1 to 573 of 573 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (1472. .3193)
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/codon_start=1
/trans1_table=11
/product="table=11ain reductase"
/protein_id="AAP16352.1"
/db_xref="GI:30040621"
                                                                                                                                                                                                                   /function="enzyme; 2-Deoxyribonucleotide metabolism"
/note="residues 1 to 321 of 321 are 95.95 pct identical to
residues 1 to 321 of 321 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (3194. .4960)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="S0887"
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                                                                                                                                                                                                                                                                                                                              locus_tag="S0888"
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TCTTCATTTAATCAGGCGGCCATTATTGGTCAAGTCGGCACGGATAATAGTGCCAGAGTA 180
                                      GCAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTÄAATGAATTGÄGTÄÄG
                                                              GCGACAAATTATGATCTGGCTCGTTCAGAATATAATTTTTGCGGTAAATGAATTAAGCAAG
                                                                                                               ATGAAAAACAAATTGTTATTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCC 210874
                                                                                                                                     ATGAAAAACAAATTGTTATTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACC
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                             /translation="MSQBYTEDKEVTLTKLSSGRRLLEALLILIVLFAVWLMAALLSF NPSDBSWSQTAWHEPIHULGGMPGAWLADTLFFIFGVWAYTIFVIIVGCCWFAWRHQS SDEYIDYFAVSLRIIGYLALLITSCGLAAINADDIWYFASGGVIGSLLSTTLQFLLHS SGGTIALLCVWAAGLTLFTGWSWVTIAEKLGGWILNILTFASNRTRRDDTWVDEDEYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trans_ table=11
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/db_xref="GI:30040623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /functTon="phenotype, Cell division"
/note="residues 1 to 737 of 1342 are 68.24 pct identical
to residues 1 to 737 of 1329 from Escherichia coli K-12
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/locus_tag="S0890"
7221. ...11249
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CLERVRRLERQGFTQGYTALLNPHYLDASLLVFVEITLNRGAPDVFEQFNTAVQKLEE
IQECHLVSGDFDYLLKTRVFDMSAYRKLLGETLLRLDGVNDTRTYVVMEEVKQSNRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="regulator for leucine (or lrp)
high-affinity branched-chain amino acid t
/protein_id="AAP16353.1"
/db_xref="G1:30040622"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="irp"
/locus tag="S0889"
/locus tag="S0889"
/function=regulator; Central intermediary metabolism:
/function=regulator; Central intermediary metabolism:
/function=regulator; Central intermediary metabolism:
/note="residues 1 to 164 of 164 are 100.00 pct identical
to residues 1 to 164 of 164 from Escherichia coli K-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MGTTKHSKILLIGSGPAGYTAAVYAARANLOPVLITGMEKGGQL
TTTTEVENWFGDPNDLTGPLLVARMHEHATKFETEIIFDHINKVDLQNRPFRLMGDNG
EYTCDALLIATGASARYLGLPSEBAEKIKGRGVSACATODGFYENGKVAVIGGGNTAVE
EALYLSNIASEVHLIHRADGFRAEKILIKGRUNGVENGNIIHTNRTLEEVTGDQMGV
TGVRLRDTQNSDNIESLDVAGLFVAIGHSPNTAIFEGQLELENGYIKVQSGIHGNATQ
TSIPGVFAAGDVNDHIYRQAITSAGTGCMAALDAERYLDGLADAK"
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/locus_tag="S0889"
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83.1%;
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0; Mismatches 77
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                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-JUN-2002) Genetics Laboratory, University of Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Welch,R.A., Burland,V., Plunkett,G.D. III, Redford,P., Roescl Rasko,D.A., Buckles,E.L., Liou,S.-R., Boutin,A., Hackett,J., Stroud,D., Mayhew,G.F., Rose,D.J., Zhou,S., Schwartz,D.C., Perna,N.T., Mobley,H.L.T., Donnenberg,M.S. and Blattner,F.R.
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1 (bases 1 to 306358)
Welch,R.A., Burland,V., Plunkett,G.D. III, Redford,P., Roesch,P.,
Rasko,D.A., Buckles,E.L., Liou,S.-R., Boutin,A., Hackett,J.,
Stroud,D., Mayhew,G.F., Rose,D.J., Zhou,S., Schwartz,D.C.,
Perra,N.T., Mobley,H.L.T., Donnenberg,M.S. and Blattner,F.R.
Extensive Mosiac Structure Revealed by the Complete Genome Sequence
of Uropathogenic Escherichia coli
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 17020-17024 (2002)
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Escherichia coli CFT073
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Escherichia coli CFT073 section
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AE016759.1 GI:26107527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTCGCATATGGCTATTCGCGTCACCCCAACGCTAA 456
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/transl_table=11
/product="ATP binding |
/protein_id="AAN79727.
                                                                                        /locus_tag=c1253"
/locus_tag=c1253"
/notes_Residues 27 to 1231 of 1245 are 80.16 pct identical to residues 1 to 1209 of 1218 from GenPept.129;
-emb[CAD05883.1] (AL627276) putative ABC transporter
                                                                                                                                                                                                      /locus_tag="c1253"
complement(83. .3820)
                                                                                                                                                                          /gene="iroC"
/locus_tag="
                                                                                                                                                                                                                                                              complement (83. .3820)
                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="CFT073"
                                                                                                                                                                                                                                                                                                                                                                            - Madison, 445 Henry
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          organism="Escherichia"
                                                                                                                                                                                                                                                                                  _xref="taxon:199310"
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    cassette
.1"
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      (ABC) transporter homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roesch, P.,
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to residues 1 to 152 o
>8p|Q57334|T200_SALTY T
element IS200"
         complement (6578. .6940)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPDRKRLLVSLGTVKPMVDGLDLIAWVMDSASEVDAEIILHISANARSDLRSLPSNVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="c1254"
complement(3882. .!
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/note="Escherichia coli O157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="iroB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [LLLDEATSCLDRTSEERLMSSLTDVVHAGKHSALIVAHRLTTAQRCDLIAVIDKGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             locus_tag="c1255"
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535. .5834
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                                                                                                                                                                               _table=11
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                                                                                                                                                                                                                                          169 of 169 are 94.07 pct identical of 152 from SwissProt.40 : Transposase for insertion sequence
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7915. .8269
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                                                                                                                                                                                                                                                                                                                                                                                                                  complement (8832.
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                                                                                                                                                                                                                                                                                       codon_start=1
transl_table=11
                                                                                                                                                                                                                                                                                                                               note="Escherichia coli O157:H7 ortholog: z4324"
                                                                                                                                                                                                                                                                                                                                                 runction="putative enzyme; Transposases Insertion equence Associated"
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table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
transl_table=
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REFERENCE
AUTHORS
TITLE
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ORGANISM
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AF275733
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Best Local Sim.
Matches 379;
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                                                                 Submitted (06-JUN-2000) USDA, ARS, Roman L. Hruska U.S. Meat
Research Center, State Spur 18D, Clay Center, NE 68933, USA
Location/Qualifiers
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                                                                                                                    2 (bases 1 to 1711)
Uhlich, G.A., Keen, J.E. and Elder, R.O.
Direct Submission
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                                                                                                                                                                                        Unlich,G.A., Keen,J.E. and Elder,R.O. Mutations in the csgD promoter associated with variations expression in certain strains of Escherichia coli O157:H7 Appl. Environ. Microbiol. 67 (5), 2367-2370 (2001)
                                                                                                                                                                                                                                                                                                                      Escherichia coli
Escherichia coli
                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Escherichia coli strain 43895 Red Variant CsgB protein (csgB) and
CsgA protein (csgA) genes, complete cds.
                                                                                                                                                                                                                                                                    Enterobacteriaceae; Escherichia.

1 (bases 1 to 1711)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTĀĀTĀĀAGĊAĀĀTĀTTĀĊĀCĀGTĀTGGTĀCTCĀAĀĀĀĀCGGCĀATTGTĀGTGCĀGĀGĀ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GÁTGCCAGTÁTTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGATTGÁTCAGACÁGGAGÁTTÁTÁÁCCTTGCATÁTÁTTGÁTCÁGGCGGGCÁGTGCCAÁC
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                                   organism="Escherichia coli"
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83.1%;
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Pred. No. 8.6e-87;
0; Mismatches 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sdo
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                                                                                                                                                         1177
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                                                                                                                                                                                                                                                                                      1057
                                                                                                                                                                                     421
                                                                                                                                                                                                                                                      361
                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                       997
                                                                                                                                                                                                                                                                                                                                                                                                                      937
                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      877
Escherichia coli O157:H7
of 155.
AE005315 AE005174
AE005315.1 GI:12514572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     757
                                                                    AE005315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                CAGTCGCATAIGGCTATICGCGTCACCCCAACGCTAA 456
                                                                                                                                                                                                     GGTAÁTAAAGCAAATÁTTÁCACAGTATGGTÁCTCAAAAAACGGCAATTGTÁGTGCÁGÁGA 1176
                                                                                                                                           CAGTCGCAAATGGCTATTCGCGTGACACAACGTTAA 1212
                                                                                                                                                                                                                                 GGAAATAAGGCCAATATTACCCAGTACGGTACGCAGAAAACAGCAGTTGTAGTGCAGAAA
                                                                                                                                                                                                                                                                        GATGCCAGTÁTTTCGCAÁGGTGCTTÁTGGTÁÁTACTGCGATGÁTTÁTCCÁGÁÁÁÁGGTTCT
                                                                                                                                                                                                                                                                                                GATGCCAGTATATCGCAAAGCGCTTACGGTAATAGTGCAGCTATTATCCAGAAAGGTTCT 360
                                                                                                                                                                                                                                                                                                                                     AAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAAT 1056
                                                                                                                                                                                                                                                                                                                                                                  AAAGTCGACCAGGCAGGGAATTATAAACTTTGGGTATATTGAGCAAACGGGCAATGCCAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                     CGGCAĞĞGAĞĞCTCAAAACTTTTĞGCĞĞTTGTTĞCĞCAAĞAAĞĞTAĞTAĞCAACCĞĞĞÇA 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTCATTTAATCAGGCGGCCATTATTGGTCAAGTCGGCACGGATAATAGTGCCAGAGTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGAAGGAGGAAATAATCGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCGACAAATTATGATCTGGCTCGTTCAGAATATAATTTTGCGGTAAATGAATTAAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGCAGGTTATGÁTTTAGCTAATTCÁGÁÁTÁTÁÁCTTCGCGGTÁÁÁTGÁÁTTGÁGTÁÁG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAĀĀĀĀĀČĀĀĀTTĢTTĀTTĀTGĀTĢTTĀĀCĀĀTĀCTĢGGTĢCĞCCTĞGGĀTTĞCĀGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAAAAACAAATTGTTATTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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757. .1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="csgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="csgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="csgB"
757. .1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="csgB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="43895 Red Variant"
/serotype="0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.6%;
82.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۰,
                                                                 10190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 331.2;
Pred. No. 2.;
                                               EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                               genome,
                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                          contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78;
                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1711;
                                          1 of
                                        BCT 21-MAR-2001
3, section 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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                                                                                                                                                                                                                                                                      1116
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REFERENCE
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JOURNAL
MEDLINE
PUBMED
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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                                                                                                                                                                                                                                                                                                                                                                                   SgS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21074935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Sao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A., and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 10190)

Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Kink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A. and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (22-OCT-2000) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome sequence of enterohaemorrhagic Escherichia coli O157:H7
Nature 409 (6819), 529-533 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli 0157:H7 EDL933
Escherichia coli 0157:H7 EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perna, N.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 10190)
                                                                                                                                                                                                                                                                                                                                                                                                 1113. .1571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  constituents: Surface structures"
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to residues 1 to 151 of 151 from Escherichia coli K-12
Strain MG1655: B1041"
                                              TLDQWNGKDSHMTVKQFGGGNGAAVDQTASNSTVNVTQVGFGNNATAHQY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SISQGAYGNTAMIIQKGSGNKANITQYGTQKTAIVVQRQSQMAIRVTQR"
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QaaiigQagtnnsaqlrQggskllavvaQegssnrakidQtgdynlayidQagsanda
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                                                                                                                                                                                                  /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="csg8"
/function="structural component; Cell exterior
                                                                                                                                                                                /product="curlin major subunit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="csg8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Escherichia coli O157:H7 EDL933"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="synonym:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      serotype="0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _xref="taxon:155864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .1072
                           .1962
                                                                                                                                                                                                                                                                                                                                                                                                        Z1676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21675"
                                                                                                                                                                                                                                                                        e g
                                                                                                                                                                                                                                                                   152 of 152 are 96.71 pct :
151 from Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 precursor,
                                                                                                                                                                              coiled
                                                                                                                                                                                                                                                                                                                                       constituents: Surface
                                                                                                                                                                              surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similar
                                                                                                                                                                                                                                                                 identical to
i K-12 Strain
                                                                                                                                                                                structures;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CagA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SgS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sgo
/gene="ymdD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="synonym:
2964. .4445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="21679"
2489. .3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2083. .2394
/gene="Z1678"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2964. .4445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EENAHLYERLLTQQGDE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MG1655: B1044"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                         WG1655: B1046"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2083. .2394
                                                                                                                                                                                                                                                                                                             codon_start=1/
transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="ymdC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="21679"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="Z1678"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /G1655: B1043"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="synonym:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="ymdC"
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PEGEMADRIELPASWHNDAMTHRYLRKMESSPFINHLVDGTLPLIWAKTRLLSDDPAK
GEGKAKRHSLLPQRLFDIMGSPSERIDISSSFVPTRAGVAQLLENVRKYKTALISDDPAK
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SLAANDVAVUHAGYARWKKKLIKTRYGVELYELKPTREGOSTLHDKRFIQSQYDAAWQLRLDR
WGRINWVDRHAKKEIVLKKEPATSFWKRVMVRLASILPVEWLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="orf; Unknown function"
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to residues 1 to 177 of 177 from Escherichia coli K-12
Strain MG1655: B1045"
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residues 1 to 103 of 103 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1630. .1962

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/function="putative structure; Not classified"
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residues 1 to 110 of 110 from Escherichia coli K-12 Strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mktrihvvQGDItkLavDVIvnaanpSLmGGGGVDGAIHRAAGp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GI:12514575"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trans] table=11
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Query Match
Best Local Similarity
Matches 378; Conserv
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                                AAAGTCGACCAGGCAGGGAATTATAACTTTGCGTATATTGAGCAAACGGGCAATGCCAAC 300
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7531. 10074
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MG1655: B1048"
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82.9%;
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Search completed: March 15, 2004, 22:49:43 Job time: 1967.17 secs

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1: geneseqn1980s:*
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Match
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Gapop 10.0 , Gapext 1.0
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ACD26496
AAC64629
AAQ73066
AAT74141
AAQ87467
AAT74141
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ABK94407
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ADA71938
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ACD68811
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Aac64618 Salmonell
Aac64620 Escherich
Acd68810 E. coli K
Acd68811 E. coli K
Aac64623 AgfA.:PT3
Ada71938 Rice gene
Aac64608 AffA (SEF
Aad32400 Chlamydia
Abk94407 DNA encod
Adc10081 Human NOV
Acd26496 Human tum
Aac64629 AgfA::PT3
Aac64629 AgfA sequ
Aat74141 Salmonel1
Aaq87467 AgfA sequ
Aat74142 Salmonel1
Aac64628 AgfA::PT3
Aac64627 AgfA::PT3
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## ALIGNMENTS

RESULT 1 AAC64618

AAC64618;

AAC64618 standard; DNA; 456

ВP

26-FEB-2001

(first entry)

Salmonella enteritidis AgfB DNA sequence SEQ ID NO:2.

WPI; 2000-672631/65. P-PSDB; AAB36342. 05-APR-1999; Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen; ds. 05-APR-2000; 2000WO-CA000356 12-OCT-2000. Salmonella enteritidis. White AP, Doran JL, WO200060102-A2. vaccine; immune response; (UYVI-) UNIV VICTORIA. 99US-0127888P Collison immunogen; SK, Kay WW

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombination of the chromosome of the homologous species, (3) directing recombination of a recombination of a recombination of a recombination of a recombination. Recombinant agfA gene having a segment replaced by a foreign DNA which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal. Disclosure; Page 134; 139pp; English. DNA sequence ant AgfA

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RESULT 2
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ID AAC6
XX AAC6
XX AAC6
XX AAC6
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XX Esch
XX Salm
KW Vacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA compression containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing the sequences grown on a Salmonella, E. coli or containing the containing the segment of recombinant and introducing the containing animal in conjunction with a carrier or diluent. (1) is contained the expression of recombinant AgfA protein which is useful for containing an immune response in an animal. In a fimbrial presentation containing an immune response in an animal. In a fimbrial presentation containing the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live contained the inserted epitope, and hybrid fimbriae are usually strong containst the inserted epitope, and hybrid fimbriae are easy and the exemplification of the present invention
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Best Local
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           WO200060102-A2
                                                      Salmonella, agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen; ds.
                                        Escherichia coli
                                                                                                     Escherichia coli CsgB DNA sequence SEQ ID NO:4.
                                                                                                                                               26-FEB-2001
                                                                                                                                                                                                 AAC64620 standard; DNA; 456
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Pred. No. 8.6e-135;
0; Mismatches 0;
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CC Regment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA, homologue fimbriae (SER17/TAF) nucleation depended CC AgfA, CsgA and AgfA, homologue fimbrian is subunits, respectively; (2) are the chromosome of the production of fimbriae comprising recombinant CC chomologous species; (3) directing recombinant gene into the chromosome of the comprising separating an amino acid polymer comprising a recombinant gene CC comprising separating an amino acid polymer comprising a recombinant agene CC comprising separating an amino acid polymer comprising a recombinant agene CC comprising separating an animal in conjunction with a carrier or diluent. (I) is collower into the expression of recombinant AgfA protein the the expression of recombinant AgfA protein which is useful for compared the heterologous antigens are presented in high numbers (up to compose the heterologous antigens are presented in high numbers (up to compose the heterologous antigens are presented in high numbers (up to compose the heterologous antigens are presented in high numbers (up to compose the inserted epitope, and hybrid fimbrin protein genesses both the carrier fimbrial subunit protein sare usually strong composers the inserted epitope, and hybrid fimbrine are easy and consensive to purify in large amount. The present sequence is given in the exemplification of the present invention
Sequence 456 BP; 146 A; 78 C; 113 G; 119 T; 0 U; 0 Other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 134; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2000; 2000WO-CA000356
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Best Loca Matches Query Match Best Local ( 121 379; 61 61 ب h 73.0%; Similarity 83.1%; rcricárthaátcaggcagccataatrggtcaagcrgggactaataatagtggtcagtta TCTTCATTTAATCAGGCGGCCATTATTGGTCAAGTCGGCACGGATAATAGTGCCAGAGTA GCGACAAATTATGATCTGGCTCGTTCAGAATATAATTTTTGCGGTAAATGAATTAAGCAAG 120 ĠĊAGĊĀGGŦŦĀŦĠĀŦŦŦĀĠĊŦĀĀŦŦĊĀĠĀĀŦĀŦĀĀĊŦŦĊĠĊĠĠŦĀĀĀŦĠĀĀŦŦGĀĞŦĀĀĠ ATGAAAAACAAATTGTTATTTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACC Conservative Score 332.8; pred. No. 1.5e 1.5e-95; 77; DB 3; Length 456; Indels

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> 181 181 121

301 241

GATGCCAGTATATCGCAAAGCGCTTACGGTAATAGTGCAGCTATTATCCAGAAAGGTTCT AAGATTGÁCCÁGACÁGGAGÁTTÁTÁACCTTGCATÁTÁTTGÁTCÁGGCGGGGGÁGTGCCAÁC

360

300 300 240 240 180 180 120

AAAGTCGACCAGGCAAGTATATAACTTTGCGTATATTGAGCAAACGGGCAATGCCAAC

CGCCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGAAGGAGGAAATAATCGGGCG cegchéegheerrehannerriegegerrerrecechnenaernernaechnecegech

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This invention describes a novel biochip comprising probe spots, each C containing many identical probes. The probes are nucleotide sequences of C 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at CC least one includes a segment of at least 20 bases identical with, or C complementary to, a segment of an open reading frame (orf) of Escherichia CC coli k12. The blochip is used for specific detection of gene expression in k12 and for determining the gene expression pattern, e.g. for C diagnostic determination of which E. coli strains are present in the gut, and to determine the effects of e.g. growth media on gene expression. The CC diagnostic determine the effects of e.g. growth media on gene expression. The CC device, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or CC other E. coli strains in a single experiment. Apart from qualitative and quantitative information about gene expression, it also allows CC measurements of population densities for the various strains. The use of synthetic oligonucleotides for preparation of probes allows free CC variation in probe length and ensures high purity (and thus selectivity, cand reproducibility), also synthetic probes are generally CC shorter than probes prepared by polymerase chain reaction. ACD68731 to in the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Donner H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MWGB-) MWG-BIOTECH
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Query Match
Best Local Similarity 84.

16.3%; 84.0%;

Score 74.4; DB 7; Pred. No. 1.6e-13; 0; Mismatches 16;

Length 100; Indels

0

Gaps

0

S

123 TTCATTTAATCAGGCGGCCATTATTGGTCAAGTCGGCACGGATAATAGTGCCAGAGTACG 182

Query Match
Best Local Similarity
Matches 79; Conserv

Conservative

14.6%;

Score 66.4; Pred. No. 5. 0; Mismatche

Mismatches

.6e-11; les 21; DB 7;

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Gaps

0

Length 100, Indels

Sequence 100 BP; 28 A; 18 C;

27 G; 27 T; 0 U; 0 Other;

Sequence 100

B₽,

27

A; 19 C; 26 G;

28 T; 0 U; 0 Other;

invention

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RESULT 4
ACD68812
ID ACD6
This invention describes a novel biochip comprising probe spots, each containing many identical probes. The probes are nucleotide sequences of 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at CC least one includes a segment of at least 20 bases identical with, or CC complementary to, a segment of an open reading frame (orf) of Escherichia CO il K12 and for determining the gene expression pattern, e.g. for cc diagnostic determination of which E. coli strains are present in the gut, and to determine the effects of e.g. growth media on gene expression. The CC diagnostic determination of which E. coli strains are present in the gut, and to determine the effects of e.g. growth media on gene expression. The CC penome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or cother E. coli strains in a single experiment. Apart from qualitative and CC quantitative information about gene expression, it also allows for measurements of population densities for the various strains. The use of synthetic oligonucleotides for preparation of probes allows free CC variation in probe length and ensures high purity (and thus selectivity, reactivity and reproducibility); also synthetic probes are generally construct than probes prepared by polymerase chain reaction. ACD68731 to in the invention
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CC This invention describes a novel biochip comprising probe spots, each CC containing many identical probes. The probes are nucleotide sequences of CC 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at CC complementary to, a segment of at least 20 bases identical with, or CC coll KI2. The biochip is used for specific detection of gene expression CC in KI2 and for determining the gene expression pattern, e.g. for CC and to determination of which E. coll strains are present in the gut, CC diagnostic determination of which E. coll strains are present in the gut, CC genome, with simultaneous analysis of many different gene expression. The CC device, and comparison of gene expression between KI2 and its mutants or CC quantitative information about gene expression, it also allows are consuments of population densities for the various strains. The use of consuments of population densities for the various strains. The use of constitutive and reproducibility); also synthetic probes are generally to constitute than probes prepared by polymerase chain reaction. ACD68731 to in the invention
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ACD68811
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                                                                             Similarity
                      GTTATTTCACAAGAAGGAAGAAATAATCGGGCGAAAGTCGACCAGGCAAGGGAATTATAAC 267
GTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCAAAGATTGACCAGACAGGAGATTATAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGGGAGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGAA 222
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drescher B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                             A; 20 C; 29 G; 20 T; 0 U; 0
                                                                           14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Huber A,
                                                        Score 64.8; DE Pred. No. 1.8e-0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weber
                                                                     1.8e-10
                                                                                    DB 7;
                                                                                                            Other;
                                                                                 Length 100;
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probe; ss
                                                     0;
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60
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Sequence 456 BP; 118 A; 109 C; 121

ü 108 T; 0

U; 0 Other

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CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA-homologue fimbriae (SERI7/TAF) nucleation depended CC AgfA, CsgA and AgfA-homologue fimbria bunits, respectively; (2) cc homologous species; (3) directing recombinant gene into the chromosome of the back into the chromosome of the books species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, CC protein containing a replacement segment or segments of foreign amino CC Enterobacteriaceae host cell, from the host cell and introducing the cuseful for the expression of recombinant AgfA protein in the animal in conjunction with a carrier or diluent. (1) is eliciting an immune response in an animal in conjunction with a carrier or diluent. (1) is cliting an immune response in an animal. In a finbrial presentation consisting an immune response in an animal. In a finbrial presentation consisting an immune response in an animal. In a finbrial presentation the carrier fimbrial subunit protein possesses both the carrier fimbrial subunit proteins are usually strong cinexpensive to purify in large amount. The present sequence is given in the examplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 136; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-672631/65.
P-PSDB; AAB36347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYVI-) UNIV VICTORIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-2000; 2000WO-CA000356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA::PT3#2 DNA sequence SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC64623 standard; DNA; 456 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 TTTGCGTATATTGAGCAAACGGGCAATGCCAACGATGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTĠĊAŤĀŤĀŤŤĠĀTĊĀGGĊĠĠĊĀGŤĠĊĊĀĀĊĠĀŤĠĊĊĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agfA; chromosomal gene replacement; fimbrin; epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response; immunogen; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SK,
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Query Match

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                                      Matches
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                        The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                        Chang H,
Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1938/c
                                                                                                                                                                                                                                                                                         Identifying at least one gene involved in plant resistance or repathogenic infection for conferring resistance or tolerance to bacterial, fungal or viral infection by determining or detecting
                                                                                        Sequence 2000 BP;
                                                                                                                                                                                                                                                                                                                                                WPI; 2003-175290/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
                                                                                                                                                                                                                                                       Claim 27; SEQ ID NO 5263; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003000898-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant; bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene,
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             14
                                     l Similarity
57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,
88
                                                                                                                                                                                                                                                                                                                                                                   נד,
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TGTTATTTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACCGCGACAAATTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATAGTGCAGCTATTATCCAGAAAGGTTCTGGAAATAAGGCCAATATTACCCAGTACGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCAGAAAACAGCAGTTGTAGTGCAGAAACAGTCGCATATGGCTATTCGCGT 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGACCATTACCCAGAGCGGTTATGGTAACGGCGCGATGTAGGCCAGGGTGCGGATAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTATATTGAGCAAACGGGCAATGCCAACGATGCCAGTATATCGCAAAAGCGCTTACGGTA
                                                                                                                                                                                                                                                                                                                                                                       Chen W,
F, Quan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                 invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection;
                                                                                     336 A; 265 C; 284 G; 363
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                                                                                                                                                                                                                                                                                                                                                                       Cooper B,
S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5263
                                                 8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.2%;
                                      195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fungal infection; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37.6; DI
Pred. No. 0.15
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                 Score 37.6; DB 7; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
                                                                                                                                                                                                                                                                                                                                                                      Glazebrook J, Goff SA, Whitham S, Xie Z, Zhu
                                                                                                                                                                                                                                                                                                                                                                                                              ĀG
                                     Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB . 15;
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                                                            Length
                                     Indels
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depende assembly system of strains of Salmonella, Escherichia coli and

are:

Example 2; Page 61; 139pp;

English.

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RESULT 8
AAC64608
ID AAC6
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                       05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                          Salmonella;
                                                                                                                                                                                                                                                                                                                                                                                                         AgfA (SEF17)
                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-2003
26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC64608;
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                                                                                                                                                                                                                                        12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                        vaccine;
                                                                                                                                      (UYVI-) UNIV VICTORIA.
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                                                                                                     ΑP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               609 TSKMSYMGKMTCTMYTSMKGSTRR 586
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                                                                                                                                                                                                                                                                                                                                                        immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WGAMRYAYYAMRRRWTYKWSWRRMYWTMTKWAWTWMTCMCMAKWYMATGWATWWWWRYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTAGGTGCTKMWRTYTRSMSWTYAMWKKYTKYMTAYSSTWKWYWAYKWRAYAWSRSRKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTATTCGCGTCACCCAACGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKWAGASMKSCWMYWRGARSMWYSKYSCSAKCCKKTRYMTSSYMSTGMYGMYSSYKSMSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATATTACCCAGTACGGTACGCA-GAAAACAGCAGTTGTAGTGCAGAAACAGTCGCATATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCTGGCTCGTTCAGAATATAATTTTGCGGTAAATGAATTAAGCAAGTCTTCATTTAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CWKAGWARWMKSRYRWKWKKYATRYYWKMWAMTWWWSWRRWKSYRMWSGMGRMRWSAWRY
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                                                                                                   Doran
                                                                                                                                                                                                                                                                                                                                                        agfA; chromosomal gene replacement; fimbrin;
mune response; immunogen; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                         recombinant agfA::PT3a generating
                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                      99US-0127888P
                                                                                                                                                                                                                                                                                                                                                       response;
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                                                                                                     Collison
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                                                                                                                                                                                                                                                                                                                                                       immunogen;
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                                                                                                     SK,
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                                                                                                                                                                                                                                                                                                                                                       primer;
                                                                                                                                                                                                                                                                                                                                                                                                           PCR primer
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RESULT 9
AAD32400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC AgfA, CByA and AgfA-homologue fimbria subunits, respectively, (2)
CC AgfA, CByA and AgfA-homologue fimbrin subunits, respectively, (2)
CC homologous species; (3) directing recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of a recombination of a recombinant gene and (4) eliciting an immune response in an animal, CC protein containing a replacement segment or segments of foreign amino
CC protein containing a replacement segment or segments of foreign amino
CC acid sequence or sequences grown on a Salmonella, E. coll or
CC interobacteriaceae host cell, from the host cell and introducing the acid sequence or sequences grown on a Salmonella, E. coll or
CC useful for the expression of recombinant AgfA protein which is useful for coliting an immune response in an animal. In a fimbrial presentation
CC System the heterologous antigens are presented in high numbers (up to System the heterologous antigens are presented in high numbers (up to communogenicity and adhesion properties relevant for an efficient live capainst the inserted epitope, and hybrid fimbria are usually strong conversed to purify in large amount. The present sequence is given in CC correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
           Timms
                                                                                18-AUG-2000; 2000AU-00009540
                                                                                                            17-AUG-2001; 2001WO-AU001021.
                                      (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                  Chlamydiaceae family; chronic infection; persistent infection; pyk; nlpD; cpn0585; regulatory pathway; biosynthetic pathway; ompA; ompB; hsp60; lipopolysaccharide; cardiovascular system; respiratory tract; therapy; genital tract; reproductive system; atherosclerotic tissue; macrophage; multiple sclerosis; conjunctiva; prophylaxis; antibacterial; gene; ds.
                                                                                                                                                                               WO200214516-A1
                                                                                                                                                                                                                                                                                                                      Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2003
18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae nlpD gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD32400 standard; DNA; 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39 BP, 13
           P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAGAAAACAGCAGTTGTAGTGCAGAAACAGTCGCATAT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                    pneumoniae
                                                                                                                                                                                                                    /product= "Chlamydia
/note= "CDS does not
                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                   /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; 7 C; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.9%;
94.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35.8; DB 3; Length 39; Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                pneumoniae nlpD protein"
include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
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ABK94407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to composition and methods for detecting organisms CC of the Chlamydiaceae family, including species of Chlamydophila and CC chlamydia, in the persistent phase of their developmental cycle and for CC chadynosis of chronic or persistent infections caused by such CC organisms. The composition is useful for modulating the expression of CC gene such as pyk, mlpD, Cpn0585, a gene belonging to same regulatory/CC lipopolysaccharide biosynthesis. It is also useful for modulating the the CC level and/or functional activity of an expression product of these genes, CC cardiovascular system, respiratory tract, genital tract, reproductive atherosclerotic tissue or associated with multiple sclerosis brain CC system or composition is useful for treatment and/or prophylaxis of a CC atherosclerotic tissue or associated with multiple sclerosis brain CC chronic infection caused by an organism of the Chlamydiaceae family in a CC developmental cycle of an organism of the Chlamydiaceae family, is useful CC in the manufacture of a medicament, for treating and/or preventing CC chlamydiaceae infection in a patient. The present sequence is Chlamydiaceae of CC pneumoniae nipD gene. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
     variation
                                                                                                           Key
variation
                                                                                                                                                                         Endothelin 3; EDN-3; endothelin converting enzyme; ECE; endothelin receptor; EDNR; signaling system; cardiovascular disease; coronary heart disease; hypertension; atherosclerosis; angiogenesis; fatty acid metabolism; diabetes; familial hypercholesterolaemia; forensic marker; transgenic animal; solid support; SNP; cardiovascular regulator; gene; ds; single nucleotide polymorphism.
                                                        variation
                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                             DNA encoding endothelin-3 (EDN-3).
                                                                                                                                                                                                                                                                                                                                                      27-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                          ABK94407;
                                                                                                                                                                                                                                                                                                                                                                                                                    ABK94407 standard; DNA; 105325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 738 BP; 231 A; 158 C; 166 G; 183 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 117-118; 196pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting Chlamydial organism in its persistent phase by detecting expression change of range of genes belonging to their respective biosynthetic pathways when expression is compared to that of organism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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P-PSDB; AAE20289.
                                                                                                                                                          sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400 ACAGCAGTTGTAGTGCAGAAACAGTCGCATATTGGCTATTCGCGTCAC 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAGCTGTCGTAGTGAATGCTATATTGCTTGTGGCTCTTTTTCGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGTTGATCÁGAGÁAATGCAGGCAGTGÁGGTAÁATÁTGÁATCGTAGAGACÁTGGTAÁTÁ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTATTATCCAGAAAGGTTCTGGAAATAAGGCCAATATTACCCAGTACGGTACGCAGAAA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                  /standard_name= "Single nucleotide polymorphism"
replace(59430,C)
/standard_name=
replace(63843,T)
                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.7%;
57.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB
Pred. No. 1.2;
   "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                    ВP
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RESULT 11
ADC10081
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Best Local S
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                 18-DEC-2003
                                                           ADC10081;
                                                                                                ADC10081 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 105325 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page; 190pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-435060/46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-SEP-2000; 2000EP-00120123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-AUG-2001; 2001WO-EP010087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200224747-A2
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                                                                                                                                                                                                                                                                                                                                                                            65;
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                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                         ATGAAAAAGCAAATTAAGAGCATAATCCTGACTGCATGGGATGTGCCCAGCCTTCTAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the invention
                                                                                                                                                                                                                                               GCGACAAATTATGATCTGGCTCGTTCAGAATATAATTTTTGCGGTAAATGAATTAA 115
                                                                                                                                                                                                     GGAĀCĀĀĀCTCTTTCCTGGCCTTTTCĀĀĀGTĀTCTGTTACTATGTĀĀTĀĀĀTTĀĀ 66633
                                                                                                                                                                                                                                                                                                                                ATGAAAAACAAATTGTTATTTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACC
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                                                                                                                                                                                                                                                                                                                                                                        7.7%;
nilarity 56.5%;
Conservative
                 (first entry)
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/standard_name= "Single nucleotide polymorphism"
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                                                                                                DNA; 2006
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                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 6
Pred. No. 8.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           25835
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Dipippo Gerlach

Gerlach VL, ( Khramtsov NV,

Rothenberg ME, Sheno Spytek KA, Stone DJ,

Spaderna SK; Alsobrook JP; Rieger DK; Kekuda

B

Lepley

DM;

2003-210149/20 DB; ADC10082.

New isolated NOVX polypeptides and nucleic acid molecules useful for treating, preventing and diagnosing pathological conditions with NOVX-associated disorders, such as cancer, obesity, diabetes and inflammatory

Claim 20; SEQ ID NO 101; 772pp; English

or CNS diseases.

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25-SEP-2001;
03-DEC-2001;
14-DEC-2001;
21-FEB-2002;
21-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2001;
18-JUN-2001;
19-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-JUN-2001;
12-JUN-2001;
14-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thyromimetic; NOVX; pathology; cancer; diabetes; obesity; endocrine disorder; CNS disorder; inflammatory disorder; chromosome mapping; tissue typing; predictive medicine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUN-2001;
03-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JUL-2001;
14-SEP-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human NOVX polypeptide coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUN-2001;
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                                                                                                                                                                                                                              (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene; cytostatic; antidiabetic; anorectic;
roprotective; antiinflammatory; gene therap;
                                                                                                                            t, Anderson DW, Berghs C, Casman SJ, Catterton E;
O VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
N VI, Gorman L, Guo X, Herrmann JL, Hjalt T, Ji W, K
SOV NV, Li L, Liu X, Malyankar UM, Millet CE, Millet
Padigaru M, Patturajan M, Pena CEA, Rastelli L, Rieg
Derg ME, Shenoy SG, Shinkets RA, Smithson G, Spaderna
EA, Stone DJ, Vernet CAM, Zhong H, Zhong M, Alsobroc
                                                                                                                                                                                                                              CURAGEN CORP.
                                                                                                                                                                                                                                                    2001US-0296418P

2001US-0296715P

2001US-029741P

2001US-0297567P

2001US-029828P

2001US-029828P

2001US-029933P

2001US-029933P

2001US-029939P

2001US-030089P

2001US-0301550P

2001US-0301890P

2001US-0308990P

2001US-0308990P

2001US-0337467P

2001US-0358950P

2001US-03591562P

2002US-03591562P

2002US-03591562P

2002US-03591562P

2002US-03591562P

2002US-0359034P

2002US-0359034P
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Best Local
        Bodian DL,
                                                                                  05-SEP-2001; 2001US-0317151P
                              (BODI/) BODIAN D L.
(LABO/) LABOW M A.
(MICK/) MICKANIN C S.
                                                                                                              28-AUG-2002; 2002US-00231426.
                                                                                                                                                                                                                            apoptotic disorder; gastrointestinal and reproductive tract disorder; cancer; ulcer; bone disorder; osteoporosis; blood disorder; hepatitis aplastic anaemia; thrombocytopenia; viral disorder; viral encephaliti
                                                                                                                                                                                                                                                                 tumour necrosis factor receptor related protein 1. Crohn's disease; AIDS; disbetes mellitus; immune disorder; autoimmune disease; multiple sclerosis; gystemic lupus erychematosus; neurodegenerative disorder; prostatitis; Alzheimer's disease; Parkinson's disease; cell proliferative disorder; cell differentiation disorder; ischaemic injury; myocardial infarction;
                                                                                                                                                                     US2003059889-A1
                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              Human; ds; gene;
                                                                                                                                                                                                                                                                                                                                                                              Human tumour necrosis factor receptor related protein-1, TRP-1,
                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACD26496 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel isolated polypeptides, mature form of the polypeptide, a sequence that is 95% identical to the polypeptide or the polypeptide is useful for treating or preventing a pathology associated polypeptide is useful for treating or preventing a pathology associated or activity of the polypeptide, such as cancer, diabetes, obesity, and various detection and screening assays, chromosome mapping, tissue typing and predictive medicine. This sequence corresponds to the coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2006 BP; 637 A; 390 C; 493 G; 486 T; 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               predictive medicine. This sequence corresone of the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAACGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTACGCA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATACTGGCCCTGGGAAAATCCCAGAAAATACCCAGAGAAAATGCATACCTAACCAAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTAATAGTGCAGCTATTATCCAGAAAGGTTCTGGAAATAAGGCCAATATTACCCAGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGTTGCTGTGGATGAGTCTGTTCATACCCTGGAAGACATAGTCAAGTGTATCAGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TŢTĢCGTAŢAŢTĢAGCĄAAÇGĢGCAĄTGCÇAACGĄTĢCÇAGTAŢATCĢCAAĄGÇGCŢTĄC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTCTTGATCTAGCAGGAĞTGATACAAAACĞTCATAGATCAĞGTĞCCAĞAĞCCTCACTAÇ
        Labow MA,
                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                  TRP-1; inflammatory disorder; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.5%;
       Mickanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34.4,
Pred. No. 2.
     cs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                            hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ,
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                                                                                                                                                                                                                                                                                                                                                                              DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC The invention relates to a new isolated tumour necrosis factor receptor CC related protein-1 polypeptide, TRP-1. The tumour necrosis factor receptor CC diagnosing and treating disorders in a human, such as an inflammatory CC disorder (e.g. rheumatoid arthritis, Crohn's disease, AIDS, allergias, CC or diabetes mellitus), an immune disorder (e.g. autoimune disease or CC systemic lupus erythematosus), a neurodegenerative disorder (e.g. attribute bowel syndrome, ulcerative colitis, multiple sclerosis cystemic lupus erythematosus), a neurodegenerative disorder (e.g. attribute), an immune disorder (e.g. attribute) colitis, multiple sclerosis cystemic lupus erythematosus), a neurodegenerative disorder (e.g. attribute) colitis, multiple sclerosis colitis, multiple sclerosis cystemic lupus erythematosus), a neurodegenerative disorder (e.g. attribute) colitis cystemic lupus erythematosus), a neurodegenerative disorder (e.g. attribute) colitis cystemic lupus cystemic lupus cystemic lupus cystemic lupus cystemic cystemic cystemic lupus cystemic cystemic lupus cystemic cystemic lupus cystemic lupus cystemic lupus cystemic lupus cystemi
                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18540 BP; 5173 A; 3532 C; 3591 G; 6244 T; 0 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New tumor necrosis factor receptor related protein-1 polypeptide and nucleic acid, useful for diagnosing and treating disorders in a human e.g. an inflammatory disorder, an immune disorder or a neurodegenerat disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Page 21-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-521912/49
P-PSDB; ABU62739.
5393 TGCAATATGAACAACAGGGAGAAAATGA 5366
                                                                                                                       5453
                                                                                                                                                                                                                              5513
                                                                                                                                                                        146
                                                                                                                                                                                                                                                                               86
                                                                                                                                                                                                                                                                                                                                  77;
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                              GTAGTAGĀGAAGAGĀCAGĀTGĀTĀGAATCĀGTGAĀCTTGAGGĀCAGĀACĀĀCĀGAĀTTTĀ
                                                                                                                                              CAGAATATAATTTTGCGGTAAATGAATTAAGCAAGTCTTCATTTAATCAGGCGGCCCATTA 145
                                                   CCGTTATTTCACAAGAAGGAGGAAATAA 233
                                                                                                                                                                                                    CAGATGGTÄÄTTATTAAAAÄTÄAAÄTGACÄĞAAÄTTTTAAAAAATTCACTĞGATĞGGCTTA
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                7.5%;
52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36pp; English
                                                                                                                                                                                                                                                                                                                    ; Score 34.4; DB; Pred. No. 6.5; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    DB 8;
                                                                                                                                                                                                                                                                                                              71;
                                                                                                                                                                                                                                                                                                                                                                 Length 18540;
                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                 5394
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AAC64629
ID AAC64629;
XX AAC64629;
XX AAC64629;
XX AC64629;
XX AC64629;
XX DT 26-FEB-2001 (first entry)
XX DT 26-FEB-2001 (first entry)
XX Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
XX Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
XX Salmonella; agfA; chromosomal gene; ds.
OS Salmonella enteritidis.
OS Salmonella enteritidis.
OS Synthetic.
XX Synthetic.
XX WO200060102-A2.
PN WO200060102-A2.
XX PF 05-APR-2000; 2000WO-CA000356.
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RESULT 14
AAQ73066
ID AAQ73
XX AAQ73
XX 27-AU
DT 25-MA
DT 26-JU
XX XX
AGFA
XX Salmc
XX Salmc
XX Salmc
XX Salmc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to CC 500,000 copies/cell), the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response CC against the inserted epitope, and hybrid fimbriae are easy and CC inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                        27-AUG-2003
25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Escherobacteriaceae for the production of fimbriae comprising recombinant and the production of the product
                                 Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                    Salmonella; AgfA; vaccine; genetic immunization;
                                                                                                                                                        AgfA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ73066 standard; DNA; 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 456 BP; 114 A; 108 C; 123 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGCAGCTATTATCCAGAAAGGTTCTGGAAATAAGGCCAATATTACCCAGT 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATGGCACATGCAGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATATTGAGCAAACGGGCAATGCCAACGATGCCAGTATATCGCAAAGCGCTTACGGTAATA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                       (revised)
                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0127888P
                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34.2; DB Pred. No. 1.8; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
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RESULT 15
AAT74141
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                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                          The DNA encodes the Salmonella enteritis27655-3b TnphoA mutant strain agfA gene cloned into pUC19. The DNA and isolated proteins are used in genetic immunization and vaccine compositions, respectively, to elicit immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1994-358275/44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                             Salmonella enteritidis 27655-3b TnphoA mutant agfA gene fragment.
                                                   25-MAR-2003
30-SEP-1997
                                                                                    AAT74141;
                                                                                                       AAT74141 standard; DNA;
                                                                                                                                                                                                                                                                                            Sequence 361 BP;
                                                                                                                                                                                                                                                                                                                 AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                 strains,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAR62761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kay WW,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9425598-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                              200
                                                                                                                                                                                 332 ATAGTGCAGCTATTATCCAGAAAGGTTCTGGAAATAAGGCCAATATTACCCAGT 385
                                                                                                                                                                                                        140
                                                                                                                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KING
                                                                                                                                                                                                                          CGTATATTGAGCAAACGGGCAATGCCAACGATGCCAGTATATCGCAAAGCGCTTACGGTA 331
                                                                                                                                                             GTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collinson SK,
                                                                                                                                                                                                        CGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATA
                                                                                                                                                                                                                                                                                                                                                                                                                 vector constructs,
                                                                                                                                                                                                                                                                                                                                                                                                                 an immune response to Salmonella - using attenuated Salmonella vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                          Fig 7A; 95pp; English.
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VICTORIA INNOVATION & DEV J.
                                                  (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-IB000207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (292.
                                                                                                                                                                                                                                                                                            94 A; 93 C; 94 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= d
note= "TAF5 primer (pair with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "TAF6 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                omplement (103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "TAF3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 60
                                                                                                                                                                                                                                                          56.1%;
                                                                                                                                                                                                                                                                                                                  တ္ထ
                                                                                                                                                                                                                                                                       7.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "TAF4 primer (pair with TAF3)"
                                                                                                                                                                                                                                                                                                                  field.)
                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clouthier SC,
                                                                                                          ВP
                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                           Score 34; DB 2;
Pred. No. 1.9;
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doran JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with TAF5)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           with TAF4)"
                                                                                                                                                                                                                                                  50;
                                                                                                                                                                                                                                                                       Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAF6) "
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                              253
                                                                                                                                                                                                         199
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Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody;

gb

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Search completed: March 15, 2004, 17:51:43
Job time : 248.684 secs
                                                                                                                                                                                                                                                                                                             Query Match 7.5%; Score 34; DB 2; Best Local Similarity 56.1%; Pred. No. 1.9; Matches 64; Conservative 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents an isolated agfA gene fragment derived from Salmonella enteritidis 27655-3b TnphoA mutant strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-WAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 361 BP; 94 A; 93 C; 94 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-309886/28.
P-PSDB; AAW23569.
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                                                                                                        200 GTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGT 253
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16. .60
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complement(294. .312)
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complement(103. .128)
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Maximum Match 100%
Listing first 45 summaries
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                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-08-956-171E-435
US-08-657-392-1
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US-08-657-392-26
PCT-US94-02539-26
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US-08-233-788A-58
US-09-328-352-2823
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Sequence 26, Appl
Sequence 45, Appl
Sequence 36, Appl
Sequence 1, Appli
Sequence 18033, A
Sequence 18491, A
Sequence 3, Appli
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Sequence 2, Appli
Sequence 313, Ap
Sequence 3386, App
Sequence 408, App
Sequence 435, App
Sequence 435, App
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Sequence 56, Appl
Sequence 58, Appl
Sequence 2823, Ap
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Sequence 26, Appl
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             Query Match
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-10	US-09-620-312D-953 US-09-526-193A-21	-09-886-149-5 -09-886-150-5	-09	US-08-471-770-56 US-08-468-059-56	US-09-268-347-35 US-08-470-202-56	US-09-328-352-3130 US-09-543-681A-934	US-08-956-171E-2326 US-08-956-171E-654	US-09-023-655-1132
18, 18,	Sequence 953, Sequence 21,	0,00	e e 56,	е е 55 56 6	56,	313C	2326	Sequence 1132
Appl Appl	App Appl	App1 App1	Appl Appl	Appl Appl	Appl Appl	, App	App App	Ap

## ALIGNMENTS

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; CLONE: pTZgpt-F1s
US-08-232-463-14
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GENERAL INFORMATION:
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                                                                                                                                                                                                      APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMPLECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                 TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                      TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 52
CORRESSONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                         TELEPHONE: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Alexandria
                                                                                  LENGTH: 7218 Lucid
                                                                               STRANDEDNESS:
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Score 41;

DB 1;

Length 7218;

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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEY 372836 SEDDAMBERRY
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-08-233-788A-56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                    OPEKA411W ...
SOFTWARE: Patentin Release #1.v, ...
CURRENT APPLICATION DATA:
US/08/233,788A
                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DORAI, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Coluthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Seattle
                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 26-APPLICATION: 43
                                                                                                                                                                                                                                                                                                                                                                   STATE: Washington COUNTRY: U.S.A. ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 AAATAAGGCCAATATTACCCAGTACGGTACGCAGAAAACAGCAGTTGTAGTGCAGAAACA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 TGCCAGTATATCGCAAAGCGCTTACGGTAATAGTGCAGCTATTATCCAGAAAGGTTCTGG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 CCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGAAGGAGGAAATAATCGGGCGAA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 TTCATTTAATCAGGCGGCCATTATTGGTCAAGTCGGCACGGATAATAGTGCCAGAGTACG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 GACAAATTATGATCTGGCTCGTTCAGAATATAATTTTGCGGTAAATGAATTAAGCAAGTC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTCGACCAGGCAGGGAATTATAACTTTGCGTATATTGAGCAAACGGGCAATGCCAACGA 302
                                                                                                                                                                                                                                                                                                                                                                                                                  6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423
                                                                                                                                                                                                                                                                                                                                                                                                                                        Seed and Berry
                                                                                                                                                                                                                                     26-APR-1994
N: 435
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                                                                                                                                                                      920043.403C2
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00; Mismatches 150;
                                                                                                                                                                                                                                                                                     Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                        US-08-233-788A-58
                                                                               Query Match
Best Local :
                                                                  Matches
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; LOCATION: 1...3
US-08-233-788A-56
                                                                                                                                                                                                                                                        TELEX: 3723836 SEEDAN INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5635617
GENERAL INFORMATION:
                                                                                                                                      FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 58,
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center,
                                                                                                                                                                                                                                                                           JLECUMINE: (206)
                                                                             Local Similarity
                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: lir
MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                         NAME: King, Joshua
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 26-APR CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.Ā.
ZIP: 98104-7092
272 CGTATATTGAGCAAACGGGCAATGCCAACGATGCCAGTATATCGCAAAGCGCTTACGGTA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 GTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 атадтесадстаттатссадавадсттствдаватавдессавтаттасссадт 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 CGACCÁTTACCCÁGAGCGGTTÁTGGTAÁCGGCGCCGATGTÁGGCCÁGGGTGCGGATAATÁ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 CGTATATTGAGCAAACGGGCAATGCCAACGATGCCAGTATATCGCAAAGCGCTTACGGTA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/08233788A
                                                                                                                                      1..456
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Kay, William W.
Collinson, Karen S.
Clouthier, Sharon C.
VENTION: METHODS AND COMPOSITIONS FOR DETECTION
VENTION: OF SALMONELLA
                                                                                                                                                     CDS
                                                                                                                                                                              linear
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                                                                                                                                                                                                                                                    SEEDANBERRY
ID NO: 58:
                                                                                                                                                                                                                                                                                   682-603
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                                                                       7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%; Score 34; DB 1; 56.1%; Pred. No. 0.091;
                                                                                                                                                                                                                                                                                                                                                                                                          US/08/233,788A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (genomic)
                                                                                                                                                                                                                                                                                                                                      35,570
                                                 Score 34; DB 1; Length 456; Pred. No. 0.1; O; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                         920043.403C2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    701 Fifth Avenue
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ADDRESSEE:

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RESULT 5
US-09-557-884-1/c
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US-09-328-352-2823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA ; ORGANISM: Acinetobacter baumannii US-09-328-352-2823
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2823
LENGTH: 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1990-06-04
NUMBER OF SEQ ID NOS: 8252
             COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION NUMBER: US/09/557,884

PILING DATE: 25-Apr-2000

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
   PRIOR
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human G
                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fleischmann et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 CGCCAGGAAGGATCAAAACTATTGTCCGTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 TCTTCATTTAATCAGGCGGCCATTATTGGTCAAGTCGGCACGGATAATAGTGCCAGAGTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   481 ATATTAAAAAAACTATTAAATCAGTTACATGCTAATAATTATTTCCCTGTCATGGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGAAAAACAAATTGTTATTTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACC
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                                                                                                                                                                                                                                             STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTTTTGATATAGATGCGCCAAATAATTATCAGCAAGTTCTGGATGAAGTTGAAAAAGCA
                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                              STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATA
   APPLICATION DATA:
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                                                                                                                                                                                          20850
                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 113; Indels
                                                                                                                                                                                                                                                                                 Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09643990A Patent No. 6528289
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 106;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 301-309-84
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,429

FILING DATE: 1995-06-07

APPLICATION NUMBER: 08/426,787
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Human G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Robert D. Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187
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                                                                                                                                                                                                                                                               STATE: MD
COUNTRY: U
                                                                                                                                                                                                                                                                                                     CITY: Rockville,
                                                                                                                                                                                                                                                                                                                       STREET: 9410 Key West
                                                                                                                                                                                                                                               ZIP: 20850
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 301-309-8504
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                                                                                                                                                                                                                                                                                                                                       Genome Sciences,
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Pred. No. 25;
                                                                                                                                                                                                                                                                                                                         Avenue
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APPLIANCE
Mark C.
Owen White
Owen White
Owen White
I Craig Venter
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd
Thereof, and Uses Thereof
COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/643,990A

FILING DATE: 23-Aug-2000

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 385654 TTTAAAAGCATAATGGGGCTTGTAAAGCCACAACAAGGCGAAATTAAAC 385606
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                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1323
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                                                                                                                                                                                           Matches
                                                                                                                                                                                                  Query Match 7.0%;
Best Local Similarity 55.3%;
                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1323
LENGTH: 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3-09-134-000C-1323/c
Sequence 1323, Application US/09134000C
PATENT NO. 6617156
GENERAL INFORMATION:
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Best Local Similarity 46.3
                                                                                                                                                                                                                                                                                                                                                                                                                                     AFFLICANT: LYTAN DOUGETTE-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION TELEFAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TORDICOX: 1:50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385654 TTTAAAAGCATAATGGGGCTTGTAAAGCCACAACAAGGCGAAATTAAAC 385606
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                             337
                                                                    277 ATTGAGCAAACGGCAATGCCAACGATGCCAGTATATCGCAAAGCGCTTACGGTAATAGT
                                                                                                                                       83;
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REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB186F1C1
TELEPHONE: 301-610-5790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1995-04-21 ATTORNEY/AGENT INFORMATION:
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GCAGCTATTATCCAGAAAGGTTCTGGAAAT 366
                                                                                                         CAAGAACTACGATAAAAGCCAGTAAAATACTCCCTGGTAGGCCTAAATAGTAATTGGCAA 119
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                                          -GGCAATCCCGCCGTTTTCACTGATTGGAĀĀĀGCCCCGĀTACTCĀTTGT 61
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46.38;
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Pred. No. 0.
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0; Mismatches
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Pred. No. 25;
0; Mismatches 123;
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                                                                                                                                                                             65; Indels
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US-09-643-990A-1

Sequence 1, Application US/09643990A Patent No. 6528289 GENERAL INFORMATION:

APPLICANT: Robert D. Fleischmann Mark D. Adams

White

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Best Local S
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                                                                                                                                                                                                                                                                                                                      TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome,
Thereof, and Uses Thereof
                                                                                                                                               617260
                                                                                                     617200
                                                                        127
                                                                                                                                                                                                                                                                                         TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
                                                                                                                67 AAITATGATCTGGCTCGTTCAGAATATAATTTTGCGGTAAATGAATTAAGCAAGTCTTCA 126
                                                                                                                                                                                                                         11 Similarity
69; Conserv.
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ADDRESSEE: Human Genome Sciences,
                                                                                                                                                                     7 AACAAATTGTTATTTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACCGCGACA
                                      TGGTAATGGGC 617270
                                                                     TTTAATCAGGC 137
                                                                                     AATTACGATACTGCCTTTTTCAAGCAACCATTTGACCGGACGAATTTCAAAAATACGTTT 617259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MD
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 301-309-8504
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OPERATING SYSTEM: MS DOS v6.22
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                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                 Score 31.8;
Pred. No. 3
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US-09-198-452A-1/c

Sequence 1, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffals, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic seq

TITLE OF INVENTION: thereof and uses thereof, in pa

TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24
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                                                                                                                                                                                                                                       RESULT 10
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Best Local Similarity
Matches 69; Conserve
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SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
UMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                  617260
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APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Human G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/643,990A FILING DATE: 23-Aug-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                              TGGTAATGGGC 617270
                                                                                                                                                                                                                                                                                                                                   TTTAATCAGGC 137
                                                                                                                                                                                                                                                                                                                                                                           AATTACGATACTGCCTTTTTCAAGCAACCATTTGACCGGACGAATTTCAAAAATACGTTT 617259
                                                                                                                                                                                                                                                                                                                                                                                                                   AATTATGATCTGGCTCGTTCAGAATATAATTTTGCGGTAAATGAATTAAGCAAGTCTTCA 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 9410 Key West Avenue
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J. Craig Venter
INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
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52.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31.8;
Pred. No. 34;
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LOCATION: (270001)..(285000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc_feature
LOCATION: (28501)..(300000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc_feature
LOCATION: (300001)..(315000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc_feature
LOCATION: (315001)..(315000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc_feature
LOCATION: (315001)..(330000)
OTHER INFORMATION: n=a or c or
NAME/KEY: misc_feature
                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (255001)..(270000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc feature
                                                                                                                                                                                                                                  OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
LOCATION: (240001)..(255000)
OTHER INFORMATION: n=a or c or g
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NAME/KEY: misc feature
LOCATION: (15001)...(30000)
OTHER INFORMATION: n=a or c
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LOCATION: (165001)..(180000)
OTHER INFORMATION: n=a or c
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NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
NAME/KEY: misc_feature
(225001)..(240000)
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NAME/KEY: misc_feature
LOCATION: (150001)..(165000)
OTHER INFORMATION: n=a or c
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NAME/KEY: misc_feature
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LOCATION: (75001)..(90000)
OTHER INFORMATION: n=a or c
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LOCATION: (30001)..
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NAME/KEY: misc feature
LOCATION: (630001)...(645000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (645001)...(660000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (660001)...(675000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (65001)...(675000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (675001)...(690000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (690001)...(705000)
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LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (585001)..(600000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (570001)..(585000)
OTHER_INFORMATION: n=a or c or g
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LOCATION: (540001)..(555000)
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LOCATION: (510001)..(525000)
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LOCATION: (525001
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LOCATION: (495001)..(510000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (480001)..(495000)
OTHER_INFORMATION: n=a or c or g
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LOCATION: (465001)...(480000)
OTHER INFORMATION: n=a or c or g
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RESULT 11
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APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever
FILE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                               Sequence 1, Application US/09198452A
Patent No. 6559294
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LOCATION: (780001)...(795000)
OTHER INFORMATION: n=a or c or g or t
LOCATION: (795001)...(810000)
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LOCATION: (900001)...(915000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
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LOCATION: (720001)..(735000)
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LOCATION: (705001)..(720000)
OTHER INFORMATION: n=a or c
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OTHER IN. (27001). (28500)
LOCATION: (27001). (28500)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature
LOCATION: (28501). (30000)
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WHER INFORMATION: n=a or c or g NME/KEY: misc\_feature OCATION: (180001)..(195000) WTHER INFORMATION: n=a or c OCATION: (105001)..(120000) OTHER INFORMATION: n=a or c JAME/KEY: misc JOCATION: (150) AME/KEY: misc feature OCATION: (25501)..(270000) WIHER INFORMATION: n=a or c or g AME/KEY: misc\_feature OCATION: (16501)..(180000) THER INFORMATION: n=a or c or g AME/KEY: misc\_feature OCATION: (135001)..(150000) THER INFORMATION: nea or c or g OCATION: (7500) WE/KEY: misc\_feature )CATION: (330001)..(345000) [HER INFORMATION: n=a or c or g or AME/KEY: misc\_feature OCATION: (240001)..(255000) AME/KEY: miec CHER INFORMATION: n=a or c or g HER INFORMATION: n=a or c or g CATION: (225001)..(240000)
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LOCATION: (495001)..(510000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc feature NAME/KEY: misc feature LOCATION: (480001)..(495000) OTHER INFORMATION: n=a or c NAME/KEY: misc fea LOCATION: (660001)..(675000)
OTHER INFORMATION: n=a or c NAME/KEY: misc\_feature
LOCATION: (510001)..(525000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc\_feature LOCATION: (405001)..(420000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc\_feature VAME/KEY: misc feature LOCATION: (55501)...(57000) DOTHER INFORMATION: n=a or c LOCATION: (525001)..(540000)
OTHER INFORMATION: n=a or c
NAME/KEY: misc\_feature NAME/KEY: misc LOCATION: (3750 VAME/KEY: misc\_featu .OCATION: (570001).. OTHER INFORMATION: n=a or c NAME/KEY: misc OCATION: (375001)..(390000)

THER INFORMATION: n=a or c THER INFORMATION: n=a or c INFORMATION: n=a or c or g or t Eeature :eature eature eature (585000) or g or g

OTHER INFORMATION: n=a or c or g NAME/KEY: misc\_feature LOCATION: (360001)..(375000) OTHER INFORMATION: n=a or c or g (390001) . (405000) RMATION: n=a or c b zo or g or g or or g or or t or t or t or t

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LOCATION: (465001)...(480000)

OTHER INFORMATION: n=a or c or g or t

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COCATION: (540001)..(555000)

THER INFORMATION: n=a or c or g or t

NAME/KEY: misc feature or g or

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NAME/KEY: misc feature LOCATION: (720001)..(735000) OTHER INFORMATION: n=a or c

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US-09-621-976-2813
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                                        SOFTWARE: Patent.pm
SEQ ID NO 2813
LENGTH: 832
                                                                                                                                                                                                           GENERAL INFORMATION:
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Best Local Similarity 56.3%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                  CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                            APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                           Sequence 2813, Application US/09621976
Patent No. 6639063
                                                                                                                                                                            APPLICANT: Dumas Milne Edwards, J.B
FEATURE:
           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or
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OTHER INFORMATION: n=a or c
NAME/KEY: misc feature
(870000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: n=a or c or g or
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LOCATION: (855001)..(870000)
DTHER INFORMATION: n=a or c or g
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OTHER INFORMATION: n=a or c or g
NAME/KEY: misc_feature
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LOCATION: (870001)..(8)
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OTHER INFORMATION: n=a or c
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OTHER INFORMATION: n=a or c or
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                                                                                                                                                                                                                                                                                                                                                                       1044632 TGATCAGAAGAAATGCAGGCAGTGAGGTAAATATGAATCGTAGAGACATGGTAATAACAG 1044691
                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                    344 ТТАТССАБАЛАССТТСТББАЛАТАЛББСССАДТАТТАСССАБТАСББТАСБСАБАЛАДСАБ
                                                                                                                                                                                                                                                                                                             CTGTCGTAGTGAATGCTATATTGCTTGTGGCTCTTTTCGTCAC 1044734
                                                                                                                                                                                                                                                                                                                                            CAGTTGTAGTGCAGAAACAGTCGCATATGGCTATTCGCGTCAC 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          feature
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US-09-543-681A-408/c
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-3386
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US-09-328-352-3386/c
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; LOCATION: 235..399
US-09-621-976-2813
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                SEQ ID NO 408
                                                                                                                                                                                                             Patent No. 6605709
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 3386
LENGTH: 1350
                                                                                                                                                                                                                                           Sequence 408, Application US/09543681A Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3386, Application US/09328352
Patent No. 6562958
                                                  APPLICANT: GARY BRETON

ITTLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR PILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 65.2%;
                                      NUMBER OF
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Best Local !
ENGTH: 1053
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                                                                                                                                                                                                                                                                                                                                                                                                                                    586 TATATGAAAAAGCTGTTTGTGAGCTAATGCCAGTATTTTCCATTAAGCTTCGGAAAATAA 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 ТАТАТСЭСАЛАЭСЭСТТАСЭТЛАТАӨТЭСАЭСТАТТАТССЛЭЛАЛАЭСЭТТСТЭЭЛАДТЛА 368
                                                                                                                                                                                                                                                                                                                                                                                                  369 СССАЛТАТ 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 YYWAATRYWWMMCWTKRWRASWWYCWWWGKARKWSTWRKSRSYASARSAKRCCYSCSWGA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 AATCAGGCGGCCATTATTGGTCAAGTCGGCACGGATAATAGTGCCAGAGTACGCCAGGAA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 MSWKYMWRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 AAATTGTTATTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACCGCGACAAAT 69
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21; Conserv
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                                      ID NOS: 8344
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11.1%; Pred. No. 1.9;
ative 92; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30.6; DB Pred. No. 2.5; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
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RESULT 15
US-08-956-171E-435
US-08-956-171E-435
; Sequence 435, Application
; Patent No. 6593114
; GENERAL INFORMATION:
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                                                                                                                                                      LENGTH: 1072 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 435:
US-08-956-171E-435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               용
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US-09-543-681A-408
                                                                          Query Match 6.6%;
Best Local Similarity 49.3%;
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.6%;
Best Local Similarity 62.7%;
Matches 47; Conservative
                                                                                                                                                                                                                                                                               TELEPHONE: (240) 314-122
TELEPAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 435:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Charles Kunsch
Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 CAGTACGGTACGCAG 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322 GCTTACGGTAATAGTGCAGCTATTATCCAGAAAGGTTCTGGAAATAAGGCCAATATTACC
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TTTTGGTAARGGAGAAAWTCAATATGAAACAGTATAARGCGTATTTAATCGATTTAGATG 65
                           TTGCGGTAAATGAATTAAGCAAGTCTTCATTTAATCAGGCGGCCATTATTGGTCAAGTCG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08956171E
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Craig A. Rosen
                                                                                                                                                                                                                                                                                                                                              (240) 314-1224
                                                                          Score 30.2; DB 4;
Pred. No. 3;
3; Mismatches 67;
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                                                                            67;
                                                                                                                  Length 1072;
                                                                            Indels
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Search completed: March 16, 2004, 04:36:29 Job time: 62.6647 secs

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Minimum
Maximum
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                   Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB BG
                                                                                                                                                                                                                                                                                                                                 Score
            seg length: 0
seg length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                 Match
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Maximum Match 100%
Listing first 45 summaries
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                                                  Length DB
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18540
18540
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12
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9
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12 US-10-231-416-3

14 US-10-231-426-3

15 US-10-027-632-241642

9 US-09-820-905-3

15 US-10-027-632-206661

US-10-027-632-206662

15 US-10-027-632-206663

15 US-10-027-632-206663

15 US-10-429-433-233

12 US-10-425-114-3093

15 US-10-425-114-3093
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Sequence 3, Appli
Sequence 3, Appli
Sequence 241642,
Sequence 206661,
Sequence 206663,
Sequence 20333, A
Sequence 20333, A
Sequence 20333, A
Sequence 18, Appl
Sequence 1500, Ap
Sequence 4167, Ap
Sequence 8045, Ap
Sequence 8045, Ap
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## ALIGNMENTS

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PRIOR APPLICATION NUMBER: PCT/AU01/01021
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 738
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: CDS
LCCATION: (1)...(738)
US-10-369-435-3
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US-10-369-435-3
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Publication No. US20040002440A1
GENERAL INFORMATION:
APPLICANT: Mathews, Sarah
APPLICANT: Timms, Peter
TITLE OF INVENTION: No. US20040002440A1el Diagnostic Agents and Uses Therefor FILE REFERENCE: 10338-15US (2615070/VPA)
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: AU PQ9540/00
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 2000-08-18
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Best Local
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Local Similarity 57.9%;
es 62; Conservative
                                        400 ACAGCAGTTGTAGTGCAGAAACAGTCGCATATGGCTATTCGCGTCAC 446
                                                                                                                 340 GCTATTATCCAGAAAGGTTCTGGAAATAAGGCCAATATTACCCAGTACGGTACGCAGAAA 399
ACAGCTGTCGTAGTGAATGCTATATTGCTTGTGGCTCTTTTCGTCAC
                                                                                    GCTGTTGATCAGAGAAATGCAGGCAGTGAGGTAAATATGAATCGTAGAGACATGGTAATA 60
                                                                                                                                                                     0,
                                                                                                                                                                   Score 35; DB 15; I
Pred. No. 1.9;
0; Mismatches 45;
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US-10-231-416-3/c

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Publication No. US20040043610A1

GENERAL INFORMATION:
APPLICANT: Bodian, Dale L.
APPLICANT: Hodian, Dale L.
APPLICANT: Mickanin, Craig S.
ITILE OF INVENTION: Tumor Necrosis Factor Related Protein-1
FILLE REFERENCE: 4-32139A
CURRENT APPLICATION NUMBER: US/10/231,416
CURRENT APPLICATION NUMBER: US/10/231,416
PRIOR APPLICATION NUMBER: 60/317,151
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                  US-10-231-426-3
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Matches
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PRIOR FILING DATE: 2002-09-05
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10231426
Publication No. US20030059889A1
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bodian, Dale L.
APPLICANT: Labow, Mark
APPLICANT: Mickanin, Craig S.
TITLE OF INVENTION: Tumor Necrosis Factor Related Protein-1
TITLE OF INVENTION: Gene and Protein
                                                                                                                                                                                       LENGTH: 18540
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/231,426
CURRENT FILING DATE: 2002-08-28
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Matches
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                                                                                                             Local Similarity 52.0 nes 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 18540
                                5513 CAGATGGTAATTAATTAAAATTAAAATGACAGAAATTTTAAAAAATTCACTGGATGGGCTTA 5454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 52.0 ses 77; Conservative
5393
                                                             86 ÇAĞAATATAATTITĞCGGTAAATGAATTAAĞCAAĞTCTTCATTTAATÇAĞĞCĞĞCCATTA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5453 GTAGTAGÁGAAGAGÁCAGATGÁTAGAATCÁGTGAÁCTTGÁGGÁCAGAACÁACAGAATTTA 5394
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                                                                                                                           7.5%;
52.0%;
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                                                                                                      0;
                                                                                                      Score 34.4; DB Pred. No. 16; 0; Mismatches
                                                                                                                                    DB 14;
                                                                                                        71;
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                                                                                                                                  Length 18540;
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; TYPE: DNA;
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(529)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-241642
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US-09-820-905-3/c
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  Sequence 3, Application US/09820905
Patent No. US20020142938A1
GENERAL INFORMATION:
APPLICANT: Yan, Chunhua
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001199
FILE REFERENCE: CL001199
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2002-04-30
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,358
PRIOR PILING DATE: 1999-09-128
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 241642
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US-10-027-632-241642
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
APPLICATION NUMBER: US/09/820,905
                                                                                                                                                                                                                                                                                      252 AG 253
                                                                                                                                                                                                                                                                                                                                                                             192
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                                                                                                                                                                                                                                                                                                                                                                                                                                      132 feárfégéctóketjágaagterregatatgáckéggáárgégagtágttckéttógkégátag
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                                                                                                                                                                                                                                                                                                                                                    ATCAATRARACTTRCCCATCTTGARCRACAGGGAGRARATRGACTGARRARARARGAGCR
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Pred. No. 3.4;
0; Mismatches 55; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      191
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SEQ ID NO 3

CURRENT FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0

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LENGTH: 203654
; TYPE: DNA
; ORGANISM: HUMAN
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(203654)
; OTHER INFORMATION: n = A,T,C or G
US-09-820-905-3
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                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-206661
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Best Local
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Best Local Similarity 50.3%;
Matches 83; Conservative
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Publication No. US20030204075A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Sing
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-08-09
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                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2000-04-20
APPLICATION NUMBER: US 60/193,483
FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
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                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1999-09-28
APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/156,358
260 ATTATAACTTTGCGTATATTGAGCAAACGGGCCAATGCCCAGTGCCAGTATATCGCAAA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION
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                                                                                         TATTATTCTTTAATTCATAGAGATCTTGTAAGAATTAGCCTAAAACAATTAAGATACATT 504
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                                                                                                                               Conservative
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51.7%;
                                                                                                                         Score 33.4; DE Pred. No. 5.5; 0; Mismatches
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Pred. No. 86
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US-10-027-632-206663/c
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US-10-027-632-206662/c
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
                                                                                                                                          APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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PRIOR FILLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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Local Similarity 51.7%;
es 76; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                   443
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Pred. No. 5.5;
0; Mismatches
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APPLICATION NUMBER: US 60/193,483

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RESULT 10
US-10-449-857A-18
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Coldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN FILL OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN FILL REFERENCE: 38-10(52052)8 MITH IMPROVED PROPERTIES CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                           ; LENGTH: 660
TYPE: DNA
; ORGANIZM: Caenorhabditis elegans
US-10-369-493-29323
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US-10-369-493-29323/c
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
PRIOR PILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTMARE: PASTSEQ for Windows Version 4.0
EENGTH: 598
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 29323
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US-10-027-632-206663
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Publication No. US20030233675A1
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Best Local S
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                                                                               310 ATATCGCAAAGCGCTTACGGTAATAGTGCAGCTATTATCCAGAAAGGTTTCTGGAA 364
                                                                                                                   339 CÁATCCGGCAÁTTTGCCGATTTGCCAGATTTGCCGAÁCAGCAÁTTGCCGCCCTTTCCTGA
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APPLICATION NUMBER: US 60/185,218
FILING DATE: 2000-02-24
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                                                  ATTATTTAGTGCATCTÁCAGTÁATATCTTÁTAGÁGTÁTCCÁTÁCÁGGCTCTGGÁÁ 225
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                                                                                                                                                                                           7.3%; Score 33.4; Di
55.7%; Pred. No. 5.8;
vative 0; Mismatches
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Pred. No. 5.5;
0; Mismatches
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Best Local :
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LENGTH: 1444
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David
APPLICANT: Screen, Steven
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                                                                                                                                                                                                                                                       APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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APPLICANT: Cao,
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CURRENT FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 89
SOFTWARE: Corixa Invention Disclosure Database
LENGTH: 535
                                                                                                                                                                                     ORGANISM: Zea mays FEATURE:
                                                                                                                                                                                                                   TYPE: DNA
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Publication No. US20040043931A1
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF INFLAMMATORY BOWEL DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hosken, Nancy A.
APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
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                                207 CCATGGAGTTGATAATCACCCACCTTACGTCAAGAAACAAGTGGTGGAAAAGTTTCCCTG 266
                                                                                   1 Similarity 65; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 ACCAGGCAGGGAATTATAACTTTGCGTATATTGAGCAAACGGGCAATGCCAACGATGCCA 307
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                                                                                                                                                                                                                                                                                                                                                            Zhou, Yinua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
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77; Conserv
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                                                                                Conservative
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                                                                                            7.3%;
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                                                                        ; Score 33.2; DE
; Pred. No. 10;
0; Mismatches
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Pred. No. 6;
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                                                                                                       DB 12;
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                                                                        53;
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                                                                                                   Length 1444;
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                                                                   Gaps
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309 TATATCGCAAAGCGCTTACGGTAATAGTGCAGCTATTATCCAGAAAGGTTCTGGAAAT 366

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267 CTCAGCGTACAGTGCTCCCTGTTCTAGTGAAGATAATTTCCAGGAAGCTTGTGCAATT 324

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US-09-815-242-4167

; Sequence 4167, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
                                                                                                                                                         RESULT 13
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; ORGANISM: Homo sapiens
US-10-094-749-1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 3381
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1500
LENGTH: 2649
TYPE: DAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.2%;
Best Local Similarity 48.4%;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVESTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                               328 GGTAATAGTGCAGCTATTATCCAGAAAGGTTCTGGAAATAAGGCCAATATTACCCAGTAC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                        91,
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                                                                                                                                                                                                                                                                            AATACTGGCCCTGGGAAAATCCAGAAAATACCCAGAGAAAATGCATACCTAACCAAGGAC 986
                                                                                                                                                                                                                                                                                                                                                  CTGGTTGCTGTGGATGAGTCTGTTCATACCCTGGAAGACATAGTCAAGTGTATCAGTAAA 926
                                                                                                                                                                                                                                                                                                                                                                                 TTTGCGTATATTGAGCAAACGGCCAATGCCAACGATGCCAGTATATCGCAAAGCGCTTAC 327
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TAMECHIKA, ICHIRO
SEKI NAOHIKO
YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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OTSUKI, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
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NAGAI, KEIICHI
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KAMAMOTO, JUN-ICHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32.8;
Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Staphylococcus aureus US-09-815-242-4167
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 4167
LENGTH: 1914
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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APPLICANT:
APPLICANT:
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TYPE: DNA
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
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CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
1121 CTATTGCTAATCAACAAAAAGCACTT 1146
                                                                                                                                                           1001 AAAATTTAGAAATTGGTTATCAAACTGCAATTACCAAACCTATCAGTATAGAGGTCTCTA 1060
                                                                                                                                                                                                    263 ATAACTTTGCGTATATTGAGCAAACGGGCAATGCCAACGATGCCAGTATATCGCAAAGCG 322
                                                                            CTTACGGTAATAGTGCAGCTATTATCCAGAAAAGGTTCTGGAAATAAAGGCCAATATTACCC 382
                                    AGTACGGTACGCAGAAAACAGCAGTT 408
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51.4%;
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Pred. No. 2:
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US-09-815-242-8045

Sequence 8045, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Trawick, John D.

APPLICANT: Trawick, John D.

APPLICANT: Yamamoto, Robert T.

APPLICANTION: John J.

FORKERY TORENTION: John J.

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/242,578
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PRIOR APPLICATION NUMBER: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: PC 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: Patentin version 3.0
SEQ ID NO 10
LENGTH: 1163020
TYPE: DNA
ORGANATOR:
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                                                                                                                                                                                                                                                                                                   ; ORGANISM: Listeria innocua ; FEBATURE; FEBATURE; ; NAME/KEY: misc feature ; LOCATION: (1). (end) ; OTHER INFORMATION: n can be any nucleotide: a, g, c US-10-398-221-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-10-398-221-10
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                                                                                                                                                                                     Query Match 7.1%; Score 32.2; DB 15; Length 1163020; Best Local Similarity 49.8%; Pred. No. 6.1e+02; Matches 108; Conservative 0; Mismatches 108; Indels 1; Gr
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; LOCATION: (1)...(1929)
US-09-815-242-8045
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Publication No. US20040018514A1
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR TILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF 55Q ID NOS: 14110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INTENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.1%; Score 32.4; DB 9; Length 1929; Best Local Similarity 51.4%; Pred. No. 21; Matches 75; Conservative 0; Mismatches 71; Indels 0; Gaps
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1136709 ATATTGAAGTAACGGGGTGATTGTAAAATGAAGATAGATGTCAGAGAATTAAATGAGATA 1136768
                                                                                        1136649 CACAAGACATAGAGAAGTTGTGCTGAATTCGTTAACTTAGATAAAAATCTTATTAACTG 1136708
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TYPE: DNA
ORGANISM: Staphylococcus aureus
FEATURE:
                                              275 ATATTGAGCAAACGGGCAATGCCAACGATGCCAGTATATCGCAAAGCGCTTACGGTAATA 334
                                                                                                                            1121 CTATTĠCTAATCAACAAAAĠĊACTT 1146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1001 AAAATTTAGAAATTGGTTATCAAACTGCAATTACCAAACCTATCAGTATAGAAGTCTCTA 1060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 CTTACGGTAATAGTGCAGCTATTATCCAGAAAGGTTCTGGAAATAAGGCCAATATTACCC 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 ATAACTTTGCGTATATTGAGCAAACGGGCAATGCCAACGATGCCAGTATATCGCAAAGCG 322
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335 GTGCAGCTATTATCCAGAAAGGTTCTGGAAATAATAAGGCCAATATTAACCCAGTACGC 394

Db 1136769 GT-TAGCGAGAATATAAGTAATGCTTAAAGAAATTTAAAATATAGCAATGAA 1136827

QY

395 AGAAAACAGCAGTTGTAGTGAAAACAGTCGCATAT 431

Db 1136828 CGCTACAACTTCACAGTAGAAACTCAGGAAATTT 1136864
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Search completed: March 17, 2004, 08:15:08 Job time: 410.736 secs

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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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   AI368352
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BJ618688
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 BI941542 dg26g06.y
AI368352 SWOvMfCAR
AL068795 Drosophil
BJ618688 BJ618688
                                                 Description
                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                           SOURCE
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VERSION
KEYWORDS
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BI941542
                                                  COMMENT
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E 1 (bases 1 to 220)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L.,
Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y.,
Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
Unpublished (1999)
Unpublished (1999)
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
WashIngton University School of Medicine
4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                              BI941542
BI941542.1 GI:16256014
EST.
                                                                                                                                                                                                         B1941542 220 bp mRNA linear EST 19-FEB-2003 dg26g66.yl Xenopus laevis gastrula non normalized Xenopus laevis cDNA clone IMAGE:3749963 5' similar to SW:CSGB_ECOLI P39828 MINOR CURLIN SUBUNIT PRECURSOR. ;, mRNA sequence.
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                           Xenopus laevis
                                                                                                                                                                    Xenopus laevis (African clawed frog)
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CC299970
CF238215
AW043435
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BP007561
AV896333
BU213938
CC310289
BU387712
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BU582719
BQ625251
BZ280200
                                                                                                                                                                                                                                                                                                                                                                                                                               CA856583
AQ055856
BM273661
BQ451444
CB389390
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BZ110007
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BJ481788
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CC211905
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CC310289 TAM32-32B
BU387712 603857374
AZ529672 ENTBM10TR
CC2211905 CH261-186
BH528896 BOGP061TR
BG226083 KQ0Bh12.y
BZ229556 CH2310-353
BH505143 BOGBM31TF
AL259887 Tetraodon
BH159159 ENTRB03TR
AM140314 SWAMCAC45
BZ756658 PUFBM68TD
BJ481788 BJ481788
CCB10770 AGENCOURT
BG548059 602575980
BX406892 BX406892
BK581316 KQ49-03.y
BH943841 odf17b10.
BW245005 BW245005
                                                                                                                                                                                                                                                                                                                  CA856583 PÉESTOBC1
AQ055856 CIT-HSP-2
BM273661 PÉESTOBA5
BQ451444 PÉESTOBA5
BQ451444 PÉESTOBA5
CB389390 OSTF116E9
BJ110432 BJ104432
BZ110007 CH230-164
AL057531 Drosophil
BUS82719 rd26b04.y
BQ625251 rd26b04.y
BQ625251 rd26b04.y
BZ280200 CH230-297
BM012028 603636451
AL549572 AL549572
CC299970 CH261-89H
CF238215 AGENCOURT
AW043435 SWAMCAC37
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AZ578608 25d10 Sho
BP007561 BP007561
AV896333 AV896333
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AI368352/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140
Genes expressed in microfilaria
Unpublished (1999)
Contact: Steven A. Williams
                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea; Onchocercidae; Onchocerca.

1 (bases 1 to 207)
                                                                                                                                                    Onchocerca volvulus
                                                                                                                                                                                                                                                                  Al368352
SWOVMFCAR04G09SK Onchocerca volvulus microfilaria cDNA
(SAW98MLW-OVMf) Onchocerca volvulus cDNA clone SWOVMfCAR04G09 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 CCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTACTGCAGGGAGGCTCAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90
                                                                                                                                                                                                               AI368352
AI368352.1 GI:4147105
                                                                                                                                                                              Onchocerca volvulus
                                                                                                                                                                                                                                                                mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTATAACTTTGCGTATATTGAGCAAACGGGCAATGC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Source lab clone id - 3749963
Trace considered overall poor quality This clone is available
royalty-free through LLNL; contact the IMAGE Consortium
(image@image.llnl.gov) for further information.
Seq primer: -40RP from Gibco
High quality sequence cross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTGGCGGTTGCTGCGCAAGAAGGTAGTAGCAACCGGGCAAAGATTGACCAGACAGGAG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCGTTCAGAATATAATTTTGCGGTAAATGAATTAAGCAAGTCTTCATTTAATCAGGCG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTAATTCĀTĀĀTĀĀĀĒTCGCGGCĀCĀTGĀĀTCGĀGTĀĀĠTCTTCĀTTTĀĀTCĀGGCĀG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="gastrula" (stages 10.5, 11.5 mixed)"
/lab host="Trop-10 F'"
/lab host="Trop-10 F'"
/clone lib="Xenopus laevis gastrula non normalized"
/clone lib="Xenopus laevis gastrula non normalized"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
KhoI; cDNA was prepared from 2 ug of poly A+ RNA (equal parts from stage 10.5 and stage 11.5 gastrulae).
EcoRI-XhoI cut cDNA was then ligated into UniZap-XR (Strategene) with EcoRI at the 5' end and XhoI at the 3' end. The library was mass excised and used to infect Top10F'. Clones were picked into freezing medium (per 11 ter 15 g tryptone, 10g yeast extract, 5g NaCl, 36 mM (X2HO04, 13 2 mM KH2PO4, 1.7 mM Na-citrate, 0.4 mM MgS04 7 hours. Original library construction by Bruce Blumberg (Cho et al 1991 Cell 67, 1111-1120)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:3749963"
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Pred. No. 5.2e-30;
0; Mismatches 53
                                  of Onchocerca volvulus
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CNS00E93
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Best Local :
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AL Submitted (02-7UN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de JOng's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was Constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 G 61
                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence TET3 end of BAC # fly), genomic survey sequence. Sequence (fruit RLOS6795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATGAĀĀĀCĊNĀĀTĪGĪCĀĪTĪĀĪGĀĪGĪTĀĀCĀĀĪĀCĪGGGĪGGGCGCGĪGGĀTĪGCĀGCC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGAAAAACAAATTGTTATTTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL068795.1
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Tel: 4135853826
Fax: 4135853786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: pBluescript SK.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Filarial nematode parasite of humans. mRNA was prepared from approximately 200,000 microfilariae isolated from the skin of infected individuals from Kumba, Cameroon and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA poll. The library has 7.8 x 10E4 independent
                                                                                                                                                                                                                                                                                                                                                                                                                                       Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinants and the average insert size is approximately lkb. The library was constructed by Michelle Lizotte-Waniewski. The library is available from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email:genome@smith.edu."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:4949039
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|mol_type="mRNA"
|db_xref="taxon:6282"
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/lab_host="XL1-Blue MRF'"
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91.8%;
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Pred. No. 1.4e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      680 bp mRNA linear EST
BJ618688 NIBB Mochii normalized Xenopus early gastrula
Xenopus laevis cDNA clone XL186b22 5', mRNA sequence.
BJ618688
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                                                                                                                                                                                                                                                                                               Expressed genes in X. laevis embryo Unpublished (2001) Contact: Tadasu Shin-i
                                                                                                                                                                                         National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
Tel: 81-559-81-6855
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                               http://xenopus.nibb.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                               Center For Genetic Resource Information
                                                                                                                                                                                                                                                                                                                                                                                       Kitayama, A., Terasaka, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSTAAWTTKGSCCKAWCCCCTTTTTTTTTTTTTTTTTTKGGVGGGAAWWTTTKKTTKGTTTT
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                                                                                                                                                tshini@genes.nig.ac.jp
formation of this clone
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/mol type="genomic DNA"
/mb xref="taxon:7227"
/clone="BARR28G06"
/clone lib="RPCI-98"
/note="end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                       Mochii, M.,
                                                                                                                                                     16
                                                                                                                                                available through the following
                                                                                                                                                                                                                                                                                                                                                                                          Ueno, N.,
                                                                                                                                                                                                                                       Japan
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AI664697
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                                                                157
217
                                                                                               305
                                                                                                                                                                 245
                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Delgado Alberto
Departamento de Biologia Molecular, Lab 303
Instituto de Parasitologia y Biomedicina
Consejo Superior de Investigaciones Cientificas C/ Ventanilla |
11, E-18001, Granada, Spain
Tel: 34 958 805058
Fax: 34 958 203323
Seg primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.

1 (bases 1 to 775)
Gonzalez Rey,E., Remisz,E., Delgado Garcia,A. and Gonzal
Characterization of ESTs from Trypanosoma cruzi epimasti-
Unpublished (1998)
                                                                                                                                                                                              70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TENG0665 T. Cruzi epimastigote cruzi cDNA clone n1059.r 5', ml A1664697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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                             <u>۲</u>
AT 218
                                                                CCTGTAGATCCAACACTGTCGTCGGTGCGACCTCAGTCATTACACACGAAGCTGGTGGAA
                                                                                             CCAGTATATCGCAAAGCGCTTACGGTAATAGTGCAGCTATTATCCAGAAAGGTTCTGGAA 364
                                                                                                                                TCGCAGTGGCAGCGAATTCGAGATTTGCATTCTGGGAGAAACACGGTCATGCCGTCTGTT
                                                                                                                                                             TCGACCAGGCAGGAATTATAACTTTGCGTATATTGAGCAAACGGGCAATGCCAACGATG 304
                               366
                                                                                                                                                                                                                                                                                                                                                                                                                                                 quality sequence stop:
Location/Qualifiers
1. .775
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                            /cell_type="epimastigote"
/clone lib="T. Cruzi epimastigote normalised cDNA Library."
/notce="Site_1: EcoRI; Site_2: NotI; cDNA library
constructed_with oligo dt primed epimastigote mRNA and
cloned in pt7t318D phagemid with modified polylinker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="XL186b22"
/tissue_type="whole embryo"
/dev_stage="stage 10.5"
/clone_11b="NIBB Mochii normalized Xenopus early gastrula
                                                                                                                                                                                                                                                                                                                                                                                               organism="Trypanosoma
/mol_type="mRNA"
/strain="Cl - Brenner"
                                                                                                                                                                                                                                                                                                                                                                 clone="n1059.r"
                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:5693"
                                                                                                                                                                                                              8.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:4775685
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Pred. No. 0.69;
0; Mismatches
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                                                                                                                                                                                                              Score 38.8; DB
Pred. No. 0.84;
                                                                                                                                                                                                Mismatches
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DNA Library Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Gonzalez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epimastigotes
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                                                                                                                                                                                                                                                                                                                                                                                178
                                                                                                                                                                                                                                                                                                                                                                                           264 TAĄCTTTGCGTATĄTTGAGCĄAĄCGGGCĄATGCCĄACGATGCCAGTĄTAŢCGCĄAAGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                        238 GTCCGTGTCTGTTCAGGAAGGCAAGGGCAATATCTCCGGAACGGCGCAGTTCGGAAAGGA 179
                                                                                                                                                                                                                                                             58
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 675)
Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
                                                                     Ciona intestinalis
Ciona intestinalis
                                                                                                                       BP007561 Nori Satoh unpublished cDNA library, young adult Ciona intestinalis cDNA clone ciad45a18 5', mRNA sequence.
                                                                                                          BP007561.1 GI:19499038 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Virginie Viprey
Laboratoire de Biologie Moleculaire des
University of Geneva
1 Chemin de 1'Imperatrice, Chambesy/Gene
Tel: +44(0)1603450000
Fax: +44(0)1603450045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viprey, V., Rosenthal, A., Broughton, W.J. and Perret, X. Genetic snapshots of the Rhizobium species NGR234 genome Biol. 1 (6), RESEARCH0014 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhizobium sp. NGR234
Rhizobium sp. NGR234
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
                                                                                                                                                                                                                                                                                    GTACGGTACG 393
                                                                                                                                                                                                                                                                                                                              TTACGGTAATAGTGCAGCTATTATCCAGAAAAGGTTCTGGAAATAAGGCCAATATTACCCA 383
                                                                                                                                                                                                                                                                                                                                                              ccácaagácáarcácccrácáááaagácácáagracáácácirteggácácgirecágrregg 119
                                                                                                                                                                                                                                                        GGACTGATCG
                                                                                                                                                                                                                                                                                                     TTACGGCAACAAATCGCTGACCCACCAGGACGGAGAAGGAAATCTCTCCATCACAGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ578608 288 bp DNA linear GSS 08-DEC-2000 Shot-gun genomic library of Rhizobium strain ANU265 Rhizobium sp. NGR234 genomic clone 25d10, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: M13; derivative strain of NGR234 cured of pNGR234a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Shot-gun genomic library of Rhizobium strainANU265"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rhizobium sp.
/mol_type="genomic DNA"
/strain="ANU265"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:394"
/clone="25d10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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                                                                                                                                                                                                                                                   Ciona intestinalis
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata;
Phlebobranchia; Cionidae; Ciona
1 (bases 1 to 715)
1 (bases 1 to 715)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289
                                                                                                                             Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                257 AATACTTTCAATGAAAAAGAAATGTCAGAAACTAAAACCTGTACTGAAACAGAGAAAAA 316
                                                                                                                                                                                          Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                Satoh, N., Satou, Y., Kohara, Y. and Shir
Expressed genes in Ciona intestinalis
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                        AV896333 Nori Satoh unpublished cDNA library, young a intestinalis cDNA clone rciad45a18 3', mRNA sequence AV896333
                                                                                                                                                                                                                                                                                                                                                     AV896333.1 GI:16885431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502,
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expressed genes in Ciona intestinalis Unpublished (2000) Contact: Nori Satoh Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAGT 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CĂAĂTĂATŤTĊTĠĊĂĂĂŤĂÁTĠAĊĂĂŤTŤCCAGĊĀĠAĂTĠAŤĂACGĀĊĀCTĀĊĀCĊĀĠAŤ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCAATGCCAACGATGCCAGTATATCGCAAAGCGCTTACGGTAATAGTGCAGCTATTATC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            satoh@ascidian.zool.kyoto-u.ac.
Location/Qualifiers
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/clone="rciad45a18"
/tissue_type="whole animal"
/dev_stage="young adult"
                                           /organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="whole animal"
/dev_stage="young adult"
/clone_lib="Nori Satoh unpublished cDNA library, young
adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="ciona intestinalis"
/mol_type="mRNA"
/db xref="texon:7719"
/clone="ciad45a18"
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                                                                                                                                                                                                                                               Kohara, Y. and Shin-i, T
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Pred. No. 1.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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BU213938
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 AATAATCGGGCGAAAGTCGACCAGGCAGGGAATTATAACTTTGCGTATATTGAGCAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae; Gallus.

1 (bases 1 to 601)

2 (bases 1 to 601)

3 (bases 1 to 601)

4 (bases 1 to 601)

5 (bases 1 to 601)

6 (bases 1 to 601)

7 (bases 1 to 601)

8 (bases 1 to 601)

8 (bases 1 to 601)

9 (bases 1 to 601)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Biomolecular Sciences
University of Manchester Institute of Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BU213938.1 GI:25389321
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Similarity 50.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Box 88, Manchester, M60 1QD, UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simon. Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                            /organism="Gallus gallus"
/mol_type="mRNA"
/strain="white Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChES751922"
/tissue_type="whole embryo"
/dev_stage="20-21"
/lab_host="HH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436
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/Clone lib="CSEQCHN04"
/Clone lib="CSEQCHN04"
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
Site_1: EcoRI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo (dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Nori Satoh unpublished cDNA library, young
adult"
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Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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ORGANISM
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VERSION
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                                                                                                            ORIGIN
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                                       Best Loc
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Best Local
                                       Local Sin hes 113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292 CAGTCTTCTTCTGGATGGACGTAATATTAAAGTGAAGGGCTATGAGAACGGCAATTCTGA 351
       71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: EC1 TACGACTCACTATAGGGCCCClass: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Sequencing Center
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasiani Phasianine; Gallus.

1 (bases 1 to 1214)

1 (bases 1 to 1214)

1 (Kremttzki, C., Higginbottham, J., Wylie, K., Carter, J., Warren, W., Graves, T., Mardis, E. and Wilson, R. Galus gallus BAC End Reads.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC310289.1 GI:30703437
GSS.
Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genomic survey sequence CC310289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAM32-32B18_EC1.1 TAM32
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                                                                                                                                                                                                                                                                                                                                                                                                                        Email: submissions@watson.wustl.edu
Insert Length: 152000 Std Error: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                      Insert Length: 152000
                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTCCCCAAGCCAAGGAAAGGGTTTGCCACCTGATTCAGAAAGGAGTAGAAGAAGGTGC
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     ATGATCTGGCTCGTTCAGAATATAATTTTGCGGTAAATGAATTAAGCAAGTCTTCATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAATATAATTTTGCGGTAAATGAATTAAGCAAGTCTTCATTTAATCAGGCGGCCATTAT 146
                                                                                                                                                                                                                                                                                                                                   quality sequence start: 20 quality sequence stop: 781 Location/Qualifiers
                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                     /cell_line="UCD001, inbred 256"
/clone lib="TAM32"
/clone lib="TAM32"
/note="Vector: pBCBAC1; Site_1: EcoRI; Site_2:
TAM32 Female Chicken library - for library and
ordering information: http://www.hbz.tamu.edu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pBluescript (KS+) vector. The library was normalized
                                                                                                                                                                                                                                                                                                 organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                      1. .1214
                                                                                                                                                                                                               'sex="female"
                                                                                                                                                                                                                              clone="TAM32-32B18"
                                                        8.2%;
47.3%;
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                                       0,
                                                      Score 37.4; DI
Pred. No. 2.6;
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Gallus
                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS 14-MAY-2003
TAM32-32B18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McPherson, J.,
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                                                                                                                                           clone;
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1027

ATATTTTGGATGGTTCAAAGTAAATTTTGAGGGGCATTTACAGATGGAAGTTTTCAAAAA

968

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ORIGIN
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BU387712
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Best Local
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                                                     Matches
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89 AATATAATTTTGCGGTAAATGAATTAAGCAAGTCTTCATTTAATCAGGCGGCCATTATTG 148
                                                     89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken cDNAs
                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archosauria; Aves; Neognathae; Phasianinae; Gallus.
1 (bases 1 to 708)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGGCAGGGAATTATAACTTTGCGTATATTGAGCAAACGGCCAATGCCAACGATGCCAGT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATCAAAACTATTGTCCGTTATTTCACAAGAAGGAGGAAATAATCGGGCGAAAGTCGACC 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACCAGGAAACAAACTATTTATCTATCCTGCTCAAACAGTTCAAGGAAGCTAATCTAAT 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAGCAAAATGGGATACCTTAAGAGAACAAAAGAAAACCTGGCCATTTGCGGTCTCCCAAA 848
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                                                   Conservative
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                                                                                                                                                         /clone_lib="CSEQCHN75"
//note="Organ: trunks; Vector: pBluescript II KS(+);
//note="Organ: trunks; Vector: pBluescript II KS(+);
Site_I: ECORI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1966): 791, except that a significantly longer
reannealing hybridization was used."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simon.Hubbard@umist.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:9031/clone="ChEST863c20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dev_stage="36"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strain="White Leghorn, Hisex"
                                                                    8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _type="mRNA"
                                           Score 36.8; DE Pred. No. 3.4; 0; Mismatches
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                                                87;
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740

GATGTTACACTTAGAAGATTTATATAAGGGGTAAAACTATTAGAGGGTATTACATTAGAA САТСТСССТСССТССАСАДТАТАТТТТССССТАЛАТСВАТТЛАССАЛСТСТССАТТТАЛТ 132

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: shotgun
High quality sequence start: 33
High quality sequence stop: 745.
Location/Qualifiers
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1 (bases 1 to 924)

Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences
HM1:IMSS sheared DNA library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Entamoeba histolytica Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ529672 924 bp
ENTBM10TR Entamoeba histolytica
                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: M13-Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic, genomic survey sequence AZ529672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bjloftus@tigr.org
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                                                                                                   C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                           Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
                                                                                                                                                                                                                                                                                                                                                /clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at
/notitute for Genomic Research (TIGR), Rockville, M
                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:5759"
                                                                                                                                                                                                                                                                                                                                                                                                                                             mol_type="genomic
strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Entamoeba histolytica"
                    8.1%;
Score 36.8; D
Pred. No. 3.7;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
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ba histolytica
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AUTHORS
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Brassica oleracea
Brassica oleracea
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                        499 bp BOGPO61TR BOGP Brassica oleracea survey sequence.
                                                                                                                                                                                                                                                                                                                        61;
                                                                   BH528896
BH528896.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 182000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kremitzki,C., Higginbotham,J., I
Warren,W., Graves,T., Mardis,E.
Gallus BAC End Reads
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archosauria; Aves; Neognathae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey CC211905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Richard K. Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC211905.1 GI:30530573
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                                                                                                                                                                                                                                                           TTTGGGTGGACTGAATTGAGCCTGTGTTCTTGTAATGTGGAAGCACAAATTGTTCCTCTC
                                                                                                                                                                                                     AGCTCAGGAAATATCTCTGTAGTTCAGGGGGAAGGAAAAAA 1084
                                                                                                                                                                                                                                                                                        TTTGCGGTAAATGAATTAAGCAAGTCTTCATTTAATCAGGCGGCCATTATTGGTCAAGTC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTAAAGAAATGTCCAGTATGTCATTGGAAGATGGGAGTTAAAACGCGAGACAAGA 915
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larity 59.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="CH261"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CH261 Female Chicken library - For library and clone
ordering information: http://www.chori.org/bacpac"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="CH261-18606"
                                                                     GI:17744694
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e_lib="CH261"
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Pred. No. 5.9;
0; Mismatches
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AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                   TGCCGACAAAGC
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Pannagrolaimoidea; Strongyloididae; StrongyLouw...

1 (bases 1 to 579)

McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,

Mylle, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,

Wylle, T., Dante, M., Mitter, E., Bennett, J., Franklin, C.,

Taggareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,

Taggareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,

Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,

Underwood, K., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,

Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
                                                                                                                                                                                                                                                                            Strongyloides stercoralis
                                                                                                                                                                                                                                                                                                                                                                                                           BG226083
579 bp mRNA linear EST 09-MAY-20
kq08h12.y1 TBN95TM-SSR Strongyloides stercoralis cDNA 5' similar
WP:ZK686.3 CE00457 ; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 499)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cdtown@tigr.org
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGCAACAGAGAAAAACCGTAATGCGTGCTCTATCACCAATGGTGAGCGCAGAAACGAA 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCCAGTATATCGCAAAGCGCTTACGGTAATAGTGCAGCTATTATCCAGAAAGGTTCTGG 362
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/strain="TO1000DH3"
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/clone_lib="BOGP"
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Pred. No. 5.4;
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linkers"
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Search completed: March 16, 2004, 04:28:38 Job time: 2238.91 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.9%; Score 36; DB 12; Length 579; Best Local Similarity 49.0%; Pred. No. 5.6; Matches 96; Conservative 0; Mismatches 100; Indels
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                                                                                                                                                                                                              391 GATACAATGGATGTTCAAATTAATGGATTTGAAGCTGATGTTTTGGCAAGATTTGTTAAA 450
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                                                                                                                                                                                                                                                                                                                                                                          67 AATTATGATCTGGCTCGTTCAGAATATAATTTTGCGGTAAATGAATTAAGCAAGTCTTCA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 AACAAATTGTTATTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACCGCGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Dr. Thomas Nutman and colleagues of NIAID, NIH (tnutman@nih.gov). DNA Sequencing by: Washington University Genome Sequencing Center St. Louis.
High quality sequence stop: 417.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
Contact: McCarter JP
                                                                                                          GAAAGAACTGAAATAT 466
                                                                                                                                                                                                                                                                                                                                 AATCTTAATACAGCTCCCGCATTTATACATTTTCCAGCTAAAGGATCTAGGAAATCTGAT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="XL" | Blue MRF' (Stratagene)"
/lab host="XL" | Blue MRF' (Stratagene)"
/clone lib="TBN95TM-SSR"
/clone="Tvector: Lambda Uni-ZAP XR (Stratagene); Site 1:
/corr | Site 2: Xho!, mRNA was purified from 2 x 10E3
rhabditiform larvae which had been isolated from gerbils
experimentally infected with larvae originally isolated
from experimentally infected dogs. cDNA was constructed
and, using adaptors, was cloned unidirectionally into the
vector from the EcoRI site to the XhoI site. The library
has an unamplified titer of 1 x 10E5 pft/ml and an
amplified, undiluted titer of 9 x 10E11 pfu/ml. The
average insert size of the unamplified library is 675 bp
(range, 100-1700)."
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/mol_type="mRNA"
/strain="Rhabditiform larvae obtained from gerbils"
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### Result O വര് ი 454.4 454.4 454.4 454.4 454.4 3955 3955 3955 3955 340.8 3340.8 3340.8 3259.2 2 Score 100.0 456 100.0 648 99.6 10346 99.6 17947 86.6 17913 86.6 327773 83.8 306358 74.7 10370 74.7 292504 68.8 5103 56.8 22411 56.5 325405 55.8 22641 56.5 32588 55.8 2067 9.5 9.5 9.5 9.3 9.3 9.1 9.0 9.0 9.0 301214 35259 165074 181047 19859 16562 19859 19970 19859 19970 196562 200368 16363 183458 Length 명 AX814811 BCCCSGABDA BCCCSGABDA BCCCSGABDA BCCCSGABDA AE000205 AE0002354 AE006759 AE016759 AE016981 AF237726 AE016840 AE016840 AE016840 STAJ2301 AE0043280 AE0143280 AE014808 AE0 SUMMARIES D90742 Escherichia 144908 Sequence 56 U53207 Salmonella AJ131756 Escherich AX814809 Sequence AX814809 Sequence AX814798 Sequence AX814798 Sequence AX814798 Sequence AX814808 Sequence AX814808 Sequence AX814798 Fesudomon AC138647 Homo sapi AC016765 Homo sapi AC016765 Homo sapi AC108448 Homo sapi AC108448 Homo sapi AC108411 Homo sapi AC108418 Homo sapi AC132799 Rattus no AP275733 Escherich AB005315 Escherich AB002554 Escherich AB016759 Escherich AB016759 Escherich AB01531 Shigella AB016981 Shigella AB016981 Shigella AP237726 Shigella AJ002301 Salmonell AE008749 Salmonell AL627269 Salmonell AL627269 Salmonell AL02380 Salmonell AB016840 Salmonell AB016840 Salmonell AB016840 Salmonell AB016840 Salmonell AB016840 Salmonell AJ515702 Enterobact AJ515701 Citrobact L04979 Escherichia X90754 E.coli csgG AE000205 Escherich D90741 Escherichia AX814811 Sequence Description Homo sapi Homo sapi Bradyrhiz

# ALIGNMENTS

nterobacteriale	obacteria; En nd Herwald,H.	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.  1 Bjoerck,L., Olsen,A., Wikstroem,M. and Herwald,H. Peptides Patent: WO 03064446-A 15 07-AUG-2003;	REFERENCE AUTHORS TITLE JOURNAL
PAT 05-DEC-2003	NA linear	AX814811 456 bp DNA Sequence 15 from Patent WO03064446. AX814811 AX814811.1 GI:39104001	AX814811 LOCUS DEFINITION ACCESSION VERSION

strain

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                                                                               Bacteria; Froteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

1 (bases 1 to 648)

Olsen, A., Arnqvist, A., Hammar, M., Sukupolvi, S. and Normark, S. The RpoS sigma factor relieves H-NS-mediated transcriptional in Escherichia coli
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/protein_id="CAE83541.1"
/protein_id="CAE83541.1"
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LNIYQYGGGNAALALQTDARMSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSAT
LNIYQYGGKNSEMTVKQFGGGNAAVDQTASNSSVNVTQVGFGNNATAHQY"
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LDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQVGFGNNATAHQY"
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/db_xref="taxon:562"
/tissue_lib="Kohara"
83. .538
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/evidence=experimental
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|mol_type="genomic DNA"
|strain="K-12"
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Pred. No. 9e-122;
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gene complement (9931409)  (gene="csgf" complement (9931409)  /gene="csgf" /codon_start=1 /transI_table=11 /product="assembly /transport component in curli /production" /protein id="CAA62278.1" /db_xref="GI:1147560" /db_xref="SWISS-PROT:P52104" /translation="MRVKHAVVLLMLISPLSWAGTMTFQFRNPNFGGNPNNGAFLLNS	/codon start=1 /transT_table=11 /product="assembly /transport component in curli /production" /db xref="G1:1147559" /db xref="G0A:952103" /db xref="G1:1147559" /db xr	repeat_region <1.\[ .>4680\] /insertion_seq="IS2 (partial)"  gene	/db xref="taxon:562"  /db xref="taxon:562"  /db xref="taxon:562"  /db xref="taxon:562"	rce	JOURNAL Mol. Microbiol. 18 (4), 661-670 (1995)  MEDLINE 96414468  PUBMED 8817489  REFERENCE 2 (bases 1 to 4680)  AUTHORS Hammar, M.  TITLE Direct Submission  Submitted (11-AUG-1995) M. Hammar, Karolinska Institutet, Microbiology and Tumorbiology Center, Box 280, S-171 77 Stockholm, SWEDEN Location/Qualifiers	orfC gene.  Bscherichia coli  SM Escherichia coli  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteri  Enterobacteriaceae; Escherichia.  1  B 1  B 1  B 1  B 1  B 1  B 1  B 1	LOCUS ECCSGABDG 4680 bp DNA linear BCT 07-JUL-2002 DEFINITION E.coli csgG, csgF, csgD, csgB, csgA, and orfC genes. ACCESSION X90754 VERSION X90754.1 GI:1147558 KEYWORDS csgA gene; csgB gene; csgB gene; csgF gene; csgG gene;
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              Direct Submission
Submitted (16-TAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                         Blattner, F.R.
                                                                                                                                                                        The complete genome sequence of Escherichia Science 277 (5331), 1453-1474 (1997)
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1 (Dases 1 to 10346)
Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V., Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F., Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J., Mau,B. and Shao,Y.
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/db_xref="G1:1147565"
/db_xref="SWISS-PROT:552107"
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SLREGSSGQSQTKQEKTLSLPANQPIALTKLSLNISPDDRVKIVVTVSDGQSLHLSQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.

This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Project and NCHGR). The entire sequence was independently Project and NCHGR). The entire sequence was independently Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 3032 [e-mail: mark@amber.gatech.edu]. Open reading frames were determined using Genemark Software, kindly supplied by 3032 [e-mail: mark@amber.gatech.edu]. Open reading frames that Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful appreciated. Updated information will be available at the E. coli (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and sequence changes. Annotation updates: updated gene identifications Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers RNA-encoding) are now designated as gene synonyms instead of names. This should allow them to be searched for in Entrez as gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (02-8EP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (bases 1 to 10346)
Plunkett, G. III.
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/note="factor:
389. .1375
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/transl_table=11
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to 58 residues of an approx. 1888 aa protein FAS2_CANAL
                                                                                                                                                                                                                                                                                                                                                                            /note="factor Sigma70; predicted
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                                                                                                                                                                                                                                                                                                                                                                                                          note="factor Sigma70; predicted +1 start at 1094689"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic
/strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Escherichia"
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                  Sigma32;
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                                                                                                                   complement(2111..2198)
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/note="syronym: b1032"
complement(2111..2198)
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SLTRYVLLSVCISTVWHLTISPLRNSDSFVTEGQWLTFKSIJALLILGVVLAINLF

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/transl_table=11
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/note="o83; This 83 aa C
to81 residues of an appr
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                                                                                   /product="tRNA-Ser"
/note="anticodon: G
                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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1253. .1280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="ycdV"
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389. .1375
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bound_moiety="DeoR predicted site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ycdU"
/function="orf; Unknown"
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        . 2365
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                       predicted
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  D90741 15047 bp
Escherichia coli K12 genomic DNA.
D90741 AB001340
D90741.1 GI:1651509
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                                                                                                                                                                                                                                                                                                                          GCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGTGGT
                                                                                                                                                                                                                                                                                                                                                 GCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGTGGT
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                                                                                                                                                             GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 9448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mrinfagresgysmbiffyhptfdtqwwiealrkafpqarvraw
Ksgdndsadyalvwhppvemlagrdlkavfalgagvdstlsklgappemlapsvplfr
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GSKVAQSLQTWRFplkcwsrtrkswpgvgsfagreelsaflsgcrvlinlipntpetv
GIINQQLLEKLPDGAYLLNLARGVHVVEDDLLAALDSGKVKGAMLDVFNREPLPPESP
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2355. .2383
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/trans1_table=11
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/db_xref="GI:1787270"
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/note="0325; This 325 aa ORF is 32 pct identical (2 gaps)
/note="0325; This 325 aa ORF is 32 pct identical (2 gaps)
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2393. .3370
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Pred. No. 3.9e-121;
D; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                           URL:
                                                                                                                                                                                                                                                                                                                                                                    Information operator:
Name: Hirotada Mori
Address: NARA Institute of Science
Ikoma, 630-01, Japan
                                                                                                                                                                                                                                                                                                                                              E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                The Japan E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yamamoto, Y. and Yano, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (29-JUL-1996) Hirotada Mori, NARA Institute and Technology, Res. & Edu. Center for Genetic Info., Takayama, Ikoma, Nara 630-01, Japan (B-mail:hmori@gtc.aist-nara.ac.jp, Tel:81-7437-2-5660, Pax:81-7437-2-5669)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name: Takashi Horiuchi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collaboration Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oshima, T., Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Ikemoto, K., Inada, T., Itoh, T., Kajihara, M., Kanai, K., Kashimoto, K., Mimura, S., Kitagawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Wishio, Y., Saito, N., Sampei, G., Seki, Y., Takemoto, Y., Yano, M. and Horiuchi, T., Takemoto, K., A 718-kb DNA sequence of the Escherichia coli K-12 genome DNA Res. 3 (3), 137-155 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lembers: (1995.4 - 1996.3)
Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A.,
Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono,
Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Japan E.coli genome DNA sequencing group
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Escherichia coli K12
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/map="23./-24.0 "..."
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/map="23.7-24.0 min"
                                                                                                                                                                         /mol_type="genomic
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                                                                                                                                                                                                                                                          3.aist-nara.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                            organism="Escherichia coli K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Institute of Basic Biology, Okazaki, 444, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                       coli genome database
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Genetic Info., 8916-5
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                                                                                                                                                                                                                                                                                                                                                                                           complement (4117. .4950)
                                                                                                                                                                                                                                                                                                                                           complement (4117. .4950)
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similar to PIR Accession Number F64035"
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SFLHSRKGSEDNCREVAAAVRDAGGWVALGSDSHTAFTMGEFEECLKILDAVDFPPER
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/note="unnamed protein product; ORF_ID:o230#5"
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GTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTCGGTAACAGC
                                                                                                                                                                                                     GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGGTAATAATAGCGGC
                                                                                                                                                                                                                                                  ATGAAACTTTTAAAAGTAGAAGCAATTGCAGCAATCGTATTCTCCGGGTAGCGCTCTGGCA 60
                                                ACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGCAGAT
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                                                                                                                                                                                                                                                                                                Conservative
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7217. . 7672
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7217. .7672
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/transI_table=11
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Pred. No. 4.1e-121;
D; Mismatches 1;
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7953 GTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTCGGTAACAGC 8012
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Submitted (06-JUN-2000) USDA, AR.
Research Center, State Spur 18D,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Which, G.A., Keen, J.E. and Elder, R.O.
Mutations in the csgb promoter associated with variations
expression in certain strains of Escherichia coli 0157:H7
Appl. Environ. Microbiol. 67 (5), 2367-2370 (2001)
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Whlich,G.A., Keen,J.E. and Blder,R.O.
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1 (bases 1 to 1711)
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Escherichia coli strain 43895 Red Variant CsgB protein (csgB)
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/product="C5gA protein"
/protein id="AAK53212.1"
/db_xref="G1:14039401"
/translation="MKLKUAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNS
ELNIYQYGGGNSALALQADARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSA
TLDQWNGKDSHMTVKQFGGGNGAAVDQTASNSTVNVTQVGFGNNATAHQY"
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/transT_table=11
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/brotein_id="AAK53211.1"
/db_xref="GI:140339400"
/table1ton="MXKLEPMLTILGAPGIAAAAGYDLANSEYNFAVNELSKSSFN
OAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGSSNRAKIDQTGDYNLAYIDQAGSANDA
                                                                                                                                                                                                                                                                                                                                        SISQGAYGNTAMIIQKGSGNKANITQYGTQKTAIVVQRQSQMAIRVTQR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="43895 Red Variant"
/serotype="0157:H7"
/db_xref="taxon:562"
                                                                                                                                                                                                                              gene="csgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="cagB"
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757. .1212
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|mol_type="genomic DNA"
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lay Center, NE 68933, USA
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86.6%;

Score 395;

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1;

Length 1711;

Matches Best Local

Similarity

92.8%;

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                                                                       Submitted (22-OCT-2000) Laboratory wisconsin, 445 Henry Mall, Madison, Location/Qualifiers
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Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N. W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A., and Blattner, F.R.
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Escherichia coli 0157:H7 EDL933
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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of 155.
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/organism="Escherichia coli O157:H7 EDL933"
/mol_type="genomic DNA"
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0; Mismatches 30;
                                                                                         of Genetics, Ur
, WI 53706, USA
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                                                                                                          University of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /serotype="0157:H7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="EDL933"
                                                                                                                                                                                                                                                                                                                                                    .2394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z1676"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surface structures;
                                                                                                                                                                                      pct identical to
coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similar
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gene

Sg

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transI tat'
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6003...7538
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/genee"Z1679"
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/functe="Residues 1 to 177 of 177 are 100.00 pct identical to residues 1 to 177 of 177 from Escherichia coli K-12
/crain MG1655: B1045"
                                                             MG1655: B1048"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MG1655: B1047"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (4453. .5610)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MG1655: B1046"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EENAHLYERLLTQQGDE"
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                                                                                                                                                                                                             Z1683"
                                                                                                                                                                                KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                        DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                             RESULT 8
AP002554
LOCUS
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                                                                                    AUTHORS
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Best Local (
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Bescherichia coli O157:H7 DNA,

AP002554 BA000007

AP002554.1 GI:13360491
       Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S., Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and Shinagawa,H.
                                                                                                                                                  Escherichia coli 0157:H7
Escherichia coli 0157:H7
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                Enterobacteriaceae; Escherichia.
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gene

gene

bp DNA 11110, complete genome,

linear near BCT section 5

T 21-DEC-2002 5/20.

Iida, T.,

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1 ATGAAACTTTTAAAAGTAGAAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCTCTGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGTTGTTCCTCAGTACGGCGGCGGTGGCGGTAACCACGGTGGTGGCGGTAATAACAGC
                                                                                                                                                            GGTGGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAG
                                                                                                                                                                                                                                                                                                        AGCGCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGT 357
                                                                                                                                                                                                                                                                                                                                                                                          GATGTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTTGGTAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCCGAATTCAGAGCTGAATATTTATCAGTACGGTGGTGAACTCTGCACTTGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCCCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTG
                                                      GTTGGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGTTGTTCCTCAGTACGGCGGC---GGCGGTAACCACGGTGGTGGCGGTAATAATAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="periplasmic glucans biosynthesis protein"
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/gene="mdoH"
/function="enzyme; Osmotic adaptation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T., Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C., Ogasawara,M., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and Shinagawa,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax:81-6-6879-2047)
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Ohnishi, M., Kurokawa, K.,
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Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
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Ohnishi,M., Mu
~~~~kawa,K., `
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/translation="MNSLFASTARGLEELLKTELENLGAVECOVVQGGVHFKGDTRLV
YQSL/MSRLASRIMLPLGECKVYSDLDLYLGVQAINWTEMFNEGATFAVHFSGLNDTI
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LAGIGELITFEVKDVAQLTNPLPKEPYGTVLSNPPYGERLDSEPALIALHSLLGRIMK
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99 in 702 aa (Conserved in E.coli K-12)"
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/db_xref="GI:13360492"
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/transl_table=11
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/mol_type="genomic DNA"
/strain="0157:H7"
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|50. .2258
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VLDSKKAGQLSPGDPVLFGGYRVGSVETSTFDTQKKAKISYQLFINAFVDRLVTSUVRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="ECs1035"
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99 in 546 aa (Conserved in E.coli K-12)"
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5565. 7205
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/codon_start=1
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4307. .5560
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QREHEOLPQLLEDLEAKLEALQTQVADASFFSQPHEQTQKVLADMAAAEQELEQAFER
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EDYANKLRKNILKKFEKWARQSIECYRLYDADLPEYNVAVDRYADWVVVQEYAPPKTI
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HLWVNLTDYLDTGLFLDHRIARMLGQMSKGNDFLMILFSYSATVHAGLGGARSTTT
VDMSRTYLEWAERNURLINGLTGRAHRLIQADCLAWLREANEQFDLIFIDPPTENSKR
MEDAFDVORDHLALMKDLKRLLRAGGTIMFSNNKRGFRMDLDGLAKLGLKAQEITQKT
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/transl_table=11
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2270. .4177
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                                                                                                                                                                                                                                                                                                                                                                                GGTGTTGTTCCTCAGTACGGCGGCGGTGGCGGTAACCACGGTGGTGGCGGTAATAACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGAAACTTTTAAAAGTAGCAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCCTCTGGCA 326480
                                                                                                                                                                                                                                                                                                                           GGCCCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTG
                     GGTGGCAACGGTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAG 417
                                                                                                                                                                        GATGTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTCCGGTAAC
                                                                                                                                                                                                                                                 CAAACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGCGGTAATGGTGCA 237
                                                                                                                                                                                                                                                                                                     GGCCCGAATTCAGAGCTGAATATTTATCAGTACGGTGGTGACTACTCTGCACTTGCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                        GGTGTTGTTCCTCAGTACGGCGGC----GGCGGTAACCACGGTGGTGGCGGTAATAATAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAAACTTTTAAAAGTAGAAGCAATTGCAGCAATCGTATTCTCCCGGTAGCGCTCTGGCA 60
                                                                                                                                                GATGTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTTGGTAAC
                                                                                                                                                                                                                           CAAGCTGATGCTCGTAACTCTGATCTTACTATTACCCAGCATGGTGGTGGTAACGGTGCA
                                                                                                             AGCGCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (8258. .8776)
/gene="EC61038"
/gene="EC61038"
/note="sinilar to FABA_ECOLI gi|1787187 percent identity
100 in 172 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="EC#1037"
8021. .8188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MTIAALWLAGCSSGEINKNYYQLPVVQSGTQSTASQGNRLLWVE
QVAVPDYLAGNGVVYQTSDVKYVIANNNLWASPLDQQLRNTLVANLSTQLPGWVVASQ
PLGSAQDTLNVTVTEFNGRYDGKVIVSGEWLLNHQGQLIKRPFRLEGVQTQDGYDEMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (8258. .8776)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REAMADRVVMA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVLAGVWSQEAASIAQEIKRLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 in 182 aa (Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="ribosome modulation
/protein_id="BAB34460.1"
/db_xref="GI:13360497"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ECs1037"
/note="identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /evidence=not_experimental
/transl_table=11
/product="hypothetical pro
/protein_id="BAB34459.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DQVLRBLQPVLKTLNEKSNALVFEAKDKKDPEPKRAKQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="EC81036"
7217. .7765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MKRQKRDRLERAHQRGYQAGIAGRSKEMCPYQTLNQRSQWLGGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="GI:13360496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      notes"similar to YMBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="ECs1036"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.6%;
92.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 395; DB 1, Pred. No. 1.3e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RMF_ECOLI gi|1787186 (Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ECOLI gi|1787185 percent identity
I in E.coli K-12)"
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SOURCE
ORGANISM
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AE016759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
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Bscherichia coli CFT073 section
AE016759 AE014075
AE016759.1 GI:26107527
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Welch,R.A., Burland,V., Plunkett,G.D. III, Redford,P., Roesch,P.,
Rasko,D.A., Burkles,E.L., Liou,S.-R., Boutin,A., Hackett,J.,
Stroud,D., Mayhew,G.F., Rose,D.J., Zhou,S., Schwartz,D.C.,
Perna,N.T., Mobley,H.L.T., Donnenberg,M.S. and Blattner,F.R.

Extensive Mosiac Structure Revealed by the Complete Genome Sequence
of Uropathogenic Escherichia coli
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 17020-17024 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-JUN-2002) Genetics Laboratory, University of Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rasko, D.A., Buckles, B.L., Liou, S.-R., Boutin, A., Hackett, J., Stroud, D., Mayhew, G.F., Rose, D.J., Zhou, S., Schwartz, D.C., Perna, N.T., Mobley, H.L.T., Donnenberg, M.S. and Blattner, F.R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 306358)
Welch,R.A., Burland,V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli CFT073
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/protein id="AATP binding cassette (ABC) transporter homolog"
/protein id="AATP 5727.1"
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VHTLLQMCPVPLAVFTYYIAGIAVMLAWSPAMTLIVVCVLVCLAITALRARRVPAQT
GMASDQLANLTEHIREVLAQISVVKSCVAEMERTHWLDRGSRQJVRVRIGAVISQAMP
GATMLALPULGGIVLLCYGGWSVMHGRIDLGTFVAFASFLAMLTGPTRVLASFLVIAQ
RTQASVERVFALIDTRRQMEDGTESINSQVVGLELENMSFDYHHGDRHILSDISFSUR
AGETVAVVGASGSGKSTLLMLLARFYLDPCSGKUMLTSERGNNLRDIRLEALRRRVGI
VFEDAFLFAGTVAENIAYGHPQATADDIRRAAAAGASDFINALPKGFDSLITERGTN
LSGGGRGRIALTRAPDVLILDDTTSAVDAVTEABINTALGRYADEGHMLLVIAR
RRSTLQLASRVVULDKGRMVDTGTPAELEARCPAFRALMTGBSDFLATSHNSHNELMP
AEPATQDDVTDTGDKGFVARMTRVPENNVQQALAGKGRKVTSLLKPVAMMFVIAALLI
ALDSAAGVGVLILLQHGIDSGVAAGDMSTIGLCALLALCLVIVGRGSYSLQTVFAARA
AESVQHSVRLRSFGHMLRLGLPHHEKHADSRITGRLALCTLVIVGRGSYSLQTVFAARA
AESVQHSVRLRSFGHMLRLGLPHHEKHADSRTFRAMVAQALESIKONSTLQE
KVSGLRVVQSHGQQBLEGGRILALTALSERFRATRVRAQKYLAVFFPFLTFCTEASYAAVL
LUGASQVAAGEMTAGVIAAFFILLGGPYGFVQQLSGIVDAMQQATASGKHIDELLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Residues 27 to 1231 of 1245 are 80.16 pct identical to residues 1 to 1209 of 1218 from GenPept.129 : 
>emb|CAD05883.1| (AL627276) putative ABC transporter protein [Salmonella enterica subsp. enterica serovar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /locus_tag="c1253"
complement(83. .3820)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (83. .3820)

    Madison, 445 Henry Mall,
Location/Qualifiers

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic
/strain="CFT073"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  locus tag="cl253"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="iroC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .306358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xref="taxon:199310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plunkett, G.D. III,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
1 5 of 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Redford, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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gene

CDS

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repeat_region
                                                                                                                                                                                                                                                 complement (6598. .6960)
/locus tag="c1257"
/function="LS, phage, Tn."
/note="Residues 8 to 120 of 120 are 98.23 pct identical residues 316 to 428 of 442 from MG1655 : b4278"
                                                                                     /translation="mpropdogyreikotmodlsrltlrskkpelveoellwgvllaynl
vryomikmaehlkgympnolsfsescomvmrmlmtlogaspgripelmrdlasmgolv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mrsgnckcqtrnqkgvpmgnekslahtrmnckyhtveapkyrrq
vfyrekkraligcilrklcemksvrileaeccadhihmlveippkmsvsgfmgylkgks
slmpyeqfgdlkfkyrnrefmcrgyyvdtvgkntaktqdyikhqleedkmgeqlsipy
                                                                           KLPTRRETAFPRVVKERP"
                              /locus_tag="c1258"
                                                                                                                                               protein_id="AAN79731.;
/db_xref="GI:26107532"
                                                                                                                                                                                                                                                                                                                                                                                                           /insertion_seq="IS4"
complement(6598. .696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (6578. .6940)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /locus_tag="c1256"
/note="Residues 18 to 169 of 169 are 94.07 pct identical to residues 1 to 152 of 152 from SwissProt.40:
>sp|057334|T200_SALTY Transposase for insertion sequence element IS200"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /producE="Hypothetical protein"
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RTPASSVSSSVYSASVSRTAADIMLLSNNPLFAPGQVSFFGCSLAASGIHVTILE"
                                                                                                                                                                 product="Putative conserved protein"
protein_id="AAN79731.1"
                                                                                                                                                                                                                     transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="c1257"
                                                                                                                                                                                                                                               codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MRRLPDLDRQAERDFLMRILFVGPPLYGILLYPVLSLAQAFRVNG HEVLIASGGQFAQKAARAGLUVFDAAFGLDSEAGYRHHEAQRKKSNIGTQMGNFSFFS EEMADHLVEFAGHWRPDLIIIYPPLGVIGPLIAAKYD I PVVMQTVGFGHTPWHLRGVTR SLTDAYKRHNUGATFRMAMIDVTPESMSILENDGEPIPWHLRGVTPNGGAVWEPWWER RDRKKLLVSLGTVKPMVDGLDLIAWVMDSASEVDAEIILHISANARSDLRSLDSNVR RVDRKKLLVSLGTVKPMVDGLDLIAWVMDSASEVDAEIILHISANARSDLRSLDSNVR LVDWIPMGVFLNGADGFIHHGGAGNTLTALHAGIPQIVFGQGADRPVNARVVAERGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="incomplete"
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protein_id="AAN79730.1"
db_xref="GI:26107531"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1/transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'insertion_seq="IS1541A-like"
5961. .6470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5535.
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PSATNEDVEIASQRAGLYEMVCNLPQGFRTPVNNGGADLSAGGRQLIALARAQLANAH
ILLLDEATSCLDRTSEERLWSSLTDVVHAGKHSALIVAHRLTTAQRCDLIAVIDKGLL
AEYGTHEQLLSAGGLYTRLWHDSVSSTALHRQHNMKEETPG"
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/protein_id="AAN79728.1"
/db_xref="GI:26107529"
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GGTGTTGTTCCTCAGTACGGCGGCGGCGGTGGCAACCACGGTGGTGGCGGTAATAACAGC 45388
                                GGTGTTGTTCCTCAGTACGGCGGCGGCGGT---AACCACGGTGGTGGCGGTAATAATAGC 117
                                                                                             ATGAAACTTTTAAAAGTAGCAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCTCTGGCA
                                                                                                                           ATGAAACTTTTAAAAGTAGAAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCTCTGGCA 60
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                        /transI tak
                                                                                                                                                                                                                                                                                                                                                                                                                            complement (9302. .9667)
/locus tag="c1261"
/note="Residues 1 to 35 of 121 are 97.14 pct identical to residues 59 to 93 of 316 from GenPept.129:
>gb|AAK18437.1|AF348706_126 (AF348706) putative transposase [Shigella flexneri]"
                                                                                                                                                                                                                                                                                                                /product="Hypothetical protein"
/protein_id="AAN79735.1"
/db_xref="GI:26107536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="masaadarrivshyerrwlieeyhkawksggtcyestrwqtrdn
Lerwyvikapiavrlgtrqbgiseetqndsckkiltptewkllwyklegkqlpsqtp
Tlkwaclklgrwhdskrtgrggwyvwwdgwfrlqdmvegypymksldqei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (9302. .9667)
/locus_tag="c1261"
                                                                                                                                                                                                                                                                                    translation="MAERLGEIQKRVITVCDREADIWHYLHYKVSHGQRFVVRTAQNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="putative enzyme; Transposases Insertion
Sequence Associated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (8832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /function="RNA; tRNA"
complement(8832, .929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Putative Transposase"
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'transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Residues 1 to 139 of 144 are 50.71 pct identical to residues 104 to 242 of 258 from GenPept.129: >gb AAK18487.1 AF348706_176 (AF348706) orf, hypothetical [Shigella flexneri]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Hypothetical protein"
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/protein id="AAN79733.1"
/db xref="G1:26107534"
/translation="MKDLSFIRFFLAILLLLVPPALEFPVIHRHITPGALTLCVITAL
IITTLASJGGRLVSVKCISEISFIRRHRIECMMAGFMIYFWTFSLIAGWYKPQFKKEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Hypothetical protein"
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LDGEQVLFSFWELNKKQYEGFEFYQIFSGNIVASCSSCSGVSSNSSAHYARCTDFMRH
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product="tRNA-Arg"
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1835. .8269
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                                                                                                                                                                                                                                                                                Jin,Q., Shen,Y., Wang,J.H., Liu,H., Yang,J., Yang,F., Zhang,X.B., Zhang,J.Y., Yang,G.W., Wu,H.T., Dong,J., Sun,L.L., Xue,Y., Zhao,A.L., Gao,Y.S., Zhu,J.P., Chen,S.X., Yao,Z.J., Wang,Y., Lu,W.C., Qiang,B.Q., Wen,Y.M. and Hou,Y.D. Direct Submission

Submitted (08-MAY-2001) Microbial Genome Center of Chinese Ministry of Public Health, 100 YingXin Jie, XuanMu Qu, Beijing 100052, P.R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jin,Q., Yuan,Z.H., Xu,J.G., Wang,Y., Shen,Y., Lu,W.C., Wang,J.H., Liu,H., Yang,J., Yang,F., Qu.D., Zhang,X.B., Zhang,J.Y., Yang,G.W., Wu,H.T., Dong,J., Sun,L.L., Xue,Y., Zhao,A.L., Gao,Y.S., Zhu,J.P., Kan,B., Chen,S.X., Yao,Z.J., He,B.K., Chen,R.S., Ma,D.L., Qiang,B.Q., Wen,Y.M., Hou,Y.D. and Yu,J. endouble sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157
Nucleic Acids Res. 30 (20), 4432-4441 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shigella flexneri 2a str. 301
Shigella flexneri 2a str. 301
Bacteria; Proteobacteria (Gammaproteobacteria; Enterobacteriales;
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Shigella flexneri
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AE015131.1 GI:24051313
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                                                                        /db_xref="taxon:198214"
complement(127. .214)
/product="tRNA-Ser"
/note="anticodon: GGA"
410. .1387
/pseudo
410. .13
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                          /organism="Shigella flexneri
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                                                    /gene="ycdW"
                                locus_tag="SF1027"
                                                                                                                                                                    serotype="2a"
                                                                                                                                                                                                                                                .10370
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/db_xref="GI:24051316"
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IVAFLMCIQAKQLLLSFVPGTFIGACATFAGQGDWKLVLPSLALGLVFGYAMKNSGLW
LAARSAKTAHREGEIKNKA"
                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus tag="SF1030"
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/notee="Residues 1 to 179 of 179 are 98 pct identical to notee="Residues 1 to 179 of a 179 aa protein from Escherichia residues 1 to 179 of a 179 aa protein from Escherichia coli K12 ref: NP_415554.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Residues 1 to 184 of 184 are 99 pct identical to residues 1 to 184 of a 184 aa protein from Escherichia coli 0157:H7 EDL933 ref: NP_287169.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus tag="SF1028"
/note="Residues 1 to 245 of 245 are 99 pct identical to residues 1 to 245 of a 245 as protein from Escherichia coli 0157:H7 EDL933 ref: NP_287168.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="ycdw"
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/locus_tag="SF1027"
/note="similar to Escherichia coli K12 putative
/note="similar to Escherichia coli K12 putative
dehydrogenase gi: 1787270 (326 aa). BLAST with identity
dehydrogenase gi: CDS contains an in-frame stop codon.
                                                                                          complement (3414. .4189)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MNEFSILCRVLGSLYYRQPQDPLLVPLFTLIREGKLAANWPLEQ
DELLTRLQKSCDMTQVSADYNALFIGDECAVPPYRSAMVEDATEAEVRAFLSERGMLL
ADTPADHIGTLLLAASWLEDQSTEDESEALETLFSEYLLPWCGAFLGKVEAHATTPFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MYPVDLHMHTVASTHAYSTLSDYIAQAKQKGIKLFAITDHGPDM
EDAPHHMHFIMMRIWPRVVDGWGILRGIBANIKNVDGBIDCSGKMFDSLDLIIAGHE
PVFAFHDKATUTQAMISTIAGGUWLIISHFGUMFXYEIDVKAVAEAAAKHQVALEIUM
SFLHSRKGSEDNCRAVAAAVRDAGGWVALGSDSHTAFTMGEFEECLKILDAVDFPLER
                                                                                                                                                                                                              complement (3414. .4189)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RTMAPLTRDAISAMWDELEEDSEE"
/gene="csgG"
/locus_tag="SF1031"
/note="similar to Escherichia coli K12 curli production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative oxidoreductase component"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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1442. .2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="SF1030"
2811. .3350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="ycdY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "LNVSPRRLLNFLESRGMAPIAEFADL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="orf, conserved hypothetical
/protein_id="AAN42652.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="orf, co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence has been checked and is believed to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="ycdZ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   locus_tag="SF1029"
203. .2757
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                                                                                                                                                locus_tag="SF1031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    locus_tag="SF1029"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="ycdX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             locus_tag="SF1028"
                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                          protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identical to
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```

gene

CDS

gene SdC

/transi\_table≈11 complement(4454.

/locus\_tag="SF1032"

.5662)

assembly-transport component, 2nd curli operon gi: 1787274 (278 aa). BLAST with identity of 97% in 257 aa. This CDS contains an in-frame stop codon. The sequence has been checked and is believed to be correct."

transI\_table=11

```
coli 0157:H7
EDL933 ref: NP_287175.1"
```

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멍 Ş д δõ B Ś 밁 Ś 맑 Ş 밁 Query Match Best Local Simi Matches 345; 9838 9778 9718 TGGCTTCGGTAÁCAGCGCCACTCTTGATCAGTGGAÁCGGCAAAAATTCTGAAATGACTGT 9658 9598 405 345 9538 CAGTAATAACGGGCCCAAATTCAGAGCTGAACATTTACCAGTACGGTGGCGGTAACTC 9597 285 105 CGGTAATAATAGCGGCCCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTC 164 chacereacreaciriescriresiraacaaceceacececreareacrairaa 9889 CAACGTGACTCACGTTGGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 456 TAPACAGTTÓGGTGGTGGCAÁCGGTGCTGCAGTTGÁCCAGACTGCÁTCGÁACTCCTCCGT TAPACAGTTCGGTGGTGGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGT 404 Similarity TGGCTTCGGTAACAGCGCTACTCTTGATCAGTGGAACGGCAAAAATTTCTGAAATGACGGT 344 TGGTAATGGTGCAGATGTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACG CGGTAATGGTGCAGATGTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACG récaerrigererada a en en receptado en en receptado receptado en recept TGCACTTGCTCTGCAAACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGG Conservative 74.7%; 98.0%; ٥, Score 340.8; DB 1 Pred. No. 5.2e-88; 0; Mismatches 7 DB 1; Indels Length 10370; <u>,</u> Gaps 9837 9777 9717 224 284 9657

gene

/product="transposase of Tn10"

protein id="AAN42655.1"

/brotein id="AAN42655.1"

/db\_xref="G1:24051317"

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GRNLPTKARTKHNIKRIDRLLGNRHLHKERLAVVRWHASFICSGNTWPIVLYDWSDIR
EQKKLMVLRASVALHGRSVTLYEKAFPLSEQCSKKAHDOFLADLASILPSNTTPLIVS
LTKSNPISCOILLYKSRSKGRKNQRSTTTHCHHSPKIYSASAKEPWILATMLPVEIR
TPKQLVNIYSKRHQIETFRDLKSPAYGLGLRHSRTSSSERFDIMLLIALMIQUTWL
TPKQLVNIYSKRHQIETFRDLKSPAYGLGLRHSRTSSSERFDIMLLTALMIQUTWL
FTHGYVLGKL"

REFERENCE AUTHORS VERSION KEYWORDS RESULT 11 AE016981 LOCUS SOURCE DEFINITION ACCESSION ORGANISM genome. AE016981 AE014073 AE016981.1 GI:30040616 AE016981 Shigella flexneri 2a str. 2457T (bases 1 to 292504)

CDS gene

complement (6389. .7069)

/locus\_tag="SF1034" locus\_tag="SF1034"

complement (6389. .7069)

gene="csgD"

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/codon\_start=1 /transl\_table=

table=11

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/note="Residues 1 to 129 of 129 are 98 pct residues 1 to 129 of a 129 as protein from coli O157:H7 EDL933 ref: NP\_287173.1"

Escherichia identical to /locus\_tag="SF1033" complement(5995...6384)

complement (5995. .6384)

/gene="csgE"

Shigella flexneri 2a str. 2457T shigella flexneri 2a str. 2457T Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae, Shigella.

DNA linear BCT 22-APR-2003 section 4 of 16 of the complete

Wei, J., Goldberg, M.B., Burland, V., Venkatesan, M.M., Deng, W., Fournier, G., Mayhew, G.F., Plunkett, G. III, Rose, D.J., Darling, A., Mau, B., Perna, N.T., Payne, S.M., Runyen-Janecky, L.J., Zhou, S., Schwartz, D.C. and Blattner, F.R. Complete Genome Sequence and Comparative Genomics of Shigella Infect. Immun. 71 (5), 2775-2786 (2003)

2 (bases 1 to 292504)

Wei,J., Goldberg,M.B., Burland,V., Venkatesan,M.M., Deng,W.,
Fournier,G., Mayhew,G.F., Plunkett,G. III, Rose,D.J., Darling
Mau,B., Perna,N.T., Payne,S.M., Runyen-Janecky,L.J., Zhou,S.,
Schwartz,D.C. and Blattner,F.R. Direct Submission Submitted (13-UUN-2002) Genetics Laboratory, University of Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA Location/Qualifiers

Darling, A.,

TITLE JOURNAL

/locus\_tag="SF1035" /note="Residues 10 to 160 of 160 are 99 pct identical | residues 1 to 151 of a 151 aa protein from Escherichia 6

/translation="mrsikkwgftmfnevhsihghtlllitkpslqatallqhlkqsl Altgklhniqrslddissgs!illdmmeadkklihymqdtlsrknnnikilllnyped Ypyrdienwphingvfyamedqervynglqgvlrgecyftqklasylithsgnyryns Tesalltherkeilnklrigasnneiarslfisentvkthlynlfkkiavknrtqavs

JOURNAL PUBMED REFERENCE AUTHORS

TITLE

/product="putative 2-component transcriptional regulator for 2nd curli operon"
(protein\_id="AAN42657.1"
/db\_xref="GI:24051319"

/note="Residues 11 to 226 of 226 are 100 pct identical to residues 1 to 216 of a 216 as protein from Escherichia coli 0157:H7 EDL933 ref: NP\_287174.1"

/codon\_start=1 /transl\_table=11

Sg gene

/locus\_tag="SF1035" 7766. .8248

gene="csg8"

/organism="Shigella flexneri 2a str. /mol\_type="genomic DNA" /strain="2457T"

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gene
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                                                                Sg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sdo
                                                                                                                                                                                                                                                        /pictein_id="AAP16350.1"
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/savagvagixsenymlpaagvrgaaitrtagryfbrlushdafyrvimuvtiglsfldf
ASAVAGVAGIXSENYMLPAAGVRGAAITRTAGRYFBRLUSHDATFRVLQHLRIYTFSK
LLPLSPAGLARYRQGELLNRVVADVDTLDHLYLRVISPLUGAFVVIMUVTIGLSFLDF
TLAFTLGSVMLLTLFLMPPLFYRAGKSTGQNLTHLRGQYRQQLFMMLGQABLGTIFGA
SDRYRTQLENTEIQWLEAQRRQSELTALSQATARVELTDGKFBVTFEDTTQTRVA
DRYRTQLENTEIQWLEAQRRQSELTALSQATARVELTDGKFBVTFEDTTQTRVA
DRYRTQLENTEIQWLEAALAPVGAFGGISLQVNAGEHIAILGRTGCGKSTLLQLLTRAWDF
QQGEILLNDSPIASLABEAALAPTGTSVVPQRVHLFSATLRDNLLLASPGSSDBALSEIL
DQGGEILLNDSPIASLABEAALRGTISVVPQRVHLFSATLRDNLLLASPGSSDBALSEIL
                                                       /gene="cydD"
/locus_tag="$0887"
complement(3194. .4960)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus tag="S0886"
/function="transport; Transport of small molecules: Othe /notes="residues 1 to 573 of 573 are 97.03 pct identical residues 1 to 573 of 573 from Escherichia coli K-12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GIFPWFSPGDPILWWSPDPRAVLWPESLHISRSMKRFHKRSPYRVTMNYAFGQVIEGC
ASDREGTWITRGVVEAYHRLHELGHAHSIEVWREDELVGGMYGVAQGTLFCGESMFS
RMENASKTALLVFCEEFIGHGGKLIDCQVLNDHTASLGACEIPRRDYLNYLNQWRLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="residues 1 to 234 of 234 are 100.00 pct identical to residues 1 to 234 of 234 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="enzyme; Aminoacyl tRNA synthetases, tRNA
modification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="S0885"
complement(726. .1430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GI:30040617"
/translation="MAKEDNIEMQGTVLETLPNTMFRVELENGHVVTAHISGKMRKNY
IRILTGDKVTVELTPYDLSKGRIVFRSR"
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                                                                                                                                                complement (3194.
                                                                                                                                                                                                                                         RRVGLEKLLEDAGLNSWLGEGGRQLSGGELRRLAIARTL1.HDAPLV1.LDEPTEGLDAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
/product="ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (1472. .3193)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (1472. .3193)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPNNFWVPRCLFSPQE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transī_table=11
/product="leucyl, phenylalanyl-tRNA-protein transferase"
/protein_id="AAP16349.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (726. .1430)
/gene="cydD"
/locus_tag="S0887"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ransport"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="protein chain
/protein_id="AAP16348.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       residues 1 to 72 of 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (223. .441)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /serotype="2a"
/db_xref="taxo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          locus_tag="S0886"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MRLVQLSRHSIAFPSPEGALREPNGLLALGGDLSPARLLMAYQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="GI:30040618"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1/transi_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note="residues 1 to 72 of 72 are 100.00 pct identical to residues 1 to 72 of 72 from Escherichia coli K-12 : B0884"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="infA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       locus tag="S0884"
function="factor; Proteins - translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              locus_tag="S0885"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    xref="taxon:198215"
                                                                                                                                                                                                          lellakmmrektvlmvthrlrglsrfqqiivmdngqiieqgthaellarqgr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             component
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/translation="mgttkhskllilgsgpagytaavyaaranlopvlitgmekggql

rtttevenwpodpridltgpellmarmeehatkreteiifdhiktdlonrpfrlweding

Eytcdaliiatgasarylgebseekekgrgvscatcdffyrnokvardfrlwediggnyny

Eytlsniasevhlherdgfraeklikrlwdkvengniilhtnrtleevtgdomgv

Egalvlsniasevhllherdgfraeklikrlwdkvengniilhtnrtleevtgdomgv

Tgvrlrdtonsdniesldvaglfvaighspntaifegolelengyikvosgihgnato

Tsifgvffaagdvmdhiyroaitsagtgcmaaldaeryldgladak"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAP16351.1"
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/db_xref="G:30040620"
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LDRLQOAGPAWIGKEAGSWAYIVLEGIDDWHDYXARYLPOMALAVSVPLLI VVAIFP
SNWAJALILLGTAPLLFPFMALVGWGAJADANKRIFLALKGHFLDRLRGMETLRI
SNWAJALILLGTAPLLFPFMALVGWGAJADANKRIFLAKTLSGHFLDRLRGMETLRI
GRGEABIESIRSASEDFRORTMEVLRLAFLSSGILEFFTSLSIALVAVYFGFSYLGEL
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ClervrrlerQgfiQgytallnphyldasllvfybitlnrgapdvfeQfntavQklee
IQeChlvsGdfdYllktrvpdmsayrkllgetllrlpgvndtrtyvvmeevkQsnrlv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pool, multipurpose conversions"
/note="residues 1 to 164 of 164 are 100.00 pct identical
to residues 1 to 164 of 164 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="trx8"
/locus_tag="S0888"
complement(5083. .6048)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFGHYDTGVTLAAGFLALĪLAPEFFQPLRDLGTFYHAKAQAVGAADSLKTFMETPLAH
PQRGEAELALTDPLTIEAEDLFITS PEGKTLAGPLKFTLPAGGRAVLVGRSGSGKSSL
LNALSGFLSYGSLRINGIERLBLSPESBWRKHLSWYGGNDLPAAKLRDWYLLARPDS
SEQELQAALDNAWVSEFLPLLPQGVDTPVGDQAARLSVGQAQRVAVARALLNPCSLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transl_table=11
/product="regulator for leucine (or lrp) regulon and/
high-affinity branched-chain amino acid transport sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transT table=11
/product="thioredoxin red
/protein_id="AAP16352.1"
/db_xref="GI:30040621"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            yeure "----"
/locus tag="S0888"
/function="enzyme; 2-Deoxyribonucleotide metabolism"
/functe="residues 1 to 321 of 321 are 95.95 pct identical
/note="residues 1 to 321 of 321 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (5083. .6048)
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YAELSVAGGPFATLLAHRQEEI"
                                                                                                                                                                          /gene="ftsK"
/locus_tag="$0890"
7221. _11249
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/note="residues 1 to 588 of 588 are 92.85
residues 1 to 588 of 588 from Escherichia
/locus tag="80890"
/functIon="phenotype; Cell division"
/note="residues 1 to 737 of 1342 are 68.24 pct identical
to residues 1 to 737 of 1329 from Bscherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAP16353.1"
/db_xref="GI:30040622"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 locus tag="S0889"
function="regulator; Central intermediary metabolism:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             locus_tag="S0889"
592. .7086
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division protein' AP16354.1"

\_table=11

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TGGCTTCGGTAACAGCGCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGT 344
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AUTHORS
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ORGANISM
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STAJ2301
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VERSION
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Best Local :
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Salmonella t
csgC genes.
AJ002301
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                   Romling, U., Bian, Z., Hammar, M., Sierralta, W.D. and Normark, S. Curli fibers are highly conserved between Salmonella typhimur and Escherichia coli with respect to operon structure and
                                                               Salmonella typhimurium
Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                         csgA gene; csgB gene; csgG gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315;
       Bacteriol, 180
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                                                                                                                                                                                                                                                                           CAACGTGACTCAGGTTGGCTT 425
                                                                                                                                                                                                                                                                                                                                                rddcrrcddraacadcdcacrcrrdarcadrddaacddcaaaaaarrchdaardacrdr 82
                                                                                                                                                                                                                                                                                                  TAAACAGTTCGGTGGCGAACGGTGCTGCAGTTGACCAGACTGCATCGAACTCCTCCGT
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Submitted (33-FEB-2000) Microbiology, Monash University, Rd., Clayton, Vic. 3800, Australia
                                                                                                                                                                                                                                                                                                                                                                 TGGCTTCGGTRACAGCGCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGT 344
                                                                                                                                                                                                                                                                                                                                                                                                               CGGTAATGGTGCAGATGTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCACTTGCTCTGCAAACTGATGCCCGTAACTCTGACTTTGACCTATTACCCAGCATGGCGG
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                                                                                                                                                                                    5103
typhimurium csgG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(1. .319,393. .437)
/note="csg locus; similar to Escheric
locus deposited in GenBank Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /insertion_seq="IS600"
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Number X05952"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Shigella_flexneri"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Shigella flexneri"
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/strain="SBA1100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:623"
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98.1%;
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   722-731 (1998)
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Pred. No. 1.2e-79;
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                                                                                                                                     gene;
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ccession Number X90754"
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TITLE
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MEDLINE
PUBMED
REFERENCE
AUTHORS

0816548

Immun, 68

3780-3783

2 (bases 1 to 437) Sakellaris,H., Hannink,N.K., Rajakumar,K., Sasakawa,C. and Adler,B.

Bulach, D.,

Hunt, M.,

REFERENCE AUTHORS

Enterobacteriaceae; Shigella.

1 (bases 1 to 437)
Sakellaris, H., Hannink, N.K., Rajakumar, K.,
Sasakawa, C. and Adler, B.
Curli loci of Shigella spp

Bulach, D.,

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

KEYWORDS SOURCE ORGANISM

Shigella flexneri Shigella flexneri

AF237726.1 GI:7582371

RESULT 12 AF237726/c DEFINITION ACCESSION VERSION

AF237726 AF237726 AF237726 AF237726 AF237726

sequence

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405

CAACGTGACTCAGGTTGGCTTTGGTAACAACGCCACCGCTCATCAGTACTAA 456 ĊĀĀĊĠſĠĀĊſĊĀĠĠſſſĠĠĊſŢſĠĠſĀĀĊĀĀĊĠĊĠĀĊĊĠĊſĊĀſĊĀĠſĀſŢŊĀ

212911

TAAACAGTTCGGTGGTGGCAACGGTGCTGCAGTTGACCAGACTGCATCGAACTCCTTCCGT TAAACAGTTCGGTGGCGAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGT

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225

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Query Match Best Local Similarity Matches 345;

Conservative

<u>,,</u>

Score 340.8; DB 1; Pred. No. 8.3e-88; 0; Mismatches 7;

\_\_DB\_1; Length 292504;

Indels

0;

Gaps

74.7%; 98.0%;

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Karolinska Institute, MTC, Box 280,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
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                                    complement (2064. .2714)
                                                                                              complement (2064. .2714)
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transI_table=
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KEYWORDS
SOURCE
                                             ACCESSION
VERSION
                                                                                                 RESULT 14
AE008749
LOCUS
                                                                                    DEFINITION
        ORGANISM
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Best Local :
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Salmonella typhimurium
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AE008749.1 GI:16419641
                                                                             Salmonella typhimurium
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LT2, s
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Pred. No. 2.9e-64;
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one mil subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EcoCyc; http://ecocyc.PangeaSystems.com/ecocyc/
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Submitted (29-MAR-2001) Genome Sequencing Center, Department Genetics, Washington University School of Medicine, 4444 Fore Park Boulevard, St. Louis, MO 63108, USA
COMMENT Supported by NIH grant 5U 01 A143283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programmer, http://www.tigr.org/softlab/glimmer/glimmer.html and GeneWark; http://opal.biology.gatech.edu/GeneWark/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.

1 (bases 1 to 22411)

McClelland,M., Sanderson,K.E., Spieth,J., Clifton,S.W., Latreille,P., Courtney,L., Porwollik,S., Ali,J., Dante,M., Du,F., Latreille,P., Courtney,L., Porwollik,S., Scott,K., Holmes,A., Hou,S., Layman,D., Leonard,S., Nguyen,C., Scott,K., Holmes,A., Grewal,N., Mulvaney,B., Ryan,E., Sun,H., Florea,L., Miller,W., Stoneking,T., Nhan,M., Waterston,R. and Wilson,R.K. Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Salmonella typhimurium Genome Sequencing Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 413 (6858), 852-856 (2001)
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/translation="mcahnrvqenagdvylqlkvlsmgrqkavikarreakrvlrrds
RSHKQREEESVTSLVQMGGVEAIGMARDSRDTSPVKARNEAQAHYLNALDSKQLIFAT
GEAGCGKTWISAAKAAEALIHKDVERIIVTRPVLQADEDLGFLPGDIAEKFAPYFRPV
                                                                                                                                                                                                                                                                                             /note="similar to E. coli PhoB-dependent, ATP-binding | regulon component; may be helicase; induced by p starvation (AAC74105.1); Blastp hit to AAC74105.1 (354 aa), 92% identity in aa 71 - 354"
                                                                                                               /protein_id="AAL20057.1"
/db_xref="GI:16419642"
                                                                                                                                                                                                          /product="PhoB-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="synonym: 434. .439
                                                                                                                                                                                                                                             transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="phoH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "gene="phoH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="LT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:99287"
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                                                                                                                                                                                                   ATP-binding
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Forest
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RBS

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PGWAAGVSVFATTLSSITFMSIPAKAFTSDWTFIIGQYLAIALIPLVFYFYIPFFRK
LKVTSAYEYLEARFDVRCRLFASMSFMLFHIGRIAITELTVLLALRPEIAIDPVILVL
LISVMCIIYTMMGGIBGVIWTDVIQGLLLSGSALLIFIVICLKVQGGIDEIFTVTQQA
DKFFFATQFHWSWTESTVPVLMIGFLFANIQQFTASQDVVQRYIVTDSIEETKKTLLT
MAKLVAVIPVFFFFAIGSALFVYYQQHPQLLPAGFNTGGILPLFVVTEMEVGIAGLIIA
AIFAAQSSISSSLWSISSCFNSDIVQRLSKKRTPENMKIAKLVILVAGLISSAAS
VMLVMADESEIWDAFNSLIGLMGGPMTGLFMLGIFFKRANAGSAVLGIIISVITVLGA
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                                                                                                                                                                                                                                                                     /product="putative inner membrane protein"
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/db xref="GI:16419645"
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                                                                                       /gene="STM1130"
5599. .6759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to E. coli putative enzyme (AAC76255.1);
Blastp hit to AAC76255.1 (229 aa), 70% identity in aa 1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (4083. .4088)
/gene="STM1128"
                                                                                                                                                                                                                      complement (5094. .5099)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (4413. .5093)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="putative RBS for STM1128; RegulonDB:STMS1H001400" complement(4413. .5099) /gene="STM1129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="putative RBS for
complement(2580. .4088)
/gene="STM1128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / translation="MEPOPRALKPGKILDTLGAMQKSITRASQRIAQYILAFPROVTO
SIADLSRETQAGEATVIRFCRTIGYKGFQDFXMDLAIFLATISDDSSFLLDAEVSE
SDIADLAIGLKLQNTISNVLSETLNLLDMQQVLGVVDALRHCHSVYIFGVGSGGITAL
MKHKLMRIGLKGDAVSNNHFMYMQATLLKAGDVAMGVSHSGTSPETVHSLRLARQAGA
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/db_xref="G1.16419643"
                             /gene="STM1130"
/note="similar to E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative sodium/glucose
/protein_id="AAL20059.1"
/db_xref="GI:16419644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (2580. . . 4076)
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/note="similar to E. coli orf, hypothetical protein
(AAC77266.1); Blastp hit to AAC77266.1 (404 aa), 41%
                                                                                                                                                                  gene="STM1129"
note="putative RBS for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to E. coli putative cotransporter
(AAC76702.1); Blastp hit to AAC76702.1 (571 aa),
identity in aa 7 -.478"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to E. coli orf, hypothetical (AAC75480.1); Blastp hit to AAC75480.1 (285 identity in aa 15 - 264"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="STM1129"
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                                                                                                                                                                  STM1129; RegulonDB:STMS1H001401"
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Best Local
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Similarity
GCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGTGGT 360
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                                                                                                  GTAGGCCAGGGTGCGGATAACAGTACTATTGAACTGACTCAGAATGGTTTCAGAAACAAT 1806
                                                                                                                                                    GTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCCAACGTGGCTTCGGTAACAGC 300
                                                                                                                                                                                                                            AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 18008
                                                                                                                                                                                                                                                                                                                                                                                                                  CCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 17828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAAACTTTTAAAAGTAGAAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCTCTGGCA 60
                                                                                                                                                                                                                                                                                    ACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGCAGAT 240
                                                                                                                                                                                                                                                                                                                                                      CCGGATTCCACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 1794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative outer membrane protein"
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6793. .6798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative sugar transport protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to B. coli putative transport protein
(AAC77235.1); Blastp hit to AAC77235.1 (425 aa), 57%
identity in aa 25 - 418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="STM1132"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7768. .7773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="STM1132"
7768. .7773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WQYMGKMKQPLGYGVSVSYGDEVFLIGGENAKGKPVSSVTSFTMRDGNLLIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQEGLAGAFSGYSHGVLLVGGGANFPGAKQNYTNGKFYSHEGINKKWRDEVYGLINGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative inner membrane protein"
/protein_id="AAL20061.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.8%;
73.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 259.2; DB 1
Pred. No. 3.6e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for STM1132; RegulonDB:STMS1H001403"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for STM1131; RegulonDB:STMS1H001402"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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REFERENCE
AUTHORS
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AL627269
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ORGANISM
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MEDLINE
PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Comerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Complete genome sequence of a multiple drug resistant Salmonella Nature 413 (6858), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Details of S. typhi sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkhill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL627269 254050 bp
Salmonella enterica serovar Typhi
complete chromosome; segment 5/20.
AL627269 AL513382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enterica subsp. enterica serovar Typhi
Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; Gammaproteobacteria; En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella enterica subsp. Salmonella enterica subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 18188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 254050)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/S_typhi/).
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                                                                                                                                                                                                                                                                                                                                                                                                   notes "Orthologue of E. coli pepN (AMPN_ECOLI); Fasta to AMPN_ECOLI (869 aa), 94% identity in 869 aa overlag
                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="STY1078"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:90370"
L81. .2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Salmonella enterica subsp. enterica serovar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="synonym: pepN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="STY1078"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriales;
                                  CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Orthologue of E. coli YCBW_ECOLI; Fasta hit to YCBW_ECOLI (192 aa), 90% identity in 180 aa overlap. I discrepency in position of translational start site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="STY1080"
4174. .4719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="STY1080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to PYRD_ECOLI (336 / Codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1060.
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o PYRD_ECOLI (336 aa), 95% identity in 336 aa overlag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="STY1079"
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LARTDTATUSUTUDIEN GHEY FHANTGARYTCROMFOLSIKEGLTVFRDQEFSSDL
GSRAVURI SAVURIGHOY FABDAS PMAH PIR PDKVI EMNUF YILTVYZKGAEV IRMIL
TLLGEENFOKGMOLY FERHOGSAATCODF VQAMEDASAVUDLSHERRWYSQSGT PI UTV
KODYNPETEGYYILTI SGRT PATADQAEKQPLH EPA LELYDNEGNVI PLQKGGHPVNA
KODYNPETEDROYFORVPALLCEFSAPVKLEYKWSDQOLTFLWRHARNDFSRWD
VLNVTQAEQTFTEDNYYFORVPALLCEFSAPVKLEYKWSDQOLTFLWRHARNDFSRWD
AAQSLATYI KLNVARHQQGOPLSLEVHVADAFRAVULDEKIDPALAAEILTLPSANE
AAQSLATYI KLNVARHQCGOPLSLEVHVADAFRAVULDEKIDPALAAEILTLPSANE
ACLREIJ IPEYID RIA AQVIBALTRILAAELADEFLAY INANHLDEKVEVHGDIGKRTLKH
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      AQDGSGYQFLVEMLTDLNSRNPQVASRL1EPL1RLKRYDDKRQEKMRAALEQLKGLEN
LSGDLYEKITKALA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLDRAPWAMTSLKNSMKWDETRFGLEYDLDIYMIVAVDFFNMGAMENKGLNIFNSKYV
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zinc-binding region note="synonym: pyrD" note="PS00142 Neutral zinc 'gene="STY1078" note="Pfam match to family M1, score 245. gene="STY1079" entry PF01433 Peptidase\_M1, .10, E-value 1.9e-84" Peptidase

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uoua hit voverlap"

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1.4e-165" /note="PS00911 Dihydroorotate gene="STY1079" gene="STY1079" dehydrogenase, entry PF01180 DHOdehase, rogenase, score 563.50, E-value dehydrogenase signature 1"

note="PS00912 Dihydroorotate 174. .4719 dehydrogenase signature 2"

Note

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gene

SdC

	AATAGCGGC AATAGCGGC AATAGCGGC AGTTCCGGG GCTCTGCAA AATAGCGCAAT AATAGCGAAT AATAGCAAT AATAGCAAT AATAGCAAT AATAGCAAT AATAGCAAT AATAGCAAT AATAGCAAT AATAGCAAT AATAGACAAT A
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Search completed: March 15, 2004, 22:49:48 Job time : 1966.17 secs

gene

CDS

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Regult
No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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                                            1 US-08-233-788A-58

1 US-08-233-788A-56

4 US-09-252-991A-4429

4 US-09-252-991A-2024

4 US-09-252-991A-1852

4 US-09-252-991A-1931

2 US-09-103-840A-1

4 US-09-557-884-1

4 US-09-643-990A-1

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9 US-09-103-840A-1

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1 US-09-072-967-190
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Sequence 4181, Ap
Sequence 4182, Ap
Sequence 2024, Ap
Sequence 1852, Ap
Sequence 1, Appli
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Sequence 7, Appli
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Sequence 9
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#### ALIGNMENTS

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Cliv:
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILLAGIANT: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: K.ng, Joshua
REGISTRATION UNMBER: 35,570
REFERENCE/DOCKST NUMBER: 920043.403C2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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FEATURE:
NAME/KEY:
LOCATION:
US-08-233-788A-58
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                                                                                                                                                                                                            TELEX: 3723836 SEEDAN INFORMATION FOR SEQ ID NO:
                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                      TELEPHONE: (206) 622-49UU
TELEPAX: (206) 682-6031
TELEX: 372336 SEEDANBERRY
                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 CCITY: Seattle
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                                                CDS
                                                                                              linear
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RESULT 2
US-08-233-788A-56
                                                                                                                                                    COMPUTER READABLE FORM.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, vc
APPLICATION NOMBER: US/08/233,788A
PILING DATE: 26-APR-1994
ATTORNEY/AGENT INFORMATION: 43
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403
TELEPHONE: (206) 682-6031
TELEPAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 56, Application US/08233788A
Patent No. 5635617
GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: OF SALMONELLA
TITLE OF INVENTION: OF SALMONELLA
                                                                               TELEX: 3723836 SEEDANBERRY INFORMATION FOR SEQ ID NO: 56:
                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GGCGTCGTTCCACAATGGGGGGGGGGGGGGTAATCATAACGGCGGGGGGAATAGTTCCGGC 120
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Sequence 4632, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196,136

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR FILING DATE: 1998-02-18

PRIOR PRICE SEQ ID NOS: 33142

LENGTH: 1788

TYPE: DNA

ORGANIUM: Pseudomonas aeruginosa
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Best Local Similarity 69.9%;
Matches 234; Conservative
                                                                                                                                                                                                                                                                                      Local Similarity
les 53; Conserv
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STRANDEDNESS;
TOPOLOGY: line
MOLECULE TYPE; D
FEATURE;
1331 TGATCAGGGTGCCGGTGAGCAT 1310
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                                                                                                 AGCGGGTĠTÀŤŤĊĠĊĊĠĠŤGCĊĠĠAĊŤĠCGĊĠŤĠGCĠAŤĊGGĊÁĠGÁAĠCĊĠĠĊĠĠĊĠĠ 1332
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Pred. No. 7.3e-45;
0; Mismatches 101;
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FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 4429

SEQ ID NO 4429
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PRILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
SEQ ID NO 4181
LENGTH: 250
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2024/c
; Sequence 2024, Application US/09252991A
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US-09-252-991A-4429/c
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                                               RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                             1411 AGCGGGTGTATTCGCCGGTGCCGGACTGCGCGGTGGCGATCGGCAGGAAGCCGGCGGCGG
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107196.136
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N: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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Pred. No. 0.3;
0; Mismatches 29;
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Pred. No. 0.26;
0; Mismatches 29;
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GENERAL INFORMATION:

APPLICANT: MARC J. Rubenfield et al.

APPLICANT: MARC J. RUDENFIELD AND AMINO AC

TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTIC

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT ETLING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-07-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27
RESULT 8
US-09-252-991A-1931
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NUMBER OF SEQ ID NOS:
SEQ ID NO 1852
LENGTH: 669
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SEQ ID NO 2024
LENGTH: 552
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                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196:136
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                               Local Similarity 56.1%; es 64; Conservative
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                                                                                                                               207 TATTACCCAGCATGGCGGCGGTAATGGTGCAGATGTTGGTCAGGGCTCAGATGA 260
                                                                                                                                                                                                                      147 GTACGGTGGCGGTAACTCTGCACTTGCTCTGCAAACTGATGCCCGTAACTCTGACTTGAC 206
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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56.1%;
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Pred. No. 0.44;
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Pred. No. 0.48;
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Sequence 1931, Appli Patent No. 6551795 GENERAL INFORMATION:

Application US/09252991A

APPLICANT:

Marc J. Rubenfield et al.

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US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 629428
; Patent No. 629428
                                                                                                                   RESULT 10
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GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
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US-09-103-840A-2
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Applic Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R. APPLICANT: FRASER, Claire M. APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1931
                                                                                                                                                                                                                                                                                       OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Mycobacterium tuberculosis
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
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TITLE OF INVENTION:
FILE REFERENCE: 107
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43; Conservative
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56.1%;
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72.9%;
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BER: US 60/074,788
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Pred. No. 30;
0; Mismatches
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Pred. No. 0.62;
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US-09-557-884-1
                                            Query Match
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Patent No. 6506581
GENERAL INFORMATION:
                                                                                                                                                                       TELEPHONE: 301-309-8504
TELEPAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA SEQUENCES TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                             Local
                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIF: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 4411529
                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/476,102
APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371189
                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Scient STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
               l Similarity
63; Conserv
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                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 41,971
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: -Unknown>
                                                                                                                                                    SENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MD
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                         55.8%;
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72.9%;
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     Score 33; DB (
Pred. No. 30;
0; Mismatches
            0,
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Pred. No. 30;
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                                                                                        <u>:</u>
                        DB 4;
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      50;
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     Indels
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Gaps
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122 CAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAAA 181

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                                                                                                                                                                        Query Match 7.2%;
Best Local Similarity 55.8%;
Matches 63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 310-309-8439 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      740985 TTGATGTCTGTTTTTAAAACCAAATTATTTTTGAATGTCGGCGTTAAGGGT 741037
740985 TTGATGTCTGTTTTTAAAACCAAATTATTATTTTGAATGTCGGCGTTAAGGGT 741037
                                                                                     740925 CGATTTTTCGCAAGATCGTTTÄAATGAÄTATCGCCTACÄÄTTCTGCCTTGGTTATGCÄCÄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diekette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF
                                       182 CTGATGCCCGTAACTCTGACTATTACCCAGCATGGCGGCGGTAATGGT 234
                                                                                                                            122 CAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGATTTTTCGCAAGATCGTTTAAATGAATATCGCCTACAATTCTGCCTTGGTTATGCACA 740984
                                                                                                                                                                                                                                                                                                          LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/643,990A FILING DATE: 23-Aug-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 9410 Key West Avenue CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09643990A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 301-610-5790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Craig Venter
INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20850
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                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                           Score 33; DB 4; Length 1830121; Pred. No. 30;
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                                                                                     740984
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RESULT 13

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LOCATION: US-08-225-488-6
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Query Match
Best Local Similarity 46.4%;
Matches 104; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                   LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: burn, Albert APPLICANT: Hinnen, Albert Visser, Jacob
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 13-APR-1993
                                                                                                                                                   FEATURE:
NAME/KEY:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                            STRAIN: N400 | IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
HYPOTHETICAL: 1
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APPLICATION NUMBER: US
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                     NAME/KEY:
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LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                              LOCATION: ..2233)
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                 NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
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TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 2993 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
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1..829
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1154..1204
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1650..1696
                                                                                     1786..1840
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PEPD of Aspergillus niger; product of gene pepD"
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        0;
     Score 32; DB 2; Length 2993; Pred. No. 3.9; O; Mismatches 120; Indels
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RESULT 15
US-09-252-991A-10989/c
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    Sequence 10989, Application US/09252991A
PATENT NO. 6551795
GRNERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-103-840A-2
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US-09-103-840A-2/c
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
SEQ ID NO 22
SEQ ID NOS: 2
SEQ ID NOS
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Matches 108; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANIAM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                       4028916 GGCTCCCCGGGCGTTGGGCCTGCGGGCGTGGCGGCGACGGCAACCTCGGCCAGT 4028862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4029036 GGCGGAGACCGCCGCCGGCCGGCCGGCCCGGTTCCGGCTAGCTCCGGG 4028977
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REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 TACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAAACTGATGCCCGTAACTCTGAC 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001 GAGTTCGAGCCGGTCCATGCAGAAAGTACTTGCTCTCCCGGGGC 1958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 GGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGCCCAAATTCTGAGCTGAACATT 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGACTATTACCCAGCATGGCGGCGCTAATGGTGCAGATGTTGGTCAGGGCTCAGATGAC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGGAGATGTTG
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; Pred. No. 72;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
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Search completed: March 16, 2004, 04:36:54 Job time: 72.6647 secs
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US-09-252-991A-10989
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 10989
LENGTH: 1317
                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 PRIOR FILING DATE: 1998-07-27 NUMBER: OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                               393
                                                                                                                                                  453 GCCACTGCGCAGCGCCTTGTCCAGTTCCTCGGCGGTGGCGAAGGTGTGGTACTCGACGCG 394
                                                                                                                                                                                  124 AATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAAACT 183
                                                                                                                 184 GATGCCCGT 192
                                                                                                                                                                                                                                                               64 GTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGCCCA 123
                                                                                                                                                                                                                                                                                                                68;
                                                                                                                                                                                                                           GTTGTCCTTCAGCAGGGCAGGGTGTCGTGGGAGGGGACGGCGACGTCGATCGCCTC
                                                                                                                                                                                                                                                                                                          6.9%; ilarity 52.7%; Conservative
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Pred. No. 4.2;
0; Mismatches
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Gaps

454

Copyright

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2432557 seqs, 1840798884 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications NA:*
1: /cgn2_6/ptodata/2/pubpna/US07
2: /cgn2_6/ptodata/2/pubpna/FCT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atgaaacttttaaaagtaga.....cgaccgctcatcagtactaa 456
                                                                                    /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                    gn2_6/ptcdata/2/pubpna/PCT_NEW_PUB.seq:*
gn2_6/ptcdata/2/pubpna/US06_NEW_PUB.seq:*
gn2_6/ptcdata/2/pubpna/US06_PUBCOMB.seq:*
gn2_6/ptcdata/2/pubpna/PCTUS_PUBCOMB.seq:*
gn2_6/ptcdata/2/pubpna/PCTUS_PUBCOMB.seq:*
gn2_6/ptcdata/2/pubpna/PCTUS_PUBCOMB.seq:*
gn2_6/ptcdata/2/pubpna/US08_NEW_PUB.seq:*
gn2_6/ptcdata/2/pubpna/US08_PUBCOMB.seq:*
gn2_6/ptcdata/2/pubpna/US08_PUBCOMB.seq:*
_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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15	14	13	12	11	10	9	8	7	o	U	4	w	N	٢	No.
34.6	35	35.6	35.6	35.6	35.6	35.8	37	37	37.4	37.4	38.2	39	39	42.6	Score
7.6	7.7	7.8	7.8	7.8	7.8							8.6		9.3	Query
532	785	4389	3078	2122	992	1493	3309400	2580	1972	1972	625	1390	1390	135259	Length DB
14	14	15	12	15	12	14	9	9	15	14	14	15	14	12	
US-10-029-386-7202	US-10-029-386-22627	US-10-369-493-46798	US-10-389-647-226	US-10-108-260A-1242	US-10-425-114-31747	US-10-029-386-25133	US-09-738-626-1	US-09-738-626-1857	US-10-292-798-1629	US-10-017-161-1981	US-10-029-386-24675	US-10-292-798-1437	US-10-017-161-1781	US-10-240-425-1585	ID
Sequence 7202, Ap	Sequence 22627, A	Sequence 46798, A	Sequence 226, App	Sequence 1242, Ap	Sequence 31747, A	Sequence 25133, A	Sequence 1, Appli	Sequence 1857, Ap	Sequence 1629, Ap	Sequence 1981, Ap	Sequence 24675, A	Sequence 1437, Ap	Sequence 1781, Ap	Sequence 1585, Ap	Description

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70242 GTÄATGGTGGTGATGGTGATGGTGGTAATGATGGTGGTGCTGATCACAGTGATGGTG 70183

GTAGCGCTCTGGCAGGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCG 106

Matches

Best Local Query Match

Similarity

9.3%;

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Score 42.6; DB 12; Pred. No. 0.011; 0; Mismatches 174;

Length 135259;

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Gaps

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45	44	43	42	41	40	39	38	37	36	35	<u>د</u>	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
<b>33</b>	33	33	33	33	33	33	33	33.2	33.2	33.2	33.4	33.4	33.6	33.6	33.6	33.8	34	34	34.2	34.2	34.2	34.2	34.2	34.2	34.2	34.2	34.6	34.6	
7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.3	7.3	7.3				7.4	7.4	7.4	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5		7.6	
9590	3897	1973	1959	867	652	569	379	11475	1377	832				1197	652	765	1976	570	38918	38918	12981	3532	3532	1692	666	528	155074	1633	
12	12	9 (	9	12	14	14	14	14	14	12	12	12	14	14	15	15	9	9	15	14	15	15	14	14	14	14	13	15	
US-10-282-122A-33351	US-10-282-122A-22081	US-09-864-761-3471	US-09-864-761-4012	US-10-282-122A-19705	US-10-029-386-22783	US-10-029-386-3710	US-10-029-386-19106	US-10-238-075-1250	US-10-238-075-1261	US-10-282-122A-19206	US-10-282-122A-28180	US-10-282-122A-26364	US-10-156-761-1	US-10-156-761-4579	US-10-260-238-4681	US-10-369-493-44503	US-09-864-761-5052	US-09-864-761-21778	US-10-292-798-1695	US-10-017-161-2049	US-10-369-493-33865	US-10-292-798-1569	US-10-017-161-1913	US-10-355-430-33	US-10-029-386-25948	US-10-029-386-5350	US-10-026-188-6	US-10-292-798-1475	
Sequence 33351, A	Sequence 22081, A	Sequence 3471, Ap	Sequence 4012, Ap	Sequence 19705, A		Sequence 3710, Ap	Sequence 19106, A		Sequence 1261, Ap		28180,	Sequence 26364, A	Sequence 1, Appli	Sequence 4579, Ap	Sequence 4681, Ap	Sequence 44503, A	Sequence 5052, Ap	Sequence 21778, A	1695	Sequence 2049, Ap	3386		1913	Sequence 33, Appl	Sequence 25948, A		Sequence 6, Appli	Sequence 1475, Ap	der denomination of

### ALIGNMENTS

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US-10-240-425-1585
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US-10-240-425-1585/c
                                                                                                                              SOFTWARE: PatentIn Ver.
SEQ ID NO 1585
LENGTH: 135259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1585, Application US/10240425 Publication No. US20040033502A1
                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/193,446 PRIOR FILING DATE: 2000-03-31 NUMBER OF SEQ ID NOS: 1588
                                                                                                                                                                                                                                                                                                     APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Scheft, Uwe
APPLICANT: Vockley, Joseph G.
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
FILE REFERENCE: 44921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: PCT/US01/09847
PRIOR FILING DATE: 2001-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
                                                                         ORGANISM: Homo sapiens
                          OTHER INFORMATION: Genbank Accession No. US20040033502A1 Z83838
                                                    FEATURE:
                                                                                                               TYPE: DNA
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; NAME/KEY: CDS
; LOCATION: (201)
US-10-017-161-1781
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CURRENT FILLING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
SOFTWARE: Patentin Ver. 2.1
LENGTH: 1390
TYPE: DMA
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Best Local Similarity
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APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: AKUYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENITION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 094335/0152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: source
LOCATION: (1)..(1390)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                1033 GTGGTGATGGTAATAGTGATGGTGATGGCAGTGATAGTGATAGTGATGGTGATGGCAGTG
                                                                                                               302 стастсттватсавтваасвесадалаттствалатвасветталаслеттсветветв 361
                                                                                                                                                                                                                                                                             242 тторгодоростовал прасвостольтуват столосод в стротовот в стротов в стр
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 CAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 GIGTIGTICCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69945 GTGÁTCATÓGTGGTGGTGGTGGTGATGGTGCTCÁ 69909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70065 ATTATGGTGATGGTGGTGTTGATGGTGCTGATCACAGTGATGATGATAATGGCGATCATG
                                  Gregregregreatagreategrearescagregregregregreatagreategreategreategrearegrearegrearegrearegrearegrearegrearegr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287 GCTTCGGTAACAGCGCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTA 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.6%; Score 39; DB 14; Length 1390;
45.1%; Pred. No. 0.02;
ative 0; Mismatches 175; Indels (
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            RESULT 4
US-10-029-386-24675

i Sequence 24675, Application US/10029386
i Publication No. US20030194704A1
i GENERAL INFORMATION:
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Penn, Sharron G.
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Sequence 1437, Application US/10292798
Publication No. US20030235833A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
CURRENT APPLICATION NUMBER: US/10/292,798
PRIOR APPLICATION NUMBER: US/10/292,798
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR APPLICATION NUMBER: JD 2001-12-18
PRIOR APPLICATION NUMBER: JD 2001-246789
INUMBER OF SEQ ID NOS: 2007
SEQ ID NO 1437
LENGTH: 1390
TYPE: DNA
CRGANISM: Homo sapiens
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; LOCATION: (201) ... (1190)
US-10-292-798-1437
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LOCATION: (1)..(1390)
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LOCATION: source
1153 GCAATGGTGGTGATGGTGA 1171
                                                                                                                                                                          1033 GTGGTGATGGTAATAGTGATGGTGATGGCAGTGATAGTGATAGTGATGGTGATGGCAGTG
                                                                                                      362 GCAACGGTGCTGCAGTTGA 380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 СТĢĀГĢСССĢТĀАСТСТĢАСТТВАСТАТТАСССАВСĀГĢĢСĢВСĢЯТĀĀГĢĢГĢСАВАТĢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 CAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              853 Gréarégregrearegaregeageséregéagrégrégrégrégregradiation 912
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45.1%; Pred. No. 0.02;
ive 0; Mismatches 175; Indels
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Gaps

401

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APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
TITLE OF INVENTION: NOVEL G POTEIN-COUPLED REFILE REFERENCE: 08435/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: US/10/246789
PRIOR FILING DATE: 2001-06-18
ORTMARE: PAECHLIN VOE: 2430
SOPTMARE: PAECHLIN VOE: 2.1
SEQ ID NO 1981
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US-10-017-161-1981/c
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                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.8
OTHER INFORMATION: EXT HUMAN HIT: BI015471.1, EVALUE 1.00e-03
OTHER INFORMATION: NT HIT: AE000415.1, EVALUE 9.30e+00
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                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 625
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 CAGCAATCGTATTCTCCGGTAGCGCTCTGGCAGGTGTTGTTCCTCAGTACGGCGGCGGCGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTACCCAGCATGGCGGCAGTAATGGTGCAGATGTTGGTCAGGGCTCAGATGACAGCTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTCTGAAATGACGGTTAAACAGTTCGGTGGTGGCAACGGTGCTGCAGTTG 379
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                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 2001-06-18
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1629
LENGTH: 1972
TYPE: DNA
OPCANYTY.
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                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABUKATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
                                          FEATURE:
FEATURE:
NAME/KEY: modified base
FORTION: (975)...(994)
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LOCATION:
FEATURE:
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LOCATION:
                                LOCATION: (975)..(994)
OTHER INFORMATION: a, t,
                                                                                                                                  FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: modified base LOCATION: (975)..(994) OTHER INFORMATION: a, t,
                                                                                                                                                                                             FEATURE:
NAME/KEY: modified_base
                                                                                                                                                                                                             LOCATION: source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                            OCATION: (201) .. (1772)
                                                                                                                                                                         OCATION: (1)..(1972)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 GTGGTGGTGGCTGATTA 262
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(201)..(1772)
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(1)..(1972)
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                                      unknown or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown or other
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; LOCATION: (1319)..(1328); OTHER INFORMATION: a, t, US-10-292-798-1629

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g, unknown

or other

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PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 7059

SOFTWARE: Patentin ver. 3.0

SEQ ID NO 1857

LENGTH: 2580

TYPE DAA

ORGANISM: Corynebacterium glutamicum
US-09-738-626-1857
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APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKTHIRO
APPLICANT: SENOH, AKTHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, MASATO
FILLE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                    Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equence 1857, Application US/09738626
ublication No. US20020197605A1
ENERAL INFORMATION:
                                                                                                                                                                                                     Local Similarity
les 140; Conserv
                       1166
                                                                                                                       1046 AGGGTGACGCTGGCGCCGATGGCGAAGACGGCGCAGATGGTGAATCAATTACTGTTA
                          194 ACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGCAGATGTTGGTCAGGGCT 253
                                                                                       137 АСАТТТАССАСТАСССТСЯСССТААСТСТСВСАСТТССТСТССАААСТС---АГСССССТА 193
                                                                                                                                                 77 Ассессессесся таксенсе тестессе тактаране с поставаться в 136
CĈATTAĀTAAĠGGTGATĀAGGGTGĀCĠCTĠĠĊĠCCGĀTĠĠŤĠAĀĠĀŤĠGAAĠŤAĀTĠĠĊG 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280 GTGGTGGTGGTGATTA 262
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47.8%;
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                                                                                                                                                                                    Score 37; DB 9; Length 2580;
Pred. No. 0.13;
0; Mismatches 150; Indels
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Pred. No. 0.085;
0; Mismatches 101;
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RESULT 9
US-10-029-386-25133/c
/ Sequence 25133, Application US/10029386
/ Publication No. US20030194704A1
/ GENERAL INFORMATION:
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APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
NUMBER OF SEQ ID NOS: 7059
SEQ ID NO 1
IERNOTH: 3100AAA
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TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 8.1%; Score 37; DB 9; Length 3309400; Best Local Similarity 47.8%; Pred. No. 4.5; Matches 140; Conservative 0; Mismatches 150; Indels 3;
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APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
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                                                                                                                                                                                                                                                                        254 CAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTCGGTAACAGCGCTACTCTTGATC 313
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                                                                                                                                                          TGGTGTTCTCGAACGGCACTGAAATCACCATCAACAAGGGTGAGAAGGGCGAC 1784136
                                                                                                                                                                                                AGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGTGGTGGCAAC
                                                                                                                                                                                                                                                                                                              CCATTAATAAGGGTGATAAGGGTGACGCTGGCGCCGATGGTGAAGATGGAAGTAATGGCG 1784249
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
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RESULT 10
US-10-425-114-31747/c
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                                                                   CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 31747
LENGTH: 992
                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     Sequence 31747, Application US/10425114
Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                     APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: HARZEL, DAVIG K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATE 2001-12-20
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
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OTHER INFORMATION: EXPRESSED IN PLAC
OTHER INFORMATION: EXPRESSED IN HELA
OTHER INFORMATION: EXPRESSED IN LUNG
                    ORGANISM: Zea mays
                                                      TYPE: DNA
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TYPE: DNA
   OTHER INFORMATION: Clone ID: UC-ZMFLB73212F11_FLI
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IN LUNG, SIGNAL = 3.
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Pred. No. 0.26;
0; Mismatches
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US-10-108-260A-1242
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                                                                                                    Sequence 226, Application US/10389647 Publication No. US20040033549A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1242, Application US/10108260A publication No. US20040005560A1 GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: No. US20040005560A1e1 FILE REFERENCE: H1-A0106 CURRENT APPLICATION NUMBER: US/10/108,260A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT FILING DATE: 2002-
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN VEr. 2.:
SEQ ID NO 1242
LENGTH: 2122
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APPLICANT: GREENBERG, E. Peter
APPLICANT: SCHUSTER, Martin
APPLICANT: LOSTROH, Candi
TITLE OF INVENTION: QUORUM SENSING SIGNALING
FILE REFERENCE: UIZ-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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nes 71; Conserv
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150 CGGTGGCGGTAACTCTGCACTTGCTCTGCAAACTGATGCCCGTAACTCTGACTAT 209
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                                                                                                                                                                                                                                                                                                                                                                                        CGCCACCCAAGTGGAGGAAGCACTTGCGCCACTGCTGAGCGGTTGGAAGGGGAACA
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Pred. No. 0.37;
0; Mismatches 129;
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXERESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT SPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION OF STATE OF STATE
            US-10-029-386-22627/c
US-10-029-386-22627/c
Sequence 22627, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
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; ORGANISM: Pseudomonas
US-10-389-647-226
APPLICANT:
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Publication No. US20030233675A1
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PRIOR APPLICATION NUMBER: 09/653730
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/153022
PRIOR FILING DATE: 1999-09-03
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                                                                                                                                                                                                                 GTAGATGTGTCAAATGAGCCCAAGCTGAAATCATTTGTCAAAAAGCCGCA 2390
                                                                                                                                                                                                                                                                          GGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCA 416
                                                                                                                                                                                                                                                                                                                                                                                            CTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGTGGTGGCAAC
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Pred. No. 0.52;
0; Mismatches 84;
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Pred. No. 0.44;
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                                                                                                                                                                                                      SEQ ID NO 7202
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7202, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
                                                                                                                                                                                                APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
FEATURE:

OTHER INFORMATION: MAP TO AC003693.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
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SEQ ID NO 22627
LENGTH: 785
                                                                                                                                      LENGTH: 532
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE
FITTLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
RUMBER OF SEQ ID NOS: 34288
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5

OTHER INFORMATION: EXTRESSED IN HELA, SIGNAL = 0.73

OTHER INFORMATION: EST HUMAN HIT: BE767903.1, EVALUE 1.00e-03

OTHER INFORMATION: NT HIT: AJ252124.1, EVALUE 1.20e-02
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TYPE: DNA
ORGANISM: Homo sapiens
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34; Conservative
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Pred. No. 0.36;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 680)
1 (bases 1 to 680)
1 (bases 1, Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
Email: tshini@genes.nig.ac.jp
The information of this clone
URL.
                                   Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, UTCL: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                         Expressed genes in X. laevis Unpublished (2001)
                                                                                                                                                                                                                                  EST
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BJ618688
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            available through the following
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EST 01-OCT-2003

BZ997124 PUGGV90TB
BZ997127 PUGGV90TB
BZ997127 PUGGV90TB
BZ997127 PUGGV90TD
CG200536 PUIJS94TD
BZ115869 CH230-255
BX342087 BX342087
CB642466 OSJNEBD92K
AL188841 Tetraodon
BE572585 601329541
BE604165 WHE1413-1
BE604165 WHE1413-1
BE604165 WHE1413-1
BE604165 WHE1413-1
BE604165 WHE1413-1
BE604165 PUIGT-HSP-20-1
BC421645 PUIGT-STV
CG101505 PUIGOSBTD
CG142634 PUFQES1TB
BC5142634 PUFQES1TB
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CC627745 OGVBG10TV
CC327866 OGVBG09TH
CC691748 OGOBQ41TV
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BJ272995 BJ272995
CD509711 CDA97-G08
BJ404131 BJ404131
BJ4349080 BJ449080
BM276856 952011H03
BM276856 952011H03
BM276856 DSC0OURT
ANTSPIOR STANDONET

bancrofti"

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REFERENCE
AUTHORS
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COMMENT
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SOURCE
ORGANISM
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CD374421/c
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Best Local Similarity
Matches 454; Conserv
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                                                       1 (Dases 1 to 558)

Ndi,J.S., Ribeiro,J.M. and Nutman,T.B.

Toward the characterization of the Wuchereria bancrofti microfilarial transcriptome with comparisons to those of Brugia Unpublished (2003)

Contact: Thomas B. Nutman Laboratory of Parasitic Diseases
  Building 4 Room 126, Bethesda, MD 20892-0425,
Email: tnutman@niaid.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233
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                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OnChocercidae; Muchereria
                                                                                                                                                                                                                                                                                                                  Wuchereria bancrofti
Wuchereria bancrofti
                                                                                                                                                                                                                                                                                                                                                                            CD374421
CD374421.1 GI:31229939
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TNWbmfC2H3T3 Wuchereria bancrofti microfilaria cDNA (SAW95SjL Wuchereria bancrofti cDNA clone TNWbmfC2H3 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ĠĠĊŦŦŦĠĠŦŔŔĊŔŔĊĠĊĠŔĊĊĠĊŦĊŔŦĊŔĠŦŔĊŦŔŔ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCÁACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĠĊŦŔĊŦĊŦŦĠŔŦĊŔĠŦĠĠĸŔĊĠĠĊŔŔĸŔĸŦŦĊŦĠĸŔŔŦĠĸĊĠĠŦŦĸĸĸĊĸĠŦŦĊĠĠŦĠġŦ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAAATTOTGAGOTGAACATTTAOCAGTACGGTGGCGGTAACTNTGCACTTGCTCTGCAA 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC 120
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Location/Qualifiers
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/dev_stage="stage 10.5"
/clone_lib="NIBB Mochii normalized Xenopus early gastrula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'organism="Xenopus laevis"
'mol_type="mRNA"
'db_xref="taxon:8355"
/clone="XL186b22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.4%;
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Pred. No. 1.5
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1.5e-114;
2;
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(SAW95SjL-WbMf)
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                         ORIGIN
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AUTHORS
TITLE
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COMMENT
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SOURCE
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BJ348812/c
LOCUS
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Best Local Similarity //...
93; Conservative
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                                                                                                                                                                                                                                                      Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6855 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum
Dictyostelium discoideum
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 607)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 TĠTTGGCACCTGCTGGCĠCĠĠŢĠĠĊĠĠŢĀĀĊĊNĊĠĠŢĠĠŤĠĠĊĠĠŢĀĀŢĀĀŢĀĀĠĊĠĠĊĊ 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 CAAATTCTGAGCTGAACATTTACC-AGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                Contact: Tadasu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BJ348812.1 GI:19219319
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BJ348812 Dictyostelium
discoideum cDNA clone d
BJ348812
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Location/Qualifiers
                                                                                                                                                                                                                             tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                         /strain="AX4"
/db_xref="taxon:44689"
/clone="dda34011"
/sex="mat A"
/dev stage="Aggregation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: Lambda Uni-ZAP XR; Site_1: Eco RI; Site_2: MNO I; Lymphatic filarial nematode parasite of humans.—
isolated strom the blood of an infected individual from Guyana, South America and converted to double-stranded CDNA using reverse transcriptase and oligo(dT) followed by independent recombinants and the average insert size is library us constructed by Sandra J. Laney. The genome@smith.edu."
/dev_stage="Aggregation stage"
/clone_lib="Dictyostelium discoideum cDNA library,
                                                                                                                                                      /organism="Dictyostelium
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Wuchereria b
/mol_type="mRNA"
/db_xref="taxon:6293"
/clone="TNWbmfC2H3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="wuchereria bancrofti microfilaria cDNA
(SAW95SjL-WbMf)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="microfilaria"
/lab_host="XL1-Blue MRF'"
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                                                                                                                                                                                                                                                                                                                                                                                              Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               607 bp mRNA linear
m discoideum cDNA library, f
c dda34oll 3', mRNA sequence.
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Pred. No. 6.8e-06;
0; Mismatches 25;
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linear EST 06-MAR-20 rary, AF Dictyostelium

EST 06-MAR-2002

Indels Length

2

Gaps

558;

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Query Match

Score 43.

DВ

12;

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JOURNAL
REFERENCE
AUTHORS
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                          Zuechtungsforschung, Carl-von-Linne-weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion cor within cor within the sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Genomics program designated 'GABI'. Information on line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL758610 282 bp 1
Arabidopsis thaliana T-DNA flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strizhov, N., Li, Y., Rosso, M., Viehoever, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            availability can be found at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROSSO, M., Strizhov, N., Li, Y. and Weisshaar, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (flanking sequence tags)
transformed lines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Weisshaar, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jnpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pipeline for automated high-throughput generation of FSTs flanking sequence tags) from Arabidopsis thaliana T-DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNTGATGACCATGACGNTGATGATNATNACCATGANGNTGATGATNATNATCATGGTGAT
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/clone="GK-160E03-013216"
/clone=lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. Sequences displaying significant similarity to the A. thalaina nuclear genome sequence were processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                    organism="Arabidopsis"
/mol_type="genomic DNA
/strain="Columbia 0"
                                                                                                                                                                                                                                   /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:21496958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NNNNNNATGGTGATGATAACTGTGGCGGTGCCGGTGGTAATAGTGAAACAACAGTGGAG
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Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various stages including seedlings treated with a variety of hormones Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays
Zea mays
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                                                                                                                                                                                                                                                                                                                                      Individual basecall and confidence value were assigned using the Phred software (http://www.phrap.org/). Overall sequence quality assessment and vector trimming was conducted using the Lucy software (version 1.16s, http://www.tigr.org/softlab/). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers using a Perl program (est_process.pl), written by Dr. Hui-Heien
                                                                                                                                                                                                                                 FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer Sp6 (ATT TAG GTG ACA CTA TAG
Seq primer: universal (GTA AAA CGA CGG CCA GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G405 Agronomy, Tov
Tel: 515-294-0975
Fax: 515-294-2299
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: schnable@iastate.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schnable Laboratory
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nilarity 46.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            State University
    /db_xref="taxon:4577"
/clone="MEST554-D07"
/tissue_type="mixed"
/lab_host="DH10B"
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                                                                                              /mol_type="mRNA"
/cultivar="B73"
                                                                                                                                             organism="Zea mays"
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Pred. No. 10;
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AUTHORS

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ACCESSION
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 AACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGCAGATGTTGGTCAGGGC 252
                                                                                                                                                           Maize Genomics Consortium Unpublished (2003) Other_GSSs: PUGGV50TB
                                                                                                                                                                                                                      1 (bases 1 to 797)
Whitelaw, C.A., Quackenbush, J., Var
Resnick, A., Fraser, C.M., Yuan, Y.,
                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1. (bases 1 to 797)
                                                                                                                                            Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                   PUGGV50TD ZM_0.6_1.0 KB Zea mays genomic clone ZMMBTa381104, BZ997127
                              Class: sheared ends.
                                              Email: whitelaw@tigr.org
Seq primer: TF
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Other_GSSs: PUGGV50TD
Contact: Cathy Whitelaw
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Resnick, A., Fraser, C.M., Yuan, Y.,
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/clone_lib="ZM_0.6_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
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/strain="B73"
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Pred. No. 27;
0; Mismatches 88;
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REFERENCE RESULT 6 BZ997124/c 밁 Вb KEYWORDS DEFINITION á Ş **TERSION** ACCESSION B Ś ORGANISM Query Match Best Local ( Matches 165 TGCACTTGCT 174 350 410 105 Zea mays Zea mays Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. BES997124 771 bp DNA linear GSS 25-MAR-2003 PUGGV50TB ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa381104, genomic survey sequence. 4 5 BZ997124.1 GI:29240541 Similarity TGGGCTCGGT 281 CGGTAATAATAGCGGCCCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTC 164 CédercAdercredecédecrinderegrerecededédedédedecrrededérédede CGGCCTTGGTGGCGGCTCAGGATCGGGTCTGGGCGGCAACGGTGGCCTTGGCGGTGGCAG 291 CGGTAGCGCTCTGGCAGGTGTTGTTCCTCAGTACGGCGGCGGCGGTGATCCACGGTGGTGG 104 /clone lib="ISUN6"
/note="Vector: pSilp7 (4.43 kb); Site\_1: EcoRI; Site\_2: NotI; Tissue samples were collected and partially pooled prior to RNA extraction. First-strand cDNAs were prepared from 21 individual pools of oligo-dT tag primers. Distinguishable 'Dar code' tags, (N)6, were used for each code tags can be used to identify the mRNA pool from which a particular cDNA clone was derived. The 'Dar code' tags ATACGC-Germinated seeds and seedlings (1, 2, 8, 11 DAG); CACAGC--Mixed mature tissues [17, 21, 38, 69, 77 DAG); CACAGC--Mixed mature tissues [17, 21, 38, 69, 77 DAG); TAACGC--Adventious roots (65 DAG); CACAGC--Tassels (3-39 SM, 53 and 56 DAG); AGGTAC--Immature ears (0,2-3) cm, 53 and 56 DAG); AGGTAC--Immature ears (0,2-3) cm, 53 AATCGG--unpollinated first ears; CTAAGG--ear shanks; GTGAC--Uplinated first ears; CTAAGG--ear shanks; GTGAC--Cycloheximide-treated callus; GTCAC--Silks; GTGGAC--Cycloheximide-treated callus; GTCAC--Anaerobic seedlings; AGGCC--AGPC (1-aminocyclopropane-1-carboxylix seedlings; CATGCC--Nama (3) Janeau-1-carboxylix seedlings; CTAGGC--ADA (3) Janeau-1-carboxylix seedlings; CTAGGC--ADA (3) Janeau-1-carboxylix seedlings; CTAGGC--ADA (3) Janeau-1-carboxylix seedlings; CTAGGC--BABA (Abscisic acid)-treated seedlings; GCAGGA--BABA (Abscis Conservative 8.2%; 0 Score 37.2; DI Pred. No. 23; 0; Mismatches DB 12; 58; Indels Length 540; <u>,</u> 351

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TITLE
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AUTHORS
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                         Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cathy Whitelaw
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Unpublished (2003)
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/clone_lib="ZM_0.6_1.0 KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
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/clone="ZMMBTa381104"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO;
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/mol_type="genomic n
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/strain="B73"
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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 255 row: D column: 7
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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Other GSSs: CH230-255D7.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BZ115869 789 bp DN CH230-255D7.TVB CHORI-230 Segment 2 R CH230-255D7, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS.
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GTTGCTGATGGTGCTGGTGATGATGCTGATGATGATGATGGTGGTGATGATGGTGAT
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                                                                                                                                                       GGTGGTGGTGGTGATGCTGATGTTGCTGATGGTGGTGGTGATGATGCTGATGAT
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                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Brain"
/clone lib="CHORI-230 Segment 2"
/clone="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
CHORI-230 Rat (BN/S8NHsd/MCW) BAC library produced by
Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10116"
/clone="CH230-255D7"
/sex="Female"
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strain="BN/SsNHsd/MCW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                               8.1%;
45.8%;
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                                                                                                                                                                                                                                                                                                                                                       Score 37;
Pred. No.
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Russell, D.,
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BX342087
LOCUS
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                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2235.f For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DK009DD04QP1
&cluster=2235.f. Contact : Feng Liang Email : fliang@lifetech.com
URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DK009DD04QP1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GC 252
                                                                                        GTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGCAGATGTTGGTCAGG 250
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                                                  KKKMKGYHHDMMMKKKSMKKKMMCKGBMCMKBKBBGCDGMKKMMCCCGCCGCKGCCCCSS 1126
                                                                                                                                                                                                                                                      CTCAGTACGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGCCCAAATTCTG
                                                                                                                                    KGGCKGGMMKSBGMMTKMMKKKKKKMMKKKKMMMAKCMMMMMMMMWKMTMMMTKMTKMMW
                                                                                                                                                                                                                CCCCKSMGGGSKSMAGMGMKCKCCMGCKCKMKGKSCMKGMRCMGMBMMGCMMMMKCMKV 1006
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                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"/note="lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSFORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="CSODK009YH08"
                                                                                                                                                                                                                                                                                                                      7.9%;
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Pred. No. 72;
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COT 25-NORMALIZED
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                      Length 1171;
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ACCESSION
VERSION
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CNS02APC/c
   KEYWORDS
                                                                                         DEFINITION
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AUTHORS
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CB642466/c
LOCUS
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 sequence.
AL188841
AL188841.1
GSS; genome
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                                                                                                                                                                                                                                                                                                                                             61;
                                                                    CNS02APC 774 bp DNA linea: Tetraodon nigroviridis genome survey sequence PU 252I15 of library G from Tetraodon nigroviridis,
                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 675)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACKWARD: gga aac agc tat gac ca
Plate: 02 row: K column: 15
Seq primer: gga aac agc tat gac
Location/Qualifiers
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OSJNEb02K15.r OSJNEb Oryza sativa (japonica cultivar-group)
Clone OSJNEb02K15 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 520 626 3967
Fax: 520 621 9288
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85721-0088, USA
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genome survey sequence.
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/note="Vector: pBluescript II KS +; Site_1: EcoRI; S: XhoI; 24 hrs after innoculation with Rice Blast (Che 86061)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Oryza sativa/mol_type="mRNA"
/cultivar="Nipponbare"
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/clone="OSJNEb02K15"
                  GI:7826945
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Pred. No. 63;
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RESULT 13
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601329541F1 NCI_CGAP_Mam6
mRNA sequence.
BE572585
BE572585.1 GI:9816305
                                                                                                                                                                                                                                                                                                                                                           97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetraodon nigroviridis Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Meopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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/note="Genoscope sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="252I15"
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MAGE:3603347 5',
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticeae; Triticeae; Triticeae; Triticeae; Triticeae; Triticeae; Triticeae; Triticeae; Triticum.

1 (bases 1 to 435)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat
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WHE1413-1416_I13_I13ZS Wheat
Triticum aestivum cDNA clone
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8792 row: a column: 12
High quality sequence stop: 679.
                                                                                                                                                                                                                                                                                               Triticum aestivum
                                                                                                                                                                                                                                                                                                                            Triticum aestivum (bread wheat)
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National Institutes of Health, Mammalian
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
1 (bases 1 to 935)
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/clone="IMAGE:3603347"
/sex="female, virgin"
/tissue_type="infiltrating di
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sa
Site_2: Not1; Cloned unidirectionally. Primer: Ōligo
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
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/mol_type="mRNA"
/strain="FVB/N"
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Pred. No. 73;
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Sciurognathi; Muridae;
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Best Local
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               1 (bases 1 to 498)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat genomes - Drought stressed leaf cDNA library Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89;
                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
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WHE1413-1416_B07_B07ZS Wheat drought stressed leaf
Triticum aestivum cDNA clone WHE1413-1416_B07_B07,
BE604467
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Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and
Sequence have been trimmed score less than 20
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Unpublished (2000)
Contact: Olin Anderson
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Olin
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/lab_host="E. coli SOLR"
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/tissue_type="Leaf"
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Pred. No. 57;
0; Mismatches
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Sequence have been trimmed to remove vector sequence
quality sequence with phred score less than 20
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                       Conservative
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/lab host="E. coli SOLR"
/lab host="E. coli SOLR"
/clone_lib="Wheat drought stressed leaf cDNA library"
/clone_lib="Wheat drought stressed leaf cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were given a gradual
stress down to 65% and 78% RWC at Texas Tech University
(D. Zhang in HT Nguyen lab). Total RNA and poly(A) RNA
were prepared, a cDNA library was made, and the cDNA
clones were in vivo excised to give pBluescript phagemids
in the TJ Close lab (Choi, Close), at the University of
California, Riverside. Plasmid DNA preparations and DNA
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/tissue_type="Leaf"
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/cultivar="TAM W101"
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Search completed: March 16, 2004, 04:28:45 Job time: 2237.91 secs

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Match Length DB ID  No. Score Match Length DB ID  Description  2 456 100.0 10346 1 AE002025  456 100.0 10346 1 AE002025  456 100.0 15047 1 D90741  3 454.4 99.6 1711 1 AF27573 AE005315 E8 AE002025 E8 AE0020	AL132848 Caenorhab AL591376 Mouse DN	521 3 CEY47H10A 489 10 AL591376	.3 31	7.	4 4 5 4	0 0
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Cuery Ratch Length DB ID  Score Match Length DB ID  1 456 100.0 4680 1 ECCSGABDG X9 456 100.0 10346 1 AE000205 2 456 100.0 15047 1 D90741 4 454.4 99.6 1711 1 AF275733 AF 5 454.4 99.6 327773 1 AE015315 5 454.4 99.6 327773 1 AE015513 AE 6 454.4 99.6 327773 1 AE015513 AE 7 454.2 98.9 306338 1 AE016759 AE 7 454.2 98.9 306358 1 AE016759 AE 8 451.2 98.9 306358 1 AE016759 AE 9 449.6 98.6 292504 1 AE016981 AE 9 449.6 98.6 292504 1 AE016981 AE 1 332.8 73.0 2067 1 SEU13280 AD 1 332.8 73.0 5103 1 STAC2301 AD 2 331.2 72.6 301983 1 AE016840 AE 5 331.2 72.6 301983 1 AE016840 AE 6 323 70.8 2920 1 CFR515701 AL 8 266.4 58.4 1048 1 STACFBA AD AD AD 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	AJ515	1 ESA51570	6.6	58	19	
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## ALIGNMENTS

REFERENCE AUTHORS TITLE RESULT 1 ECCSGABDG LOCUS SOURCE ORGANISM DEFINITION ACCESSION VERSION KEYWORDS

E.coli csgG, csgF, csgE, x90754 X90754.1 GI:1147558 ECCSGABDG 4680 bp DNA csgD, csgB, csgA, linear BCT 07-JUL-2002 and orfC genes.

CBGF

gene; csgG

gene;

csgA gene; csgB gene; csgD gene; csgE gene; csg orfC gene. Escherichia coli Escherichia coli Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia. Enterobacteriales;

Hammar, M., Arnqvist, A., Bian, Z., Olsen, A. and Normark, S. Expression of two csg operons is required for production of

Pred. No.

is the number of results predicted by chance to have

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FEATURES
Source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hammar, M.
Direct Submission
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RafsDkwesDyTgnlTinerpsarwgswiTitvnQdvIfQTflfplkkdfekTvvfal
IQTBEALNRRQINQALLSTGDLAHDEF"
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'note=""
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4 (bases 1 to 10346)
Plunkett,G. III.
Direct Submission
Submitted (13-CCT-1998) Laboratory of Genetics, Unisconsin, 445 Henry Mall, Madison, WI 53706, USA
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Direct Submission
Oleroted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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Direct Submission

(16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.

Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 10346)
Blattner, F. P., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpattick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The complete genome sequence of Escherichia coli K-12 Science 277 (5331), 1453-1474 (1997)
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Escherichia coli K12
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AE000205.1 GI:1787265
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69. .392
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                                                                                                                                                                                                                                                                                                                       note="factor
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|xref="taxon:83333"
|Dlement(<1. .48)
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                                                                                                                                                                                                                                                      b1029"
                                                                                                                                      aa ORF is 19 pct identical (4 gaps) approx. 288 aa protein Y320_MYCGE
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88 aa protein FAS2_CANAL
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1094983"

at 1098094" at 1097992"

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Gaps

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/gene="ycdw"
/note="synonym: b1033"
2393. .3370
/gene="ycdw"
/function="putative enzyme; Not classified"
/note="0325; This 325 aa ORF is 32 pct identical (2 gaps)
to 177 residues of an approx. 312 aa protein YPRA_CORGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement (2111. .2198)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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/note="synonym: b1031"
1513. .1926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1494. ....
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| Gene="bloo"
| function="orf; Unknown"
| function="orf; Unknown"
| note="o83; This 83 aa ORF is 25 pct identical (7 gaps)
| roal residues of an approx. 616 aa protein ALBU_RABIT SW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MIPDYLTFIREQDKRNLIVIYAIGLILIGFYWKNAGFTFPSEDJ
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FLRFSKRYAFLGRLFLQEIDLFFSSENALSTFFAKPLWLRLFILLVIEUWMITLVSVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="b1030"
1494. .1745
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'bound moiety="DeoR
.337, _1365
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                                                                                                                                                                                                                                             factor Sigma70;
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Oshima, T., Aiba, H., Baba, T., Fujita, K., Hayashi, K., Ho Ikemoto, K., Inada, T., Itoh, T., Kajihara, M., Kanai, K., Kimura, S., Kitagawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Mocomura, K., Nakamura, Y., Nashi Nishio, Y., Saito, N., Sampei, G., Seki, Y., Tagami, H., Tawada, C., Yamamoto, Y., Yano, M. and Horiuchi, T.
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BScherichia coli K12 genomic DNA. (23.7 - 24.0 min).

BSCHerichia coli K12 genomic DNA. (23.7 - 24.0 min).

DS90741.AB001340

DS90741.1 GI:1651509

Complete and shotgun sequencing; csgG; csgF; csgE; csgD; csgB; csgA; ycdE; cls; nov; mdoG.

BScherichia coli K12

Escherichia coli K12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3383.
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/note="factor Sigma70;
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Pred. No. 2.7e-116;
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              . Nashimoto, H.,
""" remoto, K.,
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gene CDS

CDS gene

promoter

protein\_bind

protein\_bind

Sac gene promoter promoter

Honjo,A.,
., Kashimoto,K.,

BCT 25-DEC-2002

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8676

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8556 60 0,

gene

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TITLE
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The Jap
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Collaboration Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, S., Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yamamoto, Y., and Yano, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (29-JUL-1996) Hirotada Mori, NARA Institute of Science
Submitted (29-JUL-1996) Hirotada Mori, NARA Institute of Science
and Technology, Res. & Edu. Center for Genetic Info.; 8916-5
Takayama, Ikoma, Nara 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Japan E.coli genome DNA sequencing group Members: (1995.4 - 1996.3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8905232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             information operator:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Address: National Institute E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http:bsw3.aist-nara.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Japan E. coli genome database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Address: NARA Institute of Science Ikoma, 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name: Hirotada Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name: Takashi Horiuchi
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                                                                                                                                                                                                                                                                                                                        /clone="Kohara clone #231"
/note="Nuclectide position 1097101-1112147 from
initiation site of ThrA (0 min.).-This clone is
Kohara lambda miniset library."
      similar to SwissProt
                                                                                        WRIWFEAYFLLCYVPCLIYYFFYCRFLWHNDFMMACDMYFRWGHFNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                          note="unnamed protein product; ORF_ID:o230#5"
                                                                                                                                                                                                                                                                                                                                                                                                                                               map="23.7-24.0 min"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:83333"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol_type="genomic DNA"
strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Escherichia coli K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute of Basic
Accession Number P45637"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biology, Okazaki, 444, Japan
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```
CsgG precursor."

(protein id="BAA35827.1"

/protein id="BAA35827.1"

/db xref="GI:4062610"

/translation="MGRIFFLLVAVMLLSGCLTAPPKEAARPTLMPRAQSYKDLTHLPA

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NLLNERKIIRAAQENGTVAINNRIPLQSLTAANIMVEGSIIGYESNVKSGGVGARYFG

IGADTQYQLLQIAVNLRVNVSTGBILSSVNTSKTILSYEVQAGVFRFIDYQRLLEGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="ORF_ID:0231#5
similar to SwissProt Accession Number P52103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MCSISFMAAFSAIMRGMNILLSIAITTGILSGIMGWVAVSLGLL
SWAGFLGCTAYFACPGGLKGLAISAATLLSGVVWAMVIIYGSALAPHLEILGYVITG
IVAFLMCIQAKQLLLSFVPGTFIGACATFAGQGDWKLVLPSLALGLIFGYAMKNSGLW
LAARSAKTAHREQEIKNKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="baa35824.1"
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Edaphhmhfimmriwprvdgvgilkgibaniknvdgbidcsgkmfdsldlings
PVfAPHDKATNTQAMIATIASGNVHIISHPGNPKYEIDVKAVABAAAKHQVALEINNS
SFLISRKGSBDNCREVAAAVRDAGGWVALGSDSHTAFTMGEFEECLKILDAVDFPPER
                                                                                                                                                                                                                                                                                     complement(4977. .5393)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MNEFSILCRVLGSLYYRQPQDPLLVPLFTLIREGKLAANWPLEQDELLTRLQKSCDMTQVSADYNALFIGDECAVPPYRSAWVEGATEAEVRAFLSERGMPLADTPADHIGTLLLAASWLBDQSTEDESEALETLFSEYLLPWCGAFLGKVEAHATTPFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MDIIPYHPTFDTQWWIEALRKAIPQARVRAWKSGDNDSADYALV
WHPPVEMLAGRDLKAVPALGAVDSILSKLQAHPEMLMPSVPLERLEDTGMGERQWGEY
AVSQVLHWFRFDDYRIQQNSSHWQDLPEYHREDFTIGILGAGVLGSKVAQSLQTWRF
PLRCWSRTRKSWPGVQSFAGREELSAFLSQCRVLINLLPNTPETVGIINQQLLEKLPD
Bgf precursor."
protein_id="BAA35828.1"
/db_xref="GI:4062611"
                                                                                  product="Curli
                                                                                                                                                                                                                       /gene≃"c8gF"
/note="ORF_ID:o231#6
                                                                                                                                                                                                                                                                                                                                                    complement (4977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (4117. .4950)
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/protein_id="BAA35826.1"
/db_xref="GI:4062609"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTMAPLTRDAISAMWDELEEDSEE"
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/protein_id="BAA35825.1"
/db_xref="GI:4062608"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAYLLNLARGVHVVEDDLLAALDSGKVKGAMLDVFNREPLPPESPLWQHPRVTITPHV
AAITRPAEAVEYISRTIAQLEKGERVCGQVDRARGY"
                                                                                                                          codon_start=1
transl_table=
                                                                                                                                                                                                                                                                                                                   gene="csgF"
                                                                                                                                                                                                                                                                                                                                                                                                                /GYTSNEPVMLCLMSAIETGVIFLINDGIDRGLWDLQNKAERQNDILVKYRHMSVPPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="csgG"
                                                                                                                                                                                     imilar to SwissProt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="Curli
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transI_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="unnamed protein product; ORF_ID:o231#4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
transl_table=
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                                                                                                                                                                                            Accession Number P52104"
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         456;
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                                                                                                                        CAGTCGCAAATGGCTATTCGCGTGACACAACGTTAA 456
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                                                                                                                                                                                                                                                                                                                                       GATGCCÁGTÁTTTCGCÁAGGTGCTTATGGTAÁTÁCTGCGÁTGÁTTÁTCCAGÁÁAGGTTCT
                                                                                                                                                                                                                                                                                                                                                                               GATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGCAGGGAGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGCAGGGAGGCTCAAAACTTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGGCA 7456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGCAGGTTÁTGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAG
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ilarity 100.0%;
Conservative 0;
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RSLDDissgsiilldmmeadkklihymqdtlsrknnnikiillnipedypyrdienwp
Hingvfysmedqervnglqgvlrgecyftoklasylithsgnyrynstesallihre
KEILNKLRIGASNNEIARSLFISENTVKTHLYNLFKKIAVKNRTQAVSWANDNLRR"
7217. . 7672
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7217. .7672
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similar to SwissProt Accession Number P52106"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="BAA35830.1"
db_xref="GI:4062613"
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/transl_table=
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RAFSDKWBSDYTGNLTINERPSARWGSWITITVNQDVIFQTFLFPLKRDFEKTVVFAL
IQTEEALNRRQINQALLSTGDLHDEF"
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/gene="csgD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (5812. .6462)
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/product="Curli production
CsgE precursor."
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similar to SwissProt Accession Number P52105"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MRVKHAVVLLMLISPLSWAGTMTFQFRNENFGGNENNGAFLLNS AQAQNSYKDBSYNDDFGIETBSALDNFTQAIOSQILGGLLSNINTGKPGRMVTNDYIV DIANRDGQLQLNVTDRKTGQTSTIQVSGLQNNSTDF" Complement [5418. .5807)
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|db_xref="GI:4062612"
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Best Local Similarity 99.8
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AUTHORS
TITLE
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AUTHORS
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VERSION
KEYWORDS
SOURCE
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AF275733
LOCUS
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TCTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTA
                                                                                                  GCAĞCAĞĞTTATĞATTTAĞĞTAATTCAĞAATATAAĞTTCĞĞĞTAAATĞAATTĞAĞTAAĞ
                                                                                                                                                     GCAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAG
                                                                                                                                                                                                                                                                             ATGAAAAACAAATTGTTATTTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCC
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Uhlich, G.A., Keen, J.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
1 (bases 1 to 1711)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli
Escherichia coli
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CsgA protein (csgA) genes, con
AF275733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="csgA"
/gene="csgA"
/codon_start=1
/trans1_table=11
/trans1_table=11
/product="csgA protein"
/protein_id="AAKS3212_1"
/protein_id="AAKS3212_1"
/db_xref="G:14039401"
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TLDQMNGKDSHMTVKQFGGGNGAAVDQTASNSTVNVTQVGFGNNATAHQY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="mknkilfymltilgapgiaaaagydlanseynfavnelskssfn
Qaaiigagtnnsaqlaqggskilayvaqegssnrakidqrgdynlayidqagsanda
Siggaygntamiiqkgsgnkanitqygtqktaivvqrqsqmairvtqr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="CsgB protein"
/protein_id="AAK53211.1"
/db_xref="GI:14039400"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Escherichia coli"
| mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="taxon:562"
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strain="43895 Red Variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="csg8"
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                                                                                                                                                                                                                                                                                                                                                                                      Score 454.4; I
Pred. No. 7.6e.
0; Mismatches
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43895 Red Variant CsgB protein (csgB) and
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7.6e-116;
nes 1;
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REFERENCE
AUTHORS
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AE005315
LOCUS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 10190)
Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Posfai, G., Hackett, J., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Welch, R.A., and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (22-OCT-2000) Laboratory
Wisconsin, 445 Henry Mall, Madison,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7
Nature 409 (6819), 529-533 (2001)
21074935
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Perna,N.T., Plunkett,G. III, Burland,V., Mau,B., Glasner,J.D.,
Perna,N.T., Plunkett,G. Evans,P.S., Gregor,J., Kirkpatrick,H.A.,
Rose,D.J., Mayhew,G.F., Evans,P.S., Gregor,J., Kirkpatrick,H.A.,
Posfai,G., Hackett,J., Klink,S., Boutin,A., Shao,Y., Miller,L.,
Grotbeck,E.J., Davis,N.W.; Lim,A., Dimalanta,E., Potamousis,K.,
Apodaca,J., Anantharaman,T.S., Lin,J., Yen,G., Schwartz,D.C.,
Welch,R.A. and Blattner,F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli 0157:H7 EDL933
Escherichia coli 0157:H7 EDL933
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Escherichia coli O157:H7 EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCT
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/gene="csgB"
/function="structural component; Cell exterior
constituents: Surface structures"
/note="Residues 1 to 151 of 151 are 100.00 pct identical
to residues 1 to 151 of 151 from Escherichia coli K-12
                                                                                                                                                                /note="enterohemorrhagic" 617. .1072
                                                                                                       /note="synonym: 617. .1072
                                                                                                                                           /gene="csg8"
                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/strain="EDL933"
                                                                                                                                                                                                                                                                                    organism="Escherichia coli O157:H7 EDL933"
                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                       serotype="0157:H7"
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2489. .3022

'genee"21679"

/function="orf; Unknown function"

/note="Residues 1 to 177 of 177 are 100.00

to residues 1 to 177 of 177 from Bscherichi

Strain MG1655; B1045"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative curli production protein"
/protein id="AAGS5789.1"
/db.xref="GT:1.2514575"
/translation="MNALLLLAALSSQITFNTTQQGDMYTIIPEVTLTQSCLCRVQIL
/translation="MNALLLLAALSSQITFNTTQQGDMYTIIPEVTLTQSCLCRVQIL
SLREGSSGGSQTKQEKTLSLPANQPIALTKLSLNISPDDRVKIVVTVSDGQSLHLSQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="minor curlin subunit precursor, similar ro CsgA"
/protein id="AAC55787.1"
/db_xref="GI:12514573"
/tb_aref="MI:1514573"
/translation="MINKLEYMMLTILGAPGIAAAAGYDLANSEYNFAVNELSKSSFN
OAAIIGOAGTNNSAQLRQGGSKLLAVVAQEGSSNRAKIDQTGDYNLAYIDQAGSANDA
SISQGAYGNTAMIIOKGSGNKANITQYGTQKTAIVVQRQSQMAIRVTQR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /function="orf; Unknown function"
/note="Residues 1 to 103 of 103 are 98.05
residues 1 to 103 of 103 from Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2083. .2394
/gene="Z1678"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="putative structure; Not classified"
/note="Residues 1 to 110 of 110 are 98.18 pct identical
residues 1 to 110 of 110 from Escherichia coli K-12 Stra
MG1655: B1043"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1630. .1962
/gene="csgC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mkllkvaaiaaivfsgsalagvvpqygggggnhggggnnsgpns
Elniyqygggnsalalqadarnsdltitqhgggngadvgqgsddssidltorgfgnsa
Tldqwngkdshmtvkqfgggngaavdqtasnstvnvtqvgfgnnatahqy"
/transl_table=11
/product="putative polyprotein"
/protein_id="AAG55791.1"
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                                                                                                                                                                                                                                                                                                             /protein_id="AAG55790.1"
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STQSSPVEMNCPQNGSVPGKTYSSKALMSGNVKNAQIASVKVQYLDKQKKLAVMNIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WG1655: B1044"
                                                                                                                                                                                                                                           /gene="Z1679"
                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/product="orf, h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="Z1678"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="csgC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAG55788.1"
/db_xref="GI:12514574"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="curlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MG1655: B1042"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             residues 1 to 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="csgA"
/function="regulator; Cell exterior constituents: Surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="csgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=
/transl_table
                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=1
|transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="synonym:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Residues 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .1962
                                                                            start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _table=11
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                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to 152 of 152 are 96.71 of 151 from Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                         protein"
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coli K-12 Strain
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ia coli K-12
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CDS

note="synonym: Z1680"

/transī\_table=11

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/codor start=1
/codor start=1
/transT_table=11
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VKELKYSPDYFTFGDVQHDKDTWKDLGFAFFKSFWIERPKDTDKRUTIYALLDSSRATGAY
VKELKYSPDYFTFGDVQKIYLTRDKVGKLGVAPLTSMFLFGRVQPSPANNYFBELHDSNG
GAGVYGLSARGLAIDTALPSGESFRFKGFWIERFKGFUFFSRDEDSNG
AWVTPKGERGTWYDKSKTLADKVGKLGVAPLTSMFLFGRVQPSPANNYFBELHDSNG
AWVTPKGEMGKGSVELVEIFMNDETNDNIVAYWTPDGLFBCKEMMFKYTITFSRDED
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ANDE"
IGDNGEIVESTVRYNPUTKGWRLVMRVKVKDAKKTTEMRAALVNADQTLSSTWSYQLP
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/transT table=11
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/db xref="01:2514579"
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TLPQFIHQYVKKKFSMVKLSVIFUCLGIGYAVIRRTIETIVYPFILSNGTENFIVMQTL
RNNLENSDKTNKKFSMVKLSVIFUCLGIGYAVIRTTEIVYPFILSNGTENFIVMQTTL
VITWLGLAMMVNNVFSFGHRLLNFTSBGCTLAAALAFVAYLLNQRYGSGDAWMYETES
TSNWLGFLCGLIFVVGIAIILIYBIHLRIPLLKFLFSGKPVVKRENDKAPAR"
                                                                                                                                                                                                                                                                                                                                                                                                 /function="enzyme; Osmotic adaptation"
/note="Residues 1 to 511 of 511 are 99.80
residues 1 to 511 of 511 from Escherichia
//MG1655: B1048"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ymdD"
/function="orf; Unknown function"
/note="Residues 1 to 385 of 385 are 99.22 pct identical to
residues 1 to 385 of 385 from Escherichia coli K-12 Strain
MG1655; B1047"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /traislation="MMKKTPTSTKDSLPNKEMNDLPRLASAVLPLCSOHPGQCGLFPL
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TPGGLDDLIRLDSHPRIEVRLFRPFSESFLLRFLGYITDFSELMRRHMKSFTVDGVV
TLVGGRNIGDAYFGAGEBELFSDLDVMAJGPVVEDVADDFARYWYCKSVSPLQOVLDV
PGGRADRLELPASWHNDAMTHRYLRKMESSPFINHLVDGTLFLIWAXTRLLSDDPAK
SCHANDVAVVHAGYARWRKVLLAYGVELYELKFERFROSSTLANTRAFKTKXVKIAILTN
FSIDGKTVFIGSSTFDRSTLLNTEMGFVIESETLAQLIDKRFIGSGYDDAAWQLRLDR
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FSIDGKTVAIGSTFALSTEMGFVIESETLAGLIDKRFIGSGYDDAAWQLRLDR
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/protein_id="AAG55792.1"
/db_xref="GI:12514578"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="putative enzyme; Not classified"
/note="Residues 1 to 493 of 493 are 99.59 pct identical to
residues 1 to 493 of 493 from Escherichia coli K-12 Strain
MG1655; B1046"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="GI:12514577"
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ALLDACLKVRQQQGDCPTGHAVITLAGDLPAKAVVHTVGPVMRGGEQNEDQLLQDAYL
NSLRIVVAANSYTSVAPPAISTGVYGYPRAAAABIAVKTVSEFITRHALPEQVYFVCYD
EENAHLYERLLTQQGDE"
                                                                                                                                                                                                                                                                                                                                                                                                                 pct identical to
coli K-12 Strain
                                                                                                                                                                               REFERENCE
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AUTHORS
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SOURCE
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Best Local
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                                                                                                                                                                                                                                Complete nucleotide sequence of the prophage VT2-Sakai carrying the verotoxin 2 genes of the enterohemorrhagic Escherichia coli 0157:H7 derived from the Sakai outbreak Genes Genet. Syst. 74 (5), 227-239 (1999)
                                                                                                                                                                                                                                                                                                                  Makino,K., Yokoyama,K., Kubota,Y., Yutsudo,C.H., Kimura,S., Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida, Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T., Sasakawa,C. and Shinagawa,H.
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Escherichia coli 0157:H7
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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AP002554 BA000007
AP002554.1 GI:13360491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGATTGACCAGACAGAGATTATAAACCTTGCATATATTGATCAGGCGGGCAGTGCCAAT 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CÓCCAGOGAGOCTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCA
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ilarity 99.8%;
Conservative
                                                                                                                            Murata,T., Nakayama,K., Kuhara,S., Hattori,M.,
, Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H. and
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7531. 10074
/gene="mdoH"
/function="enzyme; Osmotic adaptation"
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be,H., Iida,T.,
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CDS

/gene="ymdD" /note="synonym: Z1681" complement(4453. .5610) complement (4453. .5610)

SGD gene

/note="synonym:

Z1683"

gene="mdoG"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-JUN-2000) Ken Kurokawa, Osaka University, Ger Information Research Center; 3-1, Yamadaoka, Suita, Osaka 5 Japan (8-mail:ken@gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365, URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete genome sequence of enterohemorrhagic Escherichia coli 0157:17 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete nucleotide sequence of the prophage VT1-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli 0157:H7 strain derived from the Sakai outbreak
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Ohnishi,M., Kurokawa,K
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                                                                                                                                                                              project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to YCBY_ECOLI gi|1787181 percent identity 99 in 702 aa (Conserved in E.coli K-12)"
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in 635 aa (Conserved in E.coli K-12)"
                                                                                                                            LSQDFARNRQIHNCWLITAA"
                                                                                                                                           VDMSRTYLEWAERNLRLNGLTGRAHRLIQADCLAWLREANEQFDLIFIDPFTFSNSKR
MEDAFDVQRDHLALMKDLKRLLRAGGTIMFSNNKRGFRMDLDGLAKLGLKAQEITQKT
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/strain="0157:H7"
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SGS

/note="similar to YMBA\_ECOLI gi|1787185 percent identity 98 in 182 aa (Conserved in E.coli K-12)"

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IODSLYTDHIDYLMFKOSVRGLOPGARVEMGSLKTGNLYGNLYVDLDFYPNT
PALTGIREPMGYQIIPTVSGGLAQIQOKLMGALDKINKLPLNPMIEQATSTLSESGNT
MKXLQTTLDSMNKILASQSMOQLFTDMQSTLAELNRSMGGFQPGSAAXNKMVADMQRL
NOT BET ONLYWINGENEN WEGENEN KONG
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VTDLLGSKMPSTILAGVILLMSEGSYEVAAVIFLASIMVPTLKMIALAMLCWDAKGHG
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DI SRLVMNDSEKNIMELAKVQEQLDHINAGOLENRI NEVLAQIGLDPNVALSSLSGG
WLKKAALVSNPRVLLDESTNHLDI ETI DWLEGFLKTFRIGTI I FISHBRSI KR
MATRI VDLDRAKLIVSNPRVLLLDESTNHLDI ETI DWLEGFLKTFRIGTI I FISHBRSI KN
MATRI VDLDRAKLIVSNPRVLLDESTNHLDI ETI DWLEGFLKTFRIGTI I FISHBRSI KN
RTTRNEGRVRALKAMRRERGERREVMGTAKMQVEEASRSGKI VFEMEDVCYQVDGKQL
VKDFSAQVLAGDKI ALI GPNCCGKTTLLKLMLGQLQADSGRI HVGTKLEVAY EPQHRA
ELDPDKTVMDNLAEGKQEVMCGKFRTVLKLMLGQLQADSGRI HVGTKLEVAY EPQHRA
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I FEGGGKI GRYVGGYHDARGQOEQYVALKQPAVKKNEEPAA FKAETVKRSSSKLSYKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to PQIB ECOLI gi|1787184 percent identity
99 in 546 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="ECs1035"
5565. .7205
                                                                                                                                      dqvlrelqpvlktlneksnalvfeakdkkdpepkrakq"
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/gene="ECs1036"
/217. .7765
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/transl_table=11
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1307. .5560
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/transl_table=11
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Matches 455;
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| Shigela flexneri 2a str. 3

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                                                                                                                                                                                                                                                                                                                                GÁTGCCAGTÁTTTCGCAAGGTGCTTATGGTAÁTÁCTGCGATGÁTTATCCAGÁAAGGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                             AAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAAC 300
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100 in 172 aa (Conserved in E.coli K-12) "
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/codon_start=-
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene≈"ECs1037"
8021. .8188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MTIAALMLAGCSSGEINKNYYQLPVVQSGTQSTASQGNRLLMVEQVAVPDYLAGNGVYQTSDVKYYIANNNLWASPLDQQLRNTLVANLSTQLPGMVVASQELAGNGVTUTUTEFNGRYDGKVIVSGEWLLNHQGQLIKRPFRLEGVQTQDGYDEMVXLAGVWSQEAASIAQEIKRLP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ECs1037"
/note="identical to RMF_ECOLI gi|1787186 (Conserved
E.coli K-12)"
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                                                                       A linear BCT 18-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-MAY-2001) Microbial Genome Center of Chinese Ministry of Public Health, 100 YingXin Jie, XuanWu Qu, Beijing 100052, P.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jin, 0. Yuan, Z.H., Xu, J.G., Wang, Y., Shen, Y., Lu, W.C., Wang, J.H., Liu, H., Yang, J., Yang, F., Qu, D., Zhang, X.B., Zhang, J.Y., Yang, G.W., Wu, H.T., Dong, J., Sun, L.L., Xue, Y., Zhao, A.L., Gao, Y.S., Zhu, J.P., Kan, B., Chen, S.X., Yao, Z.J., He, B.K., Chen, R.S., Ma, D.L., Qiang, B.O., Wen, Y.M., Hou, Y.D. and Yu, J. Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli Nucleic Acids Res. 30 (20), 4432-4441 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shigella flexneri 2a str. 301
Shigella flexneri 2a str. 301
Bacteria, Proteobacteria; Game
I Enterobacteriaceae; Shigella.
1 (bases 1 to 10370)
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                                                                                                                                                          /codon_start=1
/transl table=11
/product="orf, conserved h
/protein_id="AAN42552.1"
/db_xref="GI:24051314"
                                                                         /translation="MYPVDLHMHTVASTHAYSTLSDYIAQAKQKGIKLFAITDHGGPDM EDAPHHMHFIMMRIWPRVVDGYGILRGIEANIKNVDGZIDCSGKMFDSLDLIIAGFHE PVFAPHDKATNYQAMISTIASGNVHIISHFGMPKYBIDVKAVAEAAKHQVALEINNS SFLHSRKGSEDNCRAVAAAVRDAGGWVALGSDSHTAFTMGEFEECLKILDAVDFPLER
/locus_tag="SF1029"
2203. .2757
                                                                                                                                                                                                                                   /locus_tag="SF1028"
/locus_tag="SF1028"
/note="Residues 1 to 245 of 245 are 99 pct identical to residues 1 to 245 of a 245 aa protein from Bscherichia coli 0157:H7 EDL933 ref: NP_287168.1"
                                       gene="ycdy"
                                                                   LNVSPRRLLNFLESRGMAPIAEFADL"
                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
1442. .2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus tag="SF1027"
/locus tag="SF1027"
/notes similar to Escherichia coli K12 putative
dehydrogenase gi: 1787270 (326 aa). BLAST with identity
99% in 326 aa. This CDS contains an in-frame stop codon.
The sequence has been checked and is believed to be
correct."
                                                                                                                                                                                                                                                                                                                                                                                       /gene="ycdx"
                                                                                                                                                                                                                                                                                                                                                    locus_tag="SF1028"
442. .2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:198214"
complement(127. .214)
/product="tRNA-Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="ycdw"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="anticodon: GGA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="301"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Shigella flexneri
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _tag="SF1027"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                         hypothetical protein"
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/product="transposase of Tn10"
/proteain_id="AAN42655.1"
/proteain_id="AAN42655.1"
/db_xref="GI:24051317"
/translation="MCELDILHDSLYOPCPELHLKRLNSLTLACHALLDCKTLTLTEL
GRNLPTKARTKHNIKRIDRLLGNRHLHKERLAVYRWHASFICSGNTMFIVLVDWSDIR
GQKRLMYLRASVALHGRSVTLYEKAFPLSEQCSKKAHDQFLADLASILPSNTTPLIVS
DAGFKYPWYKSVEKLGWYMLSRVRGKYQYADLASINASINGHSWTLATNLPVEIR
LTKSNFISCQILLYKSRSKGRKNQRSTRTHCHHPSPKLYSASAKEPWILATNLPVEIR
TPKQLVNIYSKUMQIEETFRDLKSPAYGLGLHSRTSSSERFDIMLLIALMLQUTCWL
TPKQLVNIYSKUMQIEETFRDLKSPAYGLGLHSRTSSSERFDIMLLIALMLQUTCWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="SF1031"
/note="similar to Escherichia coli K12 curli production
/note="similar to Escherichia coli K12 curli production
assembly-transport component, 2nd curli operon gi: 1787274
(278 aa). BLAST with identity of 97% in 257 aa. This CDS
contains an in-frame stop codon. The sequence has been
checked and is believed to be correct."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (4454..5662)

/locus tags"SF1032"

/note="Residues 1 to 402 of 402 are 100 pct identic residues 1 to 402 of a protein from Plasmid ref: NP_052925.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (4454. .5662)
/locus_tag="SF1032"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MCSISPMAAFSAIMRGMNILLSIAITTGILSGIWGWVAVSLGLL
SWAGFLGCTAYFACPQGGLKGLAISAATLLSGVVWAMVIIYGSALAPHLBILGYVITG
IVAFLMCIQAKQLLLSFVPGTFIGACATFAGQGDWKLVLPSLALGLVFGYAMKNSGLW
LAARSAKTAHREQEIKNKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="SF1030"
/note="Residues 1 to 179 of 179 are 98 pct identical to /note="Residues 1 to 179 of a 179 aa protein from Escherichia coli K12 ref: NP_415554.1"
/codon_start=1
/transl_table=11
                                                                                           complement (5995.
                                                                                                                                                                           complement (5995. .6384)
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DELLTRLQKSCDMTQVSADYNALFIGDECAVPPYRSAMVEDATEAEVRAFLSERGMLL
ADTPADHIGTLLLAASWLEDQSTEDESEALETLFSEYLLPWCGAFLGKVEAHATTPFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus tag="SF1029"
/note="Residues 1 to 184 of 184 are 99 pct identical to residues 1 to 184 of a 184 as protein from Escherichia coli 0157:H7 EDL933 ref: NP_287169.1"
/gene="csgE"
/locus_tag="SF1033"
/note="Residues 1 to 129 of 129 are 98 pct identical
                                                                                                                                                                                                                              agvhaqkqgwdkhfqantvrnrnvlstvrlgmevlrhsgytttredslvaatlltqnl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="orf, conserved hypothetical protein"
/protein_id="AAN42654.1"
/db_xref="GI:24051316"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus_tag="SF1030"
2811. .3350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon start=1
/transI_table=11
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/protein_id="AAN42653.1"
/db_xref="GI:24051315"
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/transl_table=
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                                                                                                                  _tag="SF1033"
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                                                                                           .6384)
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Plasmid R100
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Query Match
Best Local
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                                               241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGAAAAACAAATTGTTATTTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCC 60
                             AAGATTGACCAGACAGGAGATTATATACCTTGCATATATTGATCAGGCGGGCAGTGCCAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                         ATGAAAAACAAATTGTTATTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCC
                                                                                                                               CGGCAGGGAGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCA
                                                                                                                                                                                                                                                                                                      GCAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAG
                                                                                                                                                                                                                                                                                                                                                    GCAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAG
AAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAAC 8092
                                                                                                  CGGCAGGGAGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAATCGGGCA
                                                                                                                                                                                                    TCTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTA
                                                                                                                                                                                                                                    TCTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transT_table=11
/transT_table=11
/product="minor curlin subunit precursor, similar ro CsgA"
/protein id="AAN42658.1"
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NELSKSSFNQAAIIGQAGTNNSAQLRQGGSKLLAVVAQBGSSNRAKIDQTGDYNLAYI
DQAGSANDASISQGAYGNTAMIIQKGSGNKANITQYGTQKTAVVVQRQSQMAIRVTQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="SP1035"
/note="Residues 10 to 160 of 160 are 99 pct identical to residues 1 to 151 of a 151 aa protein from Escherichia coli 0157:H7 EDL933 ref: NP_287175.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MRSIKKWGFIMFNEVHSIHGHTLLLITKPSLQATALLQHLKQSL
ATTGKLHNIQRSLDDISGSGILLLDMYSADKKLIHYWQDTLSRGNNIKIKLLHXTPED
YPYRDIENWPHINGYWYAMBOQERVVNGLQGYLKJGKYFTQKLASYLLTHKGNYRYNS
TESALLTHREKEILNKLRIGASNNEIARSLFISENTVKTHLYNLFKKIAVKNRTQAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Residues 11 to 226 of 226 are 100 pct identical to residues 1 to 216 of a 216 as protein from Escherichia (157:H7 EDL933 ref: NP_287174.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (6389. .7069)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (6389. .7069)
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Rafsdkwesdytgnltinerpsarwgswititvnqdvifqtflfplkrdsektvvfal
iqteealnrrqinqallstddlahdef"
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2nd curli operon"
/protein_id="AAN42656.1"
/db_xref="GI:24051318"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 residues 1 to 129 of a 129 aa protein from Escherichia
coli 0157:H7 EDL933 ref: NP_287173.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7766. .8248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="putative 2-component transcriptional regulator
for 2nd curli operon"
protein id="AAN42857.1"
/db_xref="GI:24051319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="SF1034"
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/transl_table=11
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transl_table=
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'766. .8248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="csgB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="cagD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="csgD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 451.2; DB 1;
Pred. No. 5.8e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            assembly-transport component,
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                                                                                                  8032
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CDS

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REFERENCE
AUTHORS
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AUTHORS
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AE016759
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8213 CAGTCGCAAATGGCAATTCGCGTGACACAACGTTAA 8248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Enteropacuation, 2011 (bases 1 to 306358)

Nelch,R.A., Burland,V., Plunkett,G.D. III, Redford,P., Roesch,P.,
Rasko,D.A., Buckles,E.L., Liou,S.-R., Boutin,A., Hackett,J.,
Stroud,D., Mayhew,G.F., Rose,D.J., Zhou,S., Schwartz,D.C.,
Perna,N.T., Mobley,H.L.T., Donnenberg,M.S. and Blattner,F.R.
Extensive Mosiac Structure Revealed by the Complete Genome Sequence
of Uropathogenic Escherichia coli
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 17020-17024 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (20-JUN-2002) Genetics Laboratory, University of Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
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Welch,R.A., Burland,V., Plunkett,G.D. III, Redford,P., Roesch,P.,
Rasko,D.A., Buckles,E.L., Liou,S.-R., Boutin,A., Hackett,J.,
Stroud,D., Mayhew,G.F., Rose,D.J., Zhou,S., Schwartz,D.C.,
Perna,N.T., Mobley,H.L.T., Donnenberg,M.S. and Blattner,F.R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli CFT073 section 5
AE016759 AE014075
AE016759.1 GI:26107507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Escherichia coli CFT073
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/product="ALP binding cassette (ABC) transporter homolog"
/product="AN79727.1"
/protein_id="AAN79727.1"
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RDFIGNYVRRGYAGMLSLWVQSFTLEAALTPLTRQAVNDALAGNPARLPWLAGGILLIAF
PHTLLOWCPVPLAVFTYYIAGIAVMSPAMTLIVVCVVCLAITALRARRRVFAQT
GMASDDLANLTBHIREVLAQISVVKSCVAEMEETHWLDRQSRQIVRVEIGANISQAMP
RTQASVERVFALIDTRSQMEDCTESINSQVVGLELENWSEDYHHGDRHILSDISFSLR
RTQASVERVFALIDTRSQMEDCTESINSQVVGLELENWSEDYHHGDRHILSDISFSLR
RTQASVERVFALIDTRSQMEDCTESINSQVVGLELENWSEDYHHGDRHILSDISFSLR
VFEDAFLFAGTVAENIAYGHPQATADDIRRAAAAGASDFINALPKGFDSLLTERGTIV
LSGGORQRIALARALITAPDVLILDDTTSAVDAVTEAEINTALGRYADEGHMLLVIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTAATAAAGCAAATATTACACAGTATGGTACTCAAAAAACGGCAGTTGTAGTGCAGAGA 8212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTAATAAAGCAAATATTACACAGTATGGTACTCAAAAAACGGCAATTGTAGTGCAGAGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĠĀTĠĊĊĀĠŤĀŦŤŤĊĠĊĀĀĠĠŤĠĊŦŦĀŤĠĠŦĀĀŦĀĊŤĠĊĠĀŤĠĀŦŤĀŤĊĊĀĠĀĀĀĠĠŤŤĊŤ 8152
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                                                                                                                                                                                                                                                                                                                                                                            /note="Residues 27 to 1231 of 1245 are 80.16 pct identical to residues 1 to 1209 of 1218 from GenPept.129 : 
>emb[CAD05883.1 | (AL627276) putative ABC transporter protein [Salmonella enterica subsp. enterica serovar Typhi]"
                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /locus_tag="c1253"
complement(83. .3820)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="iroC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          locus_tag="c1253"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="iroC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:199310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/strain="CFT073"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Escherichia coli CFT073"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome.
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repeat_region
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/locus tag="n(1257"
/functIon="IS, phage, Tn"
/note="Residues 8 to 120 of 120 are 98.23 pct identical residues 316 to 428 of 442 from MG1655 : b4278"
/transT_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRSTLQLASRVVVLDKGRWVDTGTPABLEARCPAFRALMTGDSDFLATSHNSHNELWP
ARPATQDDVTDTGDKGFVARMTRVPENAVQQALAGKGRKVTSLLKPVARMFVIAALLI
ALDSAAGVGVLILLQHGIDSGVAAGDMSTIGLCALLALCLVIVGMCSYSLQTVFAARA
LBSVQBSVRLRSFGHMLRLGLFWHEKHADSRLTRMTVDVDSLARFLQNGLAGAATSLV
TMFAIAATMEWLDPILALTALSAVPVRALATMIYRLSTPAYAQARLEIGKVNSTLQB
KVSGLRVVQSHGQQELEGARLBALSBEFRATRVRAQKYLAVYFPFLTFCTEASYAAVL
LVGASQVVAAGEMTAGVLAAFFLLLGQFYGPVQOLSGIVDAWQQATASGCHIDBLLATB
TLKLLAGLSSVLPYTGALHLDEVTFSYEDSHEPALMKLTLTIFBEGMVVAVVGRSGAGKS
TLKLLAGLSFTHGNIRIGVQMLDDASLTEYRRQIGLVDQDVALSSDIAEMIRYSR
PSATNEDVEIASQRAGLYEMVCNLPQGFRTFVNNGGADLSAGQRQLIALARAQLANAH
AFVCTMEGTISTAGRAGLYGMVCNLPGGTTIFTAGRCDLIAVRGRCDLIAVRGKGLL

AGVCTWEGTISTAGRAGLYGMVCNLCGTNIUDDASLTVARLUTTAQRCDLIAVARAQLANAH
AGVCTMEGTISTAGRAGLYGMVCNLCGTNIUDDASLTVARRLUTTAQRCDLIAVARAGLANAH
AGVCTMEGTISTAGRAGLYGMVCNLCGTNIUDDASLTVARRLUTTAQRCDLIAVARAGLANAH
AGVCTMEGTISTAGRAGLYGMVCNCGTNIUDDASLTVARRLUTTAQRCDLIAVARAGLANAH
AGVCTMEGTISTAGRAGLYGMVCNCGTNIUDDASLTVARRLUTTAQRCDLIAVARAGLANAH
AGVCTMEGTISTAGRAGLYGMVCNCGTNIUDDASLTVARRLUTTAQRCDLIAVIDKGLL
                                                                                                                                                                                                                      /insertion_seq="IS4"
complement(6598. 6960)
/locus_tag="c1257"
complement(6598. 6960)
                                                                                                                                                                                                                                                                                                                                                            complement (6578. .6940)
/note="incomplete"
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Vpyrekraalgcilrki.cewksyrilbabccadhihmlvbippkyksysgfmgylkgks
slwpybqgodlkfkyrnrefmckgyyydtvgkytakiqdvikhqlebbkygbqlsipy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Hypothetical protein"
/protein_id="AAN79730.1"
/db_xref="GI:26107531"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="c1256"
/note="Residues 18 to 169 of 169 are 94.07 pct identical to residues 1 to 152 of 152 from SwissProt.40 : >sp[057334]T200_SALTY Transposase for insertion sequence element IS200"
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/transl_table=
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RTPASSVSSSVYSASVSRTAADIMLLSNNPLFAPGQVSFFGCSLAASGIHVTILE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mrklpdlrqaerdflmrilevgpplygllypvlslaqaervng/translation="mrklpdlrqaerdflmrilevgpplygllypvlslaqaervng-thytlasggqpaqxaeraglvvpdaapgldseagyrhheaqrkxsnigtqqnenfsees
EEMADHLVEFAGHWRDLIITYPPLGVIGPLIAAKYDIPVMQTVGFGHTPWHIRGVTR
SLIDAYRRHNVGATPROMATIOVTPSMSILENDGREIIFMQYVPYNGGAVWEPWWER
RPDRKRLLVSLGTVKPMVDGLDLIAWMDSASSVDAEIILHSANAKSDLRSIBSNNY
LVDWLPMGVFLNGADGFIHHGGAGNTLTALHAGIPQIVGGQGDADRPVNARVVAERGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="Hypothetical protein"
(protein id="AAN79729.1"
/db_xref="GI:26107530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        insertion_seq="IS1541A-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'codon_start=1
'transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Putative glucosyltransferase"
/protein_id="AAN79728.1"
/db_xref="GI:26107529"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (3882. .5045)
/gene="iroB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (3882. .5045)
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535. .5834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1/
transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGDVGLSSNMINAFLNNRSLRKASEEVAAEMAAQPCPGEVAKSLITMVQKG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          locus_tag="c1254"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _tag="c1256"
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gene SdC

SdC gene

gene CDS

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Query Match
Best Local Similarity
Matches 453; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sgo
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          complement (8832. .9290)
/locus tag="c1260"
/function="putative enzyme; Transposases Insertion
Sequence Associated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="c1260"
complement(8832. .9290)
/locus_tag="c1260"
                                                                                                                                                                                                                                                 /translation="MASAADARRIVSHYERRWLIEEYHKAWKSGGTCVESLRMQTRDN LERMYVIKAFIAVRMLGLRQEGISEETQNDSCKKILTPTEWKLLWVKLEGKQLPSQTP TLKWACLKLGRWHDSKRTGRPGWVVMWDGWFRLQDMVEGYPVMKSLDQEI" COMplement (9302. .9667) /locus_tag="c1261"
                                                                                                                                                      /note="Residues 1 to 35 of 121 are 97.14 pct identical residues 59 to 93 of 316 from GenPept.129 : 
-ygb|AAK18437.1|AF348706 126 (AF348706) putative transposase [Shigella flexneri]"
                                                                                                                                                                                                                                       complement (9302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus_tag="c5534"
/product="tRNA-Arg"
/function="RNA; tRNA"
complement(8832. .929)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānblation="mkdlsfirfflaillllvppalefpvihrhitpgaltlcvital
IITLLASLGGRLVSVKCISEISFIRRHRIECMMAGFMIYFWTFSLIAGWYKPQFKKEY
QTLHYENARYYVLARYDGRLVLSQSYRSGSRKFVIINGGHRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="c1259"
/notce="Residues 1 to 139 of 144 are 50.71 pct identical residues 104 to 242 of 258 from GenPept.129:
-ygb|AAK18487.1|AF348706_176 (AF348706) orf, hypothetical [Shigella flexneri]"
                                                                                                                                                                                                         /locus tag="c1261"
/note="po-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mprQpDQGYREIKQTmQLSRLTLRSKKPELVEQELWGVLLAYNL
VRYQMIKMAEHLKGYWPNQLSFSESCGMVMRMLMTLQGASPGRIPELMRDLASMGQLV
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/product="Hypothetical
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/db_xref="GI:26107536"
                                                                                                                                                                                                                                                                                                                                  /product="Putative Transposase"
/protein_id="AAN79734.1"
/db_xref="GI:26107535"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Hypothetical protein"
/protein_id="AAN79733.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db xref="G1:26107533"
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/LOSEQVLPSFWELNKKQYEGFEFYQIFSGNIVASCSSCSGVSSNSSAHYARCTDFMRH
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                                                                                                                                                                                                                                                                                                                                                                                  /transI_table=
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/transT table=11
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                                                                                                                            codon_start=1
transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                              note="Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10cus_tag="c5534"
477. .8553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                locus_tag="c1259"
835. .8269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAN79731.:
/db_xref="GI:26107532"
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|protein_id="AAN79731.1"
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651. .8013
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              98.9%;
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Score 451.2; DB 1;
Pred. No. 5.5e-115;
0; Mismatches 3;
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44773 ATGAAAAACAAATTGTTATTTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I (bases 1 to 292504)
Wei,J., Goldberg,M.B., Burland,V., Venkatesan,M.M., Deng,W.,
Fournier,G., Mayhew,G.F., Plunkett,G. III, Rose,D.J., Darling,
Mau,B., Perna,N.T., Payne,S.M., Runyen-Janecky,L.J., Zhou,S.,
Schwartz,D.C. and Blattner,F.R.
Complete Genome Sequence and Comparative Genomics of Shigella
flexneri Serotype 2a Strain 2457T
Infect. Immun. 71 (5), 2775-2786 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shigella flexneri 2a str. 2457T
Shigella flexneri 2a str. 2457T
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriacea; Shigella.
                                                                                                                                                                                                                                                                                         Submitted (13-JUN-2002) Genetics Laboratory, Wisconsin - Madison, 445 Henry Mall, Madison,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGTCGCAAATGGCTATTCGCGTGACACAACGTTAA 45228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 292504)
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locus_tag="S0884"
                                                                                                                   serotype="2a"
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str. 2457T
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., Darling, A.,
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SDRYRTQLENTES (DWLEAQRROSELTALSQAIWLLIGALAVILMLWMASGGVGGNAQP
GALIALFVFCALAAFEALAPVTGAFGHLGQVLASAVRISDLTDQKFEVTFPDTQTRVA
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                                  /locus tag="S0887"
/function="transport; Not classified"
/note="residues 1 to 588 of 588 are 92.85 pct identical to residues 1 to 588 of 588 from Escherichia coli K-12 ;
codon_start=1
                                                                                                                                                                      complement (3194. .4960)
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                                                                                                                                                                                                                                                                                       complement (3194. .4960)
                                                                                                                                                                                                                                                                                                                            TESQILELLAKWMREKTVLMVTHRLRGLSRFQQIIVMDNGQIIEQGTHAELLARQGRY
                                                                                                                                                                                                                                                              /gene="cydD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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transport"
                                                                                                                                                                                                                                 locus_tag="S0887"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  residues 1 to
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/protein_id="App16349_1"
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/translation="MRLVQLSRHSIAFPSPEGALREPNGLLALGGDLSPARLLMAYQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /locus_tag="50886"
/function="transport; Transport of small molecules: Other"
/note="residues 1 to 573 of 573 are 97.03 pct identical to
residues 1 to 573 of 573 from Escherichia coli K-12 :
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complement(1472. .3193)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPNNFWVPRCLFSPQE"
complement(1472. .3193)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RMENASKTALLVFCEEFIGHGGKLIDCQVLNDHTASLGACEIPRRDYLNYLNQMRLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1/
transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="residues 1 to 234 of 234 are 100.00 pct identical to residues 1 to 234 of 234 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="enzyme; Aminoacyl tRNA synthetases,
modification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (726. .1430)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="protein chain initiation factor IF-1"
(protein id="AAP16348.1"
/db_xref="GI:30040617"
/translation="MAKEDNIEMOGTVLETLPNTMFRVELENGHVVTAHISGKMRKNY
IRILTGDKVTYELTPYDLSKGRIVFRSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus_tag="S0885"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           locus_tag="S0885"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="residues 1 to 72 of 72 are 100.00 pct identical to residues 1 to 72 of 72 from Escherichia coli K-12 : B0884"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="aat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /locus tag="80884"
/function="factor; Proteins - translation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (223. .441)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  component of cytochrome-related
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                                                                                                                                                                                                                                                                                                                                                                           gene
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/codon start=1
/transl_table=11
/product="cell division protein"
/protein_id="AAP16354.1"
/db_xref="GI:30040623"
                                                                                                                                                                                                                                                                       /function="phenotype; Cell division"
forte="residues 1 to 737 of 1342 are 68.24 pct identical
presidues 1 to 737 of 1329 from Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="wvdskkrpgkdldridrnilnelokdgrisnvelskrvglsptp
CLERVRRLEROGFIOGYTALLNPHYLDASLLVFVEITLNRGAPDVFEOFNTAVOKLEE
IQECHLVSGDFDYLLKTRVPDMSAYRKLLGETLLRLPGVNDTRTYVVMEEVKQSNRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="S0890"
7221. .11249
/gene="ftsK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="S0889"
/function="regulator; Central intermediary metabolism:
/function="regulator; Central intermediary metabolism:
/function="regulator; Central intermediary metabolism:
/note="residues 1 to 164 of 164 are 100.00 pct identical
to residues 1 to 164 of 164 from Escherichia coli K-12 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="thioredoxin reductase"
/product="thioredoxin reductase"
/product="thioredoxin reductase"
/product="filioredoxin reductase"
/product="filioredoxin reductase"
/product="filioredoxin reductase"
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/translation="MGTTKHSkliigsgpagy"/"
/translation="MGTTKHSkliigsgpagy"/"
/translatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="ftsK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="regulator for leucine (or lrp) regulon and nigh-affinity branched-chain amino acid transport syr/protein id="AAP16353.1" /db_xref="GI:30040622"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/transl_table=11
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DFCHYDTCVTLAAGFLALILAPEFFQPLRDLGTFYHAKAQAVQAADSLKTFMETPLAH
PORGEAELALTDFUTIRAEDLFITSPEKKTLAGFLNTTLPAGQRAVLVGRSGSKSSL
LNALSGFLSYGGSLRINGIELADLSPESWRKHLSWVGQNPQLPAAKLADNVLLARFDA
SEQELQAALDNAWVSEFLFLLFQCUTFVGDQAARLSVGQAQRVAVARALLNPCSLLL
LDEPAASLDAHSEGRVWEALNAASLRQTTLMVTHQLEDLADWDVIWVMQDGRIIEQGR
VAELSVAGGFFATLLAHRQEEI"
COMplement (5083. .6048)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ocus_tag="S0890"
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592. .7086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /locus tag="S0888"
/function="enzyme; 2-Deoxyribonucleotide metabolism"
/note="residues 1 to 321 of 321 are 95.95 pct identiones 1 to 321 from Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="S0888"
complement(5083. .6048)
/gene="trxB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="waksrokeltrwlkoosvisorwlnisrligfvsgiliiaoawf
MARIIOHMIWENIPREALLLPFTLLVLTFVLRAWVWLRERVGYHAGOHIRFAIRROV
LDRLOOAGPAWIOGKPAGSWATLVLEOIDMHDYYARYLPOWALAVSVPLLIVVAIFP
SWWAAALIILIGTAPLIPLFMALVGMGAADAWRNFLALARLSGHFLDRLRGWETLRIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=
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/product="ATP-binding component of cytochrome-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAP16351.1"
/db_xref="GI:30040620"
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CDS

gene

CDS gene

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452;
Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract Infect. Immun. 72 (7), 4151-4158 (2003)
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                                                                                                                                                                                                                    Citrobacter sp. Fec2
Citrobacter sp. Fec2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                              csgA gene; csgB gene; csgD gene; curlin-csgA protein; component of curlin monomers; regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSP515700
Citrobacter sp.
                                                                                                                                                                                                                                                                                                                                                                                                  AJ515700
AJ515700.1 GI:31790491
                                                                                                                                                                                                   Enterobacteriaceae; Citrobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTAATAAAGCAAATATTACACAGTATGGTACTCAAAAAAACGGCAATTGTAGTGCAGAGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAAGGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGATTGACCAGACAGGAGATTATAAACCTTGCATATATTGATCAGGCGGGCAGTGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGCAGGGAGGCTCAAAACTTTTGGCGGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTTCATTTAATCAGGCAGCCATAATTGGTCAGGCTGGGACTAATAATAGTGCTCAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGAAAAACAAATTGTTATTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGTCGCAAATGGCAATTCGCGTGACACAACGTTAA 211270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGCAGGGAGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAATCGGGCA
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99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fec2
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Pred. No. 1.5e-114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2889
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                                                                                                                                                                                                                                                                                                                                                                nucleation
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   CGGCAGGGAGGCTCAAAACTTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCA 240
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Query Match Best Local :

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JOURNAL REFERENCE

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ACCESSION VERSION

DEFINITION

KEYWORDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Romling, U.
Direct Submission
                                                                                                                 GCAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGGTAAATGAATTGAGTAAG
                                                                                                                                                                           ATGAAAAACAAATTGTTATTATGATGTTAACAGTACTGGGTGCGCCTGGAATTGCTTCC 1682
                           TCTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTA 180
                                                                                        ATGAAAAACAAATTGTTATTTATGATGTTAACAATACTGGGGTGCGCCTGGGATTGCAGCC
TCTTCATTTAATCAGGCAGCCATTATTGGTCAAGTGGGCACGAATAATAGTGCAAAGATG 1802
                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mknkllfmmltvlgapgiasatsyplahseynfavnelskssfn
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SisQsnyGntamiiQkGsGnkanitQyGtQkTavvvQRQSQMairviQr
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RSLDDISSGIVLVDMMEADKKLIHYWQDNLSRKNNNLKTLLLNTPDDYPYRDIENWE
HINGVFYNADDEERVUNGLOGILRGECYFSOKLASYLITHSGNYRYNSSESALLTHS
KEILNKLRIGASNIEIARSLFISENTVKTHLYNLFKKIAVKNRTQAVSWANDNLRR"
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/gene="csgD"
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/protein_id="CAD56670.1"
/db_xref="GI:31790492"
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protein_id="CAD56671.1"

/db_xref="G1:31790493"
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/transl_table=
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1623. .2078
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transl_table=11
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86.4%;
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3 (bases 1 to 2067)
Collinson, S.K., Doran, J.L., Banser, P.A. and Kay Direct Submission
Submitted (13-DEC-1995) S. Karen Collinson, Bio Microbiology, University of Victoria, P.O. Box Victoria, BC VBW 3P6, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kay,W.W.
Salmonella enteritidis agfBAC operon encoding thin,
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Doran, J.L., Collinson, S.K., Burian, J., Sarlos, G., Todd, E.C., Munro, C.K., Kay, C.M., Banser, P.A., Peterkin, P.I. and Kay, W.W. DNA-based diagnostic tests for Salmonella species targeting agfA, the structural gene for thin, aggregative fimbriae

J. Clin. Microbiol. 31 (9), 2263-2273 (1993)
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Salmonella enteritidis
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                                                                                                                                                          /gene="agfB"
/note="fimbrin-like protein
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596. .1151
                                                                                                                                                                                                                                                                                                                                          /map="between putA and
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/strain="27655-3b"
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, Clouthier,S.C., Doran,J.L., Banser,P.A.
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GATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1710. .2036
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IDQWNAXNSDITVGQYGGNNAALVNQTASDSSYMVRQVGFGNNATANQY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="agfA"
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83.1%;
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/note="putative signal sequence of
fimbrin-like protein"
1193 1_1k
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753. .1148
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6.4e-82;
77;
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JOURNAL MEDLINE PUBMED REFERENCE

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AUTHORS TITLE

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Submitted (29-OCT-1997) Romling U.,
Karolinska Institute, MTC, Box 280,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhimurium
Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Salmonella typhimurium cagG,
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csgG gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGTCGCATATGGCTATTCGCGTCACCCCAACGCTAA 1151
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fibers are highly conserved between Salmonella typhimurium
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                                                                                                                                                                                                                                                                                                                                                                        complement (361. .1194)
/gene="csgG"
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                                                                                                                                                                                                                                                                                                                                              function="lipoprotein"
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CSGE,
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3469. .3531
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3371. .3376
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S"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="csgDEFG"
complement (2891
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DIANRDGQLQLnVTDRKTGTTSTIEVSGLQTQSTDF"
                                                                                                                                                                                                                                                                                                                                                                                                         3469
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                                                                                                                                                                                                                                                            /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                   /gene="csgB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="csgBA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="csgDEFG"
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transl_table=
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                                                                                                                                                                                                                                                                                                                                           function="nucleator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="SWISS-PROT:054293"
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                                                                                                                                                                                                                                                                                                                                                                              gene="csgB"
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                                                                                     61 GCAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAG 120
                                                                                                                                                                                                                   379;
Similarity
                                                               GĆGAČÁAATTÁTGÁTGTGGCTGGTTCAGAGTÁTÁÁTTTTGGGGTTÁÁÁTGÁÁTTAÁGCÁÁG 3588
                      TCTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTA 180
                                                                                                                                ATGAAAAACAAATTGTTATTTATGATGTTGACAATACTGGGTGCGCCCTGGGATTGCAACC
                                                                                                                                                   ATGAAAAACAAATTGTTATTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCC
                                                                                                                                                                                                            73.0%;
ilarity 83.1%;
Conservative
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4940. .>5103

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4940. .5103
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4534. .4806
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function="fiber subunit
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Pred. No. 6.3e-82;
0; Mismatches 77;
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alregnate chemistries or covered by high quality data (i.e., phred quality: 30); an attempt was made to resolve all sequencing problems, such

quality >=

http://kinich.cifn.unam.mx:8850/db/regulondb\_intro.frameset

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PUBMED
REFERENCE
AUTHORS
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AUTHORS
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The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and
                                                       EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EcoCyc; http://ecocyc.PangeaSystems.com/ecocyc/
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                                                                                                                                                        Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
                                                                                                                                                                                                                                            Submitted (29-MAR-2001) Genome Sequencing Center, Department Genetics, Washington University School of Medicine, 4444 Fore Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 AI43283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae; Salmonella.

1 (bases 1 to 22411)

McClelland,M., Sanderson,K.E., Spieth,J., Clifton,S.W.,

McClelland,M., Sanderson,K.E., Spieth,J., Clifton,S.W.,

Latreille,P., Courtney,L., Porwollik,S., Ali,J., Dante,M., Du,F.,

Hou,S., Layman,D., Leonard,S., Nguyen,C., Scott,K., Holmes,A.,

Grewal,N., Mulvaney,E., Ryan,E., Sun,H., Florea,L., Miller,W.,

Stoneking,T., Nhan,M., Waterston,R. and Wilson,R.K.

Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 GGTAATAAAGCAAATATTACACAGTATGGTACTCAAAAAACGGCAATTGTAGTGCAGAGA 420
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Salmonella typhimurium LT2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                         complement (2298. .2303)
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/note="putative RBS for S
complement (2580. .4088)
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454. .1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mepopprlkpgkildtlgamoksitrasoriaoyilafprovto siabisretoageatvirecritykgfodfxdlatelaftsdbsspllbaevse sblababisretoageatvirecritykgfodfxdlatelaftsdbspllbaevse sblababisretoksgitsulsetulldmogvigtopdartchsvylfgvgssgitalb mkhklæriglrodavsnnffmymoatllkagdvamgvshsgtspetvhsirllaroaga ttvatthlugsplcebadfclingnrogmlogdsigtkaaolfvrfdllytllvosspe
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DKFFPATQFHWSWTESTVPVLMIGFLFANIQQFTASQDVVQRYIVTDSIEETKKTLLT
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lkvtsayfylfarfdyrcrlfasmsfwlfhigriaitfltvlalrpfiaidpvilvl
                                                                                                                                                                                                                                                                                                                                          complement (2580. .4076)
/gene="STM1128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mcahnrvqenagdvylqlkvlsmgrqkavikarreakrvlrrds
RSHKQREEESVTSLVQWGGVEALGMARDSRDTSFVKARNEAQAHYLNALDSKQLIFAT
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LTRLGENVTVIVNGDITQCDLPRGVRSGLSDALERFEEDEMVGIVFNKDDCVRSALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="phoH"
/note="similar to E. coli PhoB-dependent, ATP-binding pho
regulon component; may be helicase; induced by P
starvation (AAC74105.1); Blastp hit to AAC74105.1 (354
aa), 92% identity in aa 71 - 354"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Salmonella typhimurium LT2"
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/note="LT2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QARESKLRTMNALDMTK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (1414. .2295)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (1414. .2303)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QRTLHAYS"
                                                                                                                                                                                                                                                             /note="similar to E. coli putative cotransporter
(AAC76702.1); Blastp hit to AAC76702.1 (571 aa),
identity in aa 7 - 478"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 component"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to E. coli orf, hypothetical protein (AAC75480.1); Blastp hit to AAC75480.1 (285 aa), 29% identity in aa 15 - 264"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="STM1127"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="PhoB-dependent ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="synonym:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="phoH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _xref="GI:16419642"
                                                                                                                                                                                                              _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RBS for phoH; RegulonDB:STMS1H001398"
                                                                                                                                                                                                                                                                                                                                                                                                                                                STM1127; RegulonDB:STMS1H001399"
                                                                                                                                                                                cotransporter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pho regulon
                                                                                                                                                                                                                                                                                         22%
                        Sg
                                                                                                   RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
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FESGPDTSIYKPYLRGQYNFDSGVYMAGRYRYDYARKTANYSDDEKTNRFDTYIGYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6805.
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AFDASFRSRPVDIDSLLTRIRLHGLLAMADCSTVNEGISCHQKGIEFIGTTLSGYTGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="STM1129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (4413.
/gene="STM1129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIFAAAQSSISSSLNSISSCFNSDIYQRLSHKKRTPENRMKIAKLVILVAGLISSAAS
VMLVWADESEIWDAFNSLIGLMGGPMTGLFMLGIFFKRANAGSAVLGIIISVITVLGA
RYATDLNFFFYGVIGSLSVVISGVIFAPLFAPAPPLTLDEKPEPKVTL"
complement(4083.4088)
/gene="STM1128"
/gene="STM1132"
7768. .7773
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to B. coli orf, hypothetical protein (AAC77267.1); Blastp hit to AAC77267.1 (241 aa), 26% identity in aa 4 - 239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGAGTAGSSSVMGNNFLMLINGELKPGLRTDVIYRAMMDNDKLTWLKNSQLPPSPGEQ
QQEGLAGAFSGYSHGVLLVGGGANFPGAKQNYTNGKFYSHEGINKKWRDEVYGLINGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (5094. .5099)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to E. coli putative enzyme (AAC76255.1);
Blastp hit to AAC76255.1 (229 aa), 70% identity in aa 1 -
                                                                                                                                                  )ELKLEYNFTWMDSDQIKFDNKKTNYEHNVALAWKLNKSFTPYVEVGNVAVRNNTDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WQYMGKMKQPLGYGVSVSYGDEVFLIGGENAKGKPVSSVTSFTMRDGNLLIK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to E. coli orf, hypothetical protein (AAC77266.1); Blastp hit to AAC77266.1 (404 aa), 41% identity in aa 40 - 403"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="STM1131"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="putative RBS for STM1131; RegulonDB:STMS1H001402"
:805. .7497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene="STM1131"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="STM1131"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="STM1130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="STM1129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="STM1130"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="putative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPVEPDLAMVTQLSHAGCRVIAEGRYNTPALAANAIEHGAWAVTVGSAITRIEHICQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .6759
                                                                             9060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RBS for STM1129; RegulonDB:STMS1H001401"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5099)
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note="similar to

. .

coli putative transport protein

note="putative"

RBS

for

STM1132;

RegulonDB:STMS1H001403"

57%

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PUBMED
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
AL627269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
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Best Local Simi
Matches 379;
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                        2 (bases 1 to 254050)
Parkhill,J.
Direct Submission
Submitted (25-OCT-2001) Submitted on
                                                                                                                                                     Parkhill, J. Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebaihia, M., Baker, S., Bahbam, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, T.T., Holroyd, S., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Stevens, K., Whitehead, S. and Barrell, B.G. Complete genome sequence of a multiple drug resistant Salmonella Nature 413 (6858), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enterica subsp. enterica serovar Typhi
Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Salmonella.
                                                                                                                                      11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL627269 254050 bp DNA linear BCT 04-J
Salmonella enterica serovar Typhi (Salmonella typhi) strain
complete chromosome; segment 5/20.
AL627269 AL513382
AL627269.1 GI:16502231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGTCGCAAATGGCTATTCGCGTGACACAACGTTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĊĀĠĪĊĠĊĀTĀĪĠĠĊĪĀĪĪĊĠĊĠĪĊĀĊĊĊĀĀĊĠĊĪĀĀ 17727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAĀĀTĀĀGĠĊĊĀĀTĀTTĀĊĊĊĀĠTĀCGĠTĀĊĢĊĀGĀĀĀĀČĀĠĊĀGŤTĠTĀĠTĠĊĀĠĀĀĀ 17691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTAATAAAGCAAATATTACACAGTATGGTACTCAAAAAACGGCAATTGTAGTGCAGAGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ĠĀTĠĊĊĀĠŦĀŦŖŤĊĠĊĀĀĀĠĊĠĊŦŦĀĊĠĠŦĀĀŦĀGŦĠĊĠĠĊŦĀŦŦĀŤĊĊĀĠĀĀĀĠĠŦŤĊŦ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGTCGÁCGÁGGAÁGGGAÁTTATAÁCTTTGCGTATÁTTGÁGCÁAACGGGCÁATGCCAÁC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 254050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGAAGGAGGAAATAATCGGGCG 17511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGGCAGGGAGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTCÁTTTÁÁTCÁGGGGGGGGGGTTÁTTGGTCÁÁGTGGGCÁGGATÁÁTÁGTGGCAGAGTÁ 17451
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83.1%;
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Pred. No. 6.2
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-hes 77; Indels
                      behalf of the Salmonalla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriales;
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) strain CT18,
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Hinxton, Cambridge CB10 1SA, UK
E-mail: parkhill@sanger.ac.uk
Notes:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAD08183.1"
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QDGLVMDKWFLOSTSARDALFNAVALDESTARDAAFH
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LVDAEGLINRMGFNNLGVDNLVENVKKAHFDGILGINIGKNKDTPVENKDDYLICME
KVYAKAGYIAINISSENTPGLRTLQYGDALDDLLTAIKNKQNDLQVIHHKYVPVAKVL
APDLCEEELIQVADSLLRHNIDGVIAINTTLDRSLVQGMKNCQQTGGLSGRPLQLKST
EIIRRLSLELKGQLFIIGVGGIDSVIAAREKIAAGATLVQIYSGFIFKGPPLIKEIVT
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                                                                                                                                                                                                                                                                            /note="Orthologue of E.
to PYRD_ECOLI (336 aa),
/codon_start=1
/transI_table=11
                                                                                                                                                                                                    /product="dihydroorotate dehydrogenase"
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/db_xref="GI:16502233"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family M1, 1060. .1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 zinc-binding region
                                                                                                                                                                                                                                                                                                                                                                                                           note="synonym: pyrb"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="STY1079"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="PS00142 Neutral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="STY1078"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mote="Pfam match to entry PF01433 Peptidase_M1, Peptidase
family M1, score 245.10, E-value 1.9e-84"
                                                                                                                                                                                                                                                                                                                                                                           gene="STY1079"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
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181. .2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Salmonella enterica subsp.
Typhi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Hote="synonym: pepN"
181. .2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="STY1078"
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signature"
                                                                                                                                                                                                                                                                                                     coli pyrD (PYRD_ECOLI); Fasta
95% identity in 336 aa overlar
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LRGYRDRTGLAPIKETLAAAIVMRSGWQPGTPLLDPMCGSGTLLIEAAMWATDRAPGL
                                                                                                                                                                                /transl take
                                                                                                                                                                                                                              /note="Similar to Haemophilus influenzae hypothetical protein hi0116 H10116 SW:YCBY HABIN (P44524; P43945) fast scores: E(); 0, 60.3% id in 710 aa Orthologue of E. coli YCBY ECOLI; Fasta hit to YCBY ECOLI (702 aa), 92% identity in 702 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTAINQWLSGFFSRDVQLCWVGPQLTRRVKRHNAVPLGFADGYPYLLTNEASLRDLQQ RCPAGYQMEQFRPNLTVSGPKAGA RCPAGYQMEQFRPNLTVSGPKAGA RCPAGYQMEQFRPNLTVSGPKAGA KYDLRIGDVIFDVXRPGSRCI ETTVSPEKGQ KHPSGEPLATLQAFRTAQDMGDVDFGQNLIARNSGVIR VGDEVEILATAPAKAYGATT LDDSVTPEKHEDGSVTILMQGQTFCGNNQQVLLEQLENQGIR I PYSCRAGICGCCRIR LLEGEVSPLKKSAMGDDGTILSCSCVPKTALRLEN"
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/db_xref="S9TREMBL:Q82757"
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                                                                                                                                                                                                                                                                                                                                                             /gene="STY1082"
5924. .8032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (4737. .4955)
/gene="STY1081"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MMRIKPDDNWRWYYDEEHDRWMLDLANGMLFRSRFSRKMLTPDA
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IMNDRLKPQVHCHSFSLEQAY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Orthologue of E. coli YCBW_ECOLI; Fasta hit to YCBW_ECOLI (192 aa), 90% identity in 180 aa overlap. 1 discrepency in position of translational start site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="STY1079"
/note="PS00912 Dihydroorotate
4174. .4719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="STY1079"
/note="Pfam match to entry PF01180 DHOdehase,
Dihydroorotate dehydrogenase, score 563.50, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                      ruore="Pfam match to entry PF00111 fer2, iron-sulfur cluster binding domains, scones.5-13"
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/gene="STY1081"
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4174. .4719
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3874. .3936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Orthologue of E. coli P75863; Fasta hit
(369 aa), 86% identity in 367 aa overlap"
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score 55.90,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                       AB016840
Salmonella enterica subsp.
16 of the complete genome.
AE016840 AE014613
AE016840.1 GI:29137797
  Salmonella enterica subsp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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SgS

gene

CDS

gene

g

301983

DNA serovar

linear BCT 21-MAR-2003 r Typhi Ty2, section 7 of

enterica ğ

enterica serovar Typhi Ty2

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88469 GCGACAAATTATGATCTGGCTCGTTCAGAGTATAATTTTTGCGGTAAATGAATTAAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGAAAAACAAATTGTTATTATTGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCC
                                       CAGTCGCAAATGGCTATTCGCGTGACACAACGTTAA 456
                                                                                                                                                                     GGTAATAAAGCAAATATTACACAGTATGGTACTCAAAAAACGGCAATTGTAGTGCAGAGA 420
                                                                                                                                                                                                                              GATGCCAGTATATCGCAAAGCGCTTACGGTAATAGTGCGGCTATTATCCAGAAAGGTTCT
                                                                                                                                                                                                                                                                        GATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAG
                                                                                                                                                                                                                                                                                                                                                AAAGTCGACCAGGCAGGGAATTATAACTTTTGCGTATATTGAGCAAACGGGCAATGCCAAC 88708
                                                                                                                                                                                                                                                                                                                                                                                    AAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGAAGGAGAAAATAATCGGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGGCAGGGAGGCTCAAAACTTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCA 240
                                                                                                               GGAAATAAGGCCAATATTACCCAGTACGGTACGCAGAAAACAGCAGTTGTAGTGCAGAAA 8882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTCATTTAATCAGGCGGCCATTATTGGTCAAGTCGGCACGGATAATAGTGCCAGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAAAAACAAATTGTTATTTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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RAGIGELITFEVKDVAQLSNPLPKGPYGTVISNPPYGERLDSDPALIALHSLLGRTMK
ROFGGWNLSLFSASPDLLGSLQLRADKQFKAKNGFLDCVQKNVHIAETTADSKPATVA
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DAQKARQRLFDIIAATLSVLGIPPNKLVLKTRERQKGNQYQKNSEKGEFLEVSEYNA
RLWVNLTDYLDTGLFLDHRIARRMLGEMSKGKDFLNLFSYTGSASVHAGLGGARNTTT
VDMSETYYLEWAERNLELNGLSGRAHHLIQADCLGWLEEANEQFDLIFIDPTTSNSKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             526 aa overlap
Fasta hit to YJJK_ECOLI (554 aa), 34% identity in 524 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Pfam match to entry PF01170 UPF0020, Uncharacterized protein family UPF0020, score 781.30, E-value 3.7e-231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5927.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="STY1083"
9045. .9952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSPDFARNRQIHNCWLIRAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="STY1083"
note="Fasta hit to YBIT_ECOLI (530 aa), 32% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="PS01261 Uncharacterized"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="STY1082"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="STY1082"
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82.9%;
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Pred. No. 1.7e-81;
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88864
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ORGANISM

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PUBMED
REFERENCE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-SEP-2002) Laboratory of Genetics, twisconsin - Madison, 445 Henry Mall, Madison, WI Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 301983)

Deng, W., Liou, S.-R., Plunkett, G. III, Mayhew, G.F., Rose, D.J.,

Burland, V., Kodoyianni, V., Schwartz, D.C. and Blattner, F.R.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enterica subsp. enterica serovar Typhi Ty2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Salmonella.

1 (bases 1 to 301983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Deng, W., Liou, S.R., Plunkett III, G., Mayhew, G.F., Rose, D.J., Burland, V., Kodoyianni, V., Schwartz, D.C. and Blattner, F.R. Comparative Genomics of Salmonella enterica Serovar Typhi Strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 185 (7), 2330-2337 (2003)
22531367
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Salmonella typhi CT18"
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complement(1812. .3473)
                                                                                                                                                                                                                         complement (1812. .3473)
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NIVDVDMNSVISSYVMQQAAIQASYKTFTDMQGMSIFQLNR"
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Salmonella typhi CT18"
                                                                                                                                             gene="flgK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (844. .1797)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (844. .1797)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    locus_tag="t1736"
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Salmonella typhi CT18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement (164. .622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=:/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="transposase for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocus_tag="t1736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="tnpA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽
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Yphi Ty2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serovar="Typhi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strain="Ty2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            species="enterica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _tag="t1735"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               insertion sequence element
                                                                                           from
                                                                                         Accession AL513382:
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CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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      /gene="flgG"
/locus_tag="t1741"
                                                                                                                                                                                                                                                                                                                                Tocas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /locus_tag="t1738"
complement(3538. .4488)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="flgJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocus_tag="t1738"
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algssvaqinnyakqianlndoisrmtgvgagaspndlloddoltssekhkiygvevs
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                                                              LBIDGLKVTVGTGAQKNDSFLLKPVSNAIVDMNVKVTNËAEIAMASESKLDPDVDTGD
SDNRNGQALLDLQNSNVVGGNKTFNDAYATLVSDVGNKTSTLKTSSTTQANVVKQLYK
complement (3538. .4488)
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                                                                                                                                        TGSLGGLLTFRSQDLDQTRNTLGQLALAFADAFNAQHTKGYDADGNKGKDFFSIGSPV
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LPARLASEQGGVPHHLILAQAALESGWGQRQILRENGEPSYNVFGVKATASWKGPVTE
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complement (4488. .5591)
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Salmonella typhi CT18"
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Query Match
Best Local Sim
Matches 378;
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Similarity 82.9%;
                                                                                     AAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAAC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAAAAACAAATTGTTATTTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCC 60
AAAGTCGACCAGGCAGGGAATTATAACTTTGCGTATATTGAGCAAACGGGCAATGCCAAC 37508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTA 180
                                                                                                                                                                                                           CGCCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGAAGGAGAAAATAATCGGGCG 37568
                                                                                                                                                                                                                                                                                                                                                                                                       TCTTCATTTAATCAGGCGGCCATTATTGGTCAAGTCGGCACGGATAATAGTGCCAGAGTA 37628
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Salmonella typhi CT18"
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Salmonella typhi CT18"
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VETSNVNVAEELVNNIQVQBAYEINSKAVSTTDQMLQKLTQL"
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complement(7146. .7901)
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Pred. No. 1.7e-81;
0; Mismatches 78;
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                                                                    GGTAATAAAGCAAATATTACACAGTATGGTACTCAAAAAACGGCAATTGTAGTGCAGAGA 420
                                                                                                CAGTCGCAAATGGCTATTCGCGTGACACAACGTTAA 456
                                                GGAMATAAGGCCAATATTACCCAGTACGGTACGCAGAAAAACAGCAGTTGTAGTGCAGAAA 37388
37352
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Search completed: March 15, Job time: 1967.17 secs 2004, 22:49:54

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Result
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Match
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1: geneseqn1980s:*
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Listing first 45 summaries
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AAT74142
AAC64622
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AAQ62647
AAQ73066
AAT74141
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AAN40272
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AAC64629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              model
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              Ada71938 Rice gene
Aac64629 AgfA: PT3
Aac64629 AgfA: PT3
Aac64629 AgfA: PT3
Aax34648 Promoter
Aaq62647 Fibronect
Aaq73066 AgfA sequ
Aat74141 Salmonel1
Aac8467467 AgfA sequ
Aat74142 Salmonel1
Aac64622 AgfA: PT3
Aac64625 AgfA: PT3
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Aac64625 AgfA: PT3
Aac64626 AgfA: PT3
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Aac64626 AgfA: PT3
Abc17054 Human MP2
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Aac64618 Salmonell
Acd68810 E. coli K
Acd68812 E. coli K
Acd68811 E. coli K
Aan40272 Sequence
Ada31934 DNA encod
Ada71938 Rice gene
Aac64623 AgfA::PT3
Aac64627 AgfA::PT3
Aax34648 Promoter
Aag62647 Fibronect
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7.1	7.1	7.1	7.1	7.2	7.2	7.2	7.2	7.3	7.3	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.4	7.5	7.5	
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AAS97288	AAS97253	AAS74657	ABX54413	ABQ67194	ABQ69245_18	ACA47731	ACA48121	AAH24065	ACA29389	ACA48239	AAC43625	ABN71527_06	ABL08488	ABL08478	ABN67963	ABN70427	ACA18571	AAA65947	AAS46482	AAS76745	PECECOGA
Aas97288	Aas97253	Aas74657	Abx54413	Abq67194	Continuat	Aca47731	Aca48121	Aah24065	Aca29389	Aca48239	Aac43625	Continuat	Ab108488	Ab108478	Abn67963	Abn70427	Aca18571	Aaa65947	Aas46482	Aas76745	ALCI CAM
Neisseria	Neisseria	DNA encod	Bovine ES	Listeria	Continuation (19 o	Prokaryot	Prokaryot	Yeast AOD	Prokaryo	Prokaryot	Arabidops	Continuation (7 of	Drosophi	Drosophi	Streptoco	Streptoco	Prokaryot	E. coli p	Tumour su	DNA encod	Transport man

## ALIGNMENTS

RESULT 1 AAC64620

AAC64620;

AAC64620 standard; DNA;

456 BP.

26-FEB-2001

(first entry)

Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;

Escherichia coli CsgB DNA sequence SEQ ID NO:4.

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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                             WPI; 2000-672631/65.
                                                                                                                                          White AP, Doran JL,
                                                                                                                                                                      05-APR-1999;
                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                    05-APR-2000; 2000WO-CA000356.
                                                                                                                                                                                                   12-OCT-2000.
                                                                                                                                                                                                                 WO200060102-A2.
                                                                                                                                                                                                                                            vaccine; immune response; immunogen;
                                                                                                                                                         (UYVI-) UNIV VICTORIA.
                                                                                                                      AAB36344.
                                                                                                                                                                       99US-0127888P
                                                                                                                                           Collison
                                                                                                                                          SK,
                                                                                                                                          Kay WW
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing recombination of a recombination of the native

Disclosure; Page 134; 139pp; English.

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61 61 Query Match Best Local

Matches

456;

Similarity

Kay

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CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Riterobacteriaceae host cell, from the host cell and introducing the CC quiteful for the animal in conjunction with a carrier or diluent. (I) is CC quiteful for the expression of recombinant AgfA protein which is useful for CC golymer into the minume response in an animal. In a fimbrial presentation CC golymer the heterologous antigens are presented in high numbers (up to CC golymer the heterologous antigens are presented in high numbers (up to comples/cell), the hybrid fimbrin protein possesses both the cracine, the carrier fimbrial proteins are usually strong consines the inserted epitope, and hybrid fimbriae are usually strong consines the inserted epitope, and hybrid fimbriae are easy and the exemplification of the present invention
                                                                                                                                                                                                                 Salmonella, agfA, chromosomal gene replacement, fimbrin, epitope, vaccine; immune response; immunogen, ds.
                                                                                                                                                                                                                                                                                                     Salmonella enteritidis AgfB DNA sequence SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC64618 standard; DNA; 456 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 CAGTCGCAAATGGCTATTCGCGTGACACAACGTTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTAATAAAGCAAATATTACACAGTATGGTACTCAAAAAACGGCAATTGTAGTGCAGAGA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGAAAAACAAATTGTTATTTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAAAAACAAATTGTTATTTATGATGTTAACAATACTGGGTGCGCCCTGGGATTGCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                llarity 100.0%; Score 456; DB 3; L
100.0%; Pred. No. 3.3e-130;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a recombinant agfA gene (I) where a CC sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SERIT/TAP) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA-homologue fimbria (SERIT/TAP) nucleation depended CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombinant of a recombinant gene into the chromosome of the comprising recombinant coli and CC comprising separating an amino acid polymer comprising a recombinant gene comprising separating an amino acid polymer comprising a recombinant or segments or sequences grown on a Salmonella, E. coli or polymer into the expression of recombinant agfA protein described host cell, from the host cell and introducing the native colymer into the expression of recombinant segments of foreign amino complements of segments of foreign amino complements of the expression of recombinant agfA protein which is useful for system the heterologous antigens are presented in high numbers (up to comprise the instruction properties relevant for an efficient live component the carrier fimbrial subunit proteins are usually strong communogenicity and adhesion properties relevant for an efficient live communogens, which may be important for directing an immune response communogens, which may be important for directing an immune response communogens of the protein possesses both the community in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 456 BP; 149 A; 87 C; 109 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 134; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                         241 AAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAAC
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                                                                                                                                                                                                                                                                                                                    121 TCTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGAAAACAAATTGTTATTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCC
GATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCT
                                                    AAAGTCGÁCCÁGGCÁGGAÁTTATÁACTTTGCGTÁTÁTTGAGCÁAACGGGCÁATGCCÁÁC 300
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                                                                                                                                                                                                           CGGCAGGGAGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGTAGGAACCGGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAG 120
                                                                                                                                                                                                                                                                                                                                                                                              ĠĊĠĀĊĀĀĀŦŦŔŤĠŔŦĊŦĠĠĊŦĊĠŦŦĊĀĠŖĀŦŔŦŔĀŦŦŤŦĠĊĠĠŦŔŔĀŦĠŖŔŦŦĀŔĠĊŔŔĠ
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(first entry)

Salmonella enteritidis

WO200060102-A2

RESULT 2 AAC64618

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ACCTTGCATATATTGATCAGGCGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTT 325

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RESULT 3
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                                                                                             In K12 and for determining the gene expression pattern, e.g. for diagnostic determination of which E. coli strains are present in the gut, and to determine the effects of e.g. growth media on gene expression. The blochip provides as comprehensive as possible detection of the K12 genome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or other E. coli strains in a single experiment. Apart from qualitative and quantitative information about gene expression, it also allows measurements of population densities for the various strains. The use of synthetic oligonucleotides for preparation of probes allows free variation in probe length and ensures high purity (and thus selectivity, reactivity and reproducibility), also synthetic probes are generally shorter than probes prepared by polymerase chain reaction. ACD69731 to ACD691540 represent oligonucleotide probes used with the biochip described in the selection of probes are generally shorter than probes of the proparation of probes are generally shorter than probes prepared by polymerase chain reaction. ACD69731 to ACD691540 represent oligonucleotide probes used with the biochip described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      containing many identical probes. The probes are nucleotide sequences 30-80 bases, are prepared ex situ from synthetic oligonucleotides and least one includes a segment of at least 20 bases identical with, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochip containing probes complementary with open reading frames in Escherichia coli K12, useful for detecting gene expression and expr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complementary to, a segment of an open reading frame (orf) of Escherichia coli K12. The biochip is used for specific detection of gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 23; 2004pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel biochip comprising probe spots, each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-241155/24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-2001; 2001EP-00112179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E. coli K12 MG1655 biochip probe SEQ ID
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Query Match Best Local Similarity Matches 100; Conserv

Conservative

21.9%; but 100.0%; Pr

Score 100; DB 7; L; Pred. No. 9.5e-21; 0; Mismatches 0;

Length 100 Indels

0,

Gaps

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S

123 TTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTACG

Query Match Best Local Similarity Matches 100;

Conservative (

21.9%;

Score 100; DB /; -; Pred. No. 9.5e-21;

Length 100; Indels

Gaps

182 0; Sequence 100 BP; 28

A; 18 C; 27 G; 27 T; 0 U; 0 Other;

Sequence 100

BP;

27

A; 19 C; 26 G; 28 T;

0 U; 0 Other;

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RESULT 4
ACD68812
ID ACD6
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                                                genome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between KL2 and its mutants or other E. coli strains in a single experiment. Apart from qualitative and quantitative information about gene expression, it also allows measurements of population densities for the various strains. The use of synthetic oligonuclectides for preparation of probes allows free variation in probe length and ensures high purity (and thus selectivity, reactivity and reproducibility); also synthetic probes are generally shorter than probes prepared by polymerase chain reaction. ACD86731 to ACD81540 represent oligonuclectide probes used with the biochip described
                                                                                                                                                                                                                                            This invention describes a novel biochip comprising probe spots, each containing many identical probes. The probes are nucleotide sequences of 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at least one includes a segment of at least 20 bases identical with or complementary to, a segment of an open reading frame (orf) of Escherichia coli K12. The biochip is used for specific detection of gene expression in K12 and for determining the gene expression pattern, e.g. for diagnostic determination of which E. coli strains are present in the gut, and to determine the effects of e.g. growth media on gene expression. The biochip provides as comprehensive as possible detection of the K12 in the strain pattern.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 23; 2004pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochip containing probes complementary with open reading frames in Escherichia coli K12, useful for detecting gene expression and expression
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                                    in the
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                                    invention
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                                                                                                                                                      Matches
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Best Local ;
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                                                                                                                                                                                                                                              Sequence 100 BP; 31 A; 20 C;
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                              208 GTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCAAAGATTGACCAGACAGGAGATTATAAC
                                                                                                                                                         100;
                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 23; 2004pp; German.
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. GTTGCGCAAGAAGGTAGTAGCAACCGGGCAAAGATTGACCAGACAGGAGATTATAAC
                                                                                                                                21.9%; Silarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drescher B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĠĊĀĠĠĠĠĠĠĠĊŦĊĀĀĀĀĊŦŦŦŦĠĠĊĠĠŦŤĠŤŦĠĊĠĊĀĀĠĀĀ 100
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                                                                                                                       Score 100; DB
; Pred. No. 9.5;
0; Mismatches
                                                                                                                                                                                                                         29 G; 20 T; 0 U; 0 Other;
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                                                                                                                                                                  Length 100;
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DB 1;

Length 779;

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Query Match
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AAN40272
                    The inventors claim a DNA SQ which comprises a nucleotide sequence corresp. to all or part of plasmodium falciparum RNA. Also claimed is synthetic peptide or polypeptide displaying the antigencity of all or part of a P.falciparum antigen. The base sequence of clone Ag16 (see AAN40772) indicates that the antigen coded for by this partial polynucleotide sequence has a homologous repeat structure of 11 AAs tandemly repeated 23 times
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                Sequence
                                                                                                 Claim 5; Fig 1; 62pp; English.
                                                                                                                                                                            Kemp DJ,
Mitchell
                                                                                                            Expression of plasmodium falciparum poly:peptide(s) from CDNA in immunisation against malaria infection.
                                                                                                                                                 WPI; 1984-201410/32
P-PSDB; AAP40376.
                                                                                                                                                                                                        (SARA-)
                                                                                                                                                                                                                          (HALL-)
                                                                                                                                                                                                                                                  26-JAN-1984;
                                                                                                                                                                                                                                                           28-JAN-1983;
10-JUN-1983;
                                                                                                                                                                                                                   AUME - )
                                                                                                                                                                                                                                                                                     27-JAN-1984;
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                                                                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malaria; vaccine; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of a clone numbered as Ag16 which corresponds to the S antigen of isolate FC27.
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                                                                                                                                                                                                    HALL INST
KEMP D J.
AUST INST
SARAMANE
       779 BP; 294 A; 125 C; 217 G; 143
                                                                                                                                                                             Anders RF, GF;
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Matches 134; Conservative
                                                                           The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial
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                                                          protein
                                                                                                                                                                                                                                                                                                                                  Example; SEQ ID NO 3221; 328pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                      vaccines, as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAGGATTAGAAGATCCTGCAAAAGCTAGTCAAGGTGGATTAGAAGATCCTGCAAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TARAGCAAATATTACACAGTATGGTACTCAAAAAACGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAGCTAGTCAAGGTGGATTAGAAGATCCCCGCAAAGGCTAGTCAAGGTGGATTAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAGTCAAGGAGGATTAGAAGATCCTGCAAAAGCTAGTCAAGGTGGATTAGAAGATCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9905-00328352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   baumannii
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0; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
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                        The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chang H,
Katagiri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rice gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADA71938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA71938 standard;
                                                                                                                                                                                                                                                                                                                                                                                             bacterial, fungal or
                                                                                                                                                                                                                                                                                                                                                                                                                      pathogenic infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JAN-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant; bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3685
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                                                                                                                                                                                                                                                                                                                                                                       expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-175290/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 AATGAATTGAGTAAGTCTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTACAAGGTCAAGCTGGGAATGACACTTATATTATAGATAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTATG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCTGTATGGTGATGATGGAGACGATACATTAGTTTCTAATACAGGCTCTGATTATTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATAGTGCTCAGTTACGGCAGGGAGGCTCAAAACTTTTGGCCGGTTGTTGCCGCAAGAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATACTATTGGTAAATTATTAGGTACTGATGCAGCAGATAATCTTCAAGCAGATGCTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W,
F, Quan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATGGTGGTGCAGGTAATGACACATTGATTTATGGCGGTAATTCCAATGTGTATACGGCT
                                                                                                                                                                                                                                                                                                                   SEQ
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                                                                                                                                                                                                                                                                                                                   NO 5263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cooper
S, Tao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                        one gene involved in plant resistance or response for conferring resistance or tolerance to a plant viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.4%;
45.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ϋ́B
                                                                                                                                                                                                                                                                                                                 899pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38.2; DB Pred. No. 0.51; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           먪
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glazebrook J, (Whitham S, Xie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goff
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©; 284 G; 363 T; 0 U; 752 Other;

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Similarity

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Score 37.8; Pred. No. 0.

0.47;

DB 7; Length 2000;

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEFI)/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and AgfA, CsgA and AgfA-homologue fimbria comprising recombinant directing recombination of a recombinant gene into the chromosome of the
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                                                                                                                  Disclosure; Page 136; 139pp; English.
                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                               WPI; 2000-672631/65.
P-PSDB; AAB36347.
                                                                                                                                                                                                                                                                                   05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis
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                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  950 WAAGRWRWAMCWYCCMWKWNKNTSCMWWKYWRTWSCWYTINWWGAMRYAYYAMRRRRWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 TAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAGTCTTCATTTAATCAGGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WKKYATRYYWKMMAMTWWWSWRRWKSYRMWSGMGRMRWSAWRYCSRMKCAKTKYASSARW 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKRAKRSYRYRRRWYWKRKGWTYRYRYWRSCRMTR 676
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                                                                                                                                                                                                                                                                                                                                                                                                                    immunogen;
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                                                                                                                                                                                                                                                                                                                                                                                                                     gene replacement; fimbrin; epitope.
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P-PSDB; AAB36353.
                                                                                                                                                                                                                                               White AP,
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Best Local
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Escherichia coli.
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                                                                                                                                                                                                                              Doran JL,
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                                                                                                                                                                                                                                   Collison
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unogen; ds.
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0; Mismatches
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Pred. No. 0.35;
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

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RESULT 11
AAX34648/c
ID AAX346
XX AAX346
XX 17-OCT
DT 17-OCT
DT 05-JUL
XX Starch
KW Starch
KW starch
KW endosp
KW grain
KW wSBE I
XX Aegilc
XX WO9914
XX WO9914
XX PP 11-SEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
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Best Local
                                                                                                                                                                                        Starch biosynthetic pathway; cereal plant; enzyme; SBE; SSS; DBE; etarch branching enzyme; starch soluble synthase; debranching enzy endosperm; wheat; barrey; granule-bound synthase; glutenin; starch grain softness protein I; bacterial isoamylase; glycogen synthase; wSBE I-D4 gene; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing recombination of a replacing the native
                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2003
05-JUL-1999
                                                                                                 WO9914314-A1
                                                                                                                                                Aegilops tauschii
                                                    25-MAR-1999.
                                                                                                                                                                                                                                                                                                                                      Promoter containing sequence of SBE I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX34648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX34648 standard; DNA; 4890 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                 (revised)
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Pred. No. 0.61;
0; Mismatches 64
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11-SEP-1998;

98WO-AU000743.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel enzyme of starch biosynthetic pathway is a cereal plant, where the enzyme is selected from starch branching enzyme (SBE) I, SBE II, starch soluble synthase (SSS) I, and debranching enzyme (DBE), with the proviso that the enzyme is not SSS I of rice, or SBE I crice or maize. The methods and products can be used for targeting expression specifically to the endosperm of the seeds of cereal plants such as wheat or barley. They can be used for the expression of e.g. antisense sequences of granule-bound synthase (GBSS), SBE II, low mol. wt. glutenin, grain softness protein I, bacterial isoamylase, bacterial glycogen synthase, and wheat high mol. wt. glutenin Bx17. They can be used for modifying the characteristics of starch produced by a plant. The present sequence represents the wheat SBE I promoter containing sequence (Updated on 17-OCT-2003 to standardise OS field)
          03-NOV-1993;
                                                                                                                                                                                                                                                                               AAQ62647 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li Z,
                                         11-MAY-1994.
                                                                                                  Escherichia
                                                                                                                                                                                                       25-MAR-2003
18-OCT-1994
                                                                                                                                                                                                                                                    AAQ62647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4890 BP; 1403 A; 1067 C; 1035 G; 1385 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated cereal plant enzyme genes used for, antisense sequences of granule bound synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CSIR )
(AUSU )
(GOOD-)
                                                                                                                                            Fibronectin binding protein; FBP; curlin;
                                                                                                                                                                           Fibronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 17; Page 63-65; 171pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-1997;
20-MAR-1998;
                                                                                                                              .mmunization; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LIMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1097
                                                                                                                                                                                                                                                                                                                                                                                                                                               318
                                                                                                                                                                                                                                                                                                                                                        977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.7%;
Similarity 55.8%;
87; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Morell M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMONWEALTH SCI & IND RES
UNIV AUSTRALIAN NAT.
GOODMAN FIELDER LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRP LIMAGRAIN PACIFIC PTY LTD
                                                                                                                                                                                                                                                                                                                                                                                  TTACACAGTATGGTACTCAAAAAACGGCAATTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                 ACTCATACATTTGAAAAATTGTTAGTTAAATGAAACTAAGGTTCTATTCTTTTAGCATGCA 978
                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGTGCTTATGGTAATACTGCGA-TGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATA 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÁGAGAAGAACTTTCCATAAAATGAACAAACAAACAGTGCCAAGTATGCCACTTGTTGGCA 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAACGATGCCAGTATTTCGCA 317
                                                                                                                                                                                                                                                                                                                                                      TTGCATTGCATTACTAGTTAGACCCGTGAATTGTAG
                                                                                                    coli
                                                                                                                                                                         binding protein fnbA gene
                                                                                                                                                                                                       (revised)
(first entry)
          93WO-US010547
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98AU-00002509.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rahman S;
                                                                                                                              fnbA gene; ss
                                                                                                                                                                                                                                                                               646
                                                                                                                                                                                                                                                                               ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35.2; DB Pred. No. 4.3; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORG
                                                                                                                                              curli pili; pilus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68;
                                                                                                                                                                                                                                                                                                                                                                                  412
                                                                                                                                                                                                                                                                                                                                                        942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
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enzyme
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PR XXX PT PT XXX PR XXX PR XXX PT PT YXX PT PT PT YXX PT PT PT YXX PT PT PT YXX PT PT PT PT YXX PT PT PT YXX PT PT PT PT PT YXX PT PT PT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                            26-APR-1993;
                                                                     26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-2003
25-MAR-2003
26-JUN-1995
                                                                                                                         10-NOV-1994.
                                                                                                                                                                        WO9425598-A2.
                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella; AgfA; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AgfA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The fnbA gene of E. coli cattle fecal isolate AO12 includes DNA encodi a new fibronectin binding protein (FBP), curlin, which is produced as curli pili when expressed in E. coli (pFbO) DSM 4585. The fnbA gene sequence from pFnb20 is given in AAQ62647, and includes the sequence encoding the 17 kDa curlin subunit (amino acids 21-142 of AAR52664). (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ73066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ73066 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New fibronectin binding protein curlin from E. coli - used for the treatment of infections caused by E. coli and for immunisation against coli infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Normark S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416
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DB; AAR52664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGACAGTCGCAAATGGCTATTCGCGTGACACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAGACAGTCGCAAATGGCTATTCGCGTGACACAA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  646 BP; 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _ay= a
/note= "AgfA"
37. .60
                       93US-00054452
                                                                   94WO-IB000207
                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/note= "TAF3 ]
                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= d
/note= "TAF5 primer
52. .69
                                                                                                                                                                                                                                                                                                                              complement (292. .402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92US-00970846.
                                                                                                                                                                                                                                                                                       note= "TAF6 primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; +1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; 146 C; 161 G; 171 T; 0 U; 0 Other;
                                                                                                                                                                                                    "TAF4 primer (pair with TAF3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetic immunization; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                        (pair
                                                                                                                                                                                                                                                                                     (pair with TAF5) "
                                                                                                                                                                                                                                                                                                                                                                                                                                 (pair with TAF6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2
2.2;
                                                                                                                                                                                                                                                                                                                                                           with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           includes DNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT 14
AAT74141
ID AAT74
AC AAT74
AC
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Matches
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                                   primer_bind
                                                                                 primer_bind
                                                                                                                              primer_bind
                                                                                                                                                                             primer_bind
                                                                                                                                                                                                                                                                              Salmonella
                                                                                                                                                                                                                                                                                                Enteropathogenic bacteria; enterobacteria; S.enteritidis; antibody;
                                                                                                                                                                                                                                                                                                                                Salmonella enteritidis 27655-3b TnphoA mutant agfA
                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
30-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                      AAT74141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT74141 standard; DNA; 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The DNA encodes the Salmonella enteritis27655-3b TnphoA mutant strain agfA gene cloned into pUC19. The DNA and isolated proteins are used in genetic immunization and vaccine compositions, respectively, to elicit immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 252-MAR-2003 to correct PN field.) (Updated on 252-348-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 7A; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eliciting an imm
strains, vector
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P-PSDB; AAR62761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYVI-)
(KING/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               277 ATTGATCAGGCGGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTGAACTGÁCTCÁGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAÁA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTATGGTACTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTACCCAGAGCGGTTATGGTÄACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTÄCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV VICTORIA INNOVATION & DEV KING \mathbf{J}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACTCCGATATTACTGT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAACGGCAATTGTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 BP; 94 A; 93 C;
                                                                                                                                                                                                                                                                          enteritidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune response to Salmonella - using attenuated Salmonella tor constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                  /label=
52. .69
                                 /label= Primer_TAF6
complement(294. .31;
                                                                /label= Primer TAF3
complement(103 .128)
/*tag= d
                                                                                                                                                                               /label=
16. .60
                                                /label=
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SK,
Primer_TAF4
                                                                                                                                          Primer_TAF5
                                                                                                                                                                                        agfA_gene_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34.6; D
Pred. No. 2.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 G; 80 T; 0
                                .312)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 361;
                                                                                                                                                                                                                                                                                                                                gene
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                10-NOV-1994
                                                                                                                                           Salmonella
                                                                                                                                                                    Salmonella;
                                                                                                                                                                                                                          25-MAR-2003
26-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 361 BP; 94 A; 93 C; 94 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                          WO9425598-A2
                                                                                                                                                                                              AgfA sequence
                                                                                                                                                                                                                                                                    AAQ87467;
                                                                                                                                                                                                                                                                                               AAQ87467 standard; DNA; 456 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Col 107-110; 85pp; English.
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                                                                                                                                                                  AgfA; vaccine; genetic immunization;
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(first entry)
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                                                                 /*tag= a
/note= "AgfA"
                                                                                               Location/Qualifiers
1. .454
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53.3%;
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Pred. No. 2.3;
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Search completed: March 15, 2004, 17:51:50 Job time: 248.684 secs

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Best Local
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                                                                                                                                                                                                           Sequence 456 BP; 117 A; 112 C; 122 G; 105 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                            Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-358275/44.
                                                                                                                                                                                                                                        field.)
                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 7B; 95pp; English.
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                                                    ATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAA 327
                        AAAACGGCAATTGTAGT
                                                                            GCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTATGGTACTCAA 396
                                                                                                       ATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACT
                                                                                                                              ATTGATCAGGCGGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATACT
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AACTCCGATATTACTGT
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nilarity 53.3%;
Conservative
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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   Query
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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                           US-09-328-352-3901
US-09-540-236-1556
US-09-107-532A-2544
US-08-956-171E-732
US-09-134-000C-3324
US-09-023-655-661
US-09-023-655-661
US-09-025-315-92
US-09-265-315-92
US-09-265-315-92
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US-09-328-352-3221
US-08-233-788A-56
US-08-233-788A-58
US-08-545-528D-1
US-09-790-9861-1
US-09-107-532A-2325
US-09-801-861-3
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US-09-540-02-32
US-09-540-02-32
US-09-540-02-32
US-09-540-03-32
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US-08-916-421B-1
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                                                                     Sequence 3, Appli
Sequence 1518, Appl
Sequence 1518, App
Sequence 398, App
Sequence 50, Appli
Sequence 1, Appli
Sequence 2813, Ap
Sequence 3901, Appli
Sequence 3901, App
Sequence 732, App
Sequence 732, App
Sequence 3324, Ap
Sequence 3324, App
Sequence 661, App
                                                                                                                                                                                                                                                                                    Sequence 58, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2325, Ap
Sequence 133, App
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Sequence 3221, Ap
Sequence 56, Appl
Sequence 58, Appl
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6.4	6.4	6.5	6.5	6.5	6.5	6.5	6.5	6.6		6.6		6.6		6.6		6.7	6.7
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Sequence 3808, Ap	Sequence 120, App	Sequence 105, App	Sequence 46, Appl	Sequence 1, Appli	Sequence 17, Appl	Sequence 16, Appl	Sequence 120, App	Sequence 295, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 10111, A	Sequence 37, Appl	Sequence 92, Appl				

## ALIGNMENTS

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US-08-232-463-14
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US-08-232-463-14/c
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Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                     IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1800 Diag
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DORNER, APPLICANT: SCHEIFLINGER, APPLICANT: FALKNER, F. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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                                                                              TYPE: nucleic
STRANDEDNESS:
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FILING DATE:
CLASSIFICATION: 435
                                                                                                                          LENGTH:
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Score 39.6;

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Length 7218;

Matches

Best Local Similarity

Conservative

10.5%; Proative 166;

Pred. No. 0.0088; 6; Mismatches 165;

Indels

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; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-3221
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 45.9
The 130; Conservative
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US-09-328-352-3221
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 3221
SEQ ID NO 3221
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                                                                 346 АГССАGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTATG 388
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                                     TTACAAGGTCAAGCTGGGAATGACACTTATATTATAGATAAAG 3727
                                                                                             TATGGTGGTGCAGGTAATGACACATTGATTTÁTGGCGGTAÁTTCCAÁTGTGTATÁCGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 TCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTACGG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCAGTATTTCGCAAGGTGCTTĄTGGTAATACTGCGATGATTATCCAGAAAGGTTCTGGT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAACGAT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGGAGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCAAAG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAGTCT 123
                                                                                                                                                                                                                                                                                                                                                                                    8.4%; Score 38.2; DB
45.9%; Pred: No. 0.021;
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 4860;
                                                                                                                                                                                                                                                                                                                                                                153; Indels
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RESULT 4
US-08-233-788A-58
; Sequence 58, Application US/08233788A
; Patent No. 5635617
; GENERAL INFORMATION:
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Matches 73; Conserv
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Best Local (
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US-08-233-788A-56
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TELEX: 372333 SEEDANBERRY
INFORMATION FOR SEE ID NO. 56:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver.
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
CTASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 1in
MOLECULE TYPE;
FEATURE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 56, Application US/08233788A Patent No. 5635617 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 30-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 1...
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STREET: 6300 Columb
CITY: Seattle
STATE: Washington
                                                                                                                                            265 AACTCCGATATTACTGT
                                                                                                                                                                        397 ААААССССААТТСТАСТ 413
                                                                                                                                                                                           205 ATTGAACTGÁCTCÁGÁÁTGGTTTCAGAÁÁTÁÁTGCCÁCCÁTGGACCÁGTGGAACGCTAÁÁ
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                                                                                                                                                                                                                                                                               277 ATTGATCAGGCGGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATACT
                                                                                                                                                                                                                      GCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTATGGTACTCAA 396
                                                                                                                                                                                                                                                         ATTACCCÁGAGCGGTTATGGTAÁCGGCGCGGTGTAGGCCÁGGGTGCGGÁTAATÁGTÁCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 base pairs nucleic acid DNESS: double
                                                                                                                                                                                                                                                                                                                                           Conservative
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E: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                      7.6%;
53.3%;
                                                                                                                                                                                                                                                                                                                           Score 34.6; DB 1; Length 361;
Pred. No. 0.087;
0; Mismatches 64; Indels
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William W.

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Praser et al.
TITLE OF INVENTION: Nucleotide Sequence of the Myc
Patent No. 6537773
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB193P1
CURRENT APPLICATION NUMBER: US/08/545,528D
CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR PRILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
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US-08-545-528D-1
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C2
TELEPHONE: (206) 622-4900
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TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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APPLICATION NUMBER: US 08/473,545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337
                                                                                                                                                                                                                                                                                                                                                                                                                               268 ATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 ATTGATCAGGCGGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATACT 336
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Similarity 53.3%;
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                                                                                                                                                                                                                                                                                                                                                                                        AAAACGGCAATTGTAGT 413
                                                                                                                                                                                                                                                                                                                                                  AACTCCGATATTACTGT 344
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6300 Columbia Center,
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Pred. No. 0.098;
0; Mismatches 64;
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                                                                                                                                                            Mycoplasma Genitalium Genome,
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                                                                                                                                                                                                                                                                                                               SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.:
SEQ ID NO 1
                                                                                                                                                      Matches
                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Sin Matches 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICÂNT: SHIGENOBU, SHUJI
APPLICANT: WATNANBE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF
FILE REFERENCE: 081356/0159
                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Buchnera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 580073
TYPE: DNA
ORGANISM: Mycoplasma
                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181503 ATCACCAAAATAAAACGATTACTTTTATTGATACTCCTGGGCATGAAGCATTTAC 181557
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                                                                                                                                                                       ocal Similarity
79913 AAACÁGGACTTCTAAAÁGGCAÁAGAGGGAGAACACTTTGTTGAAAAATAAÁTTAAATGÁTT
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                                 62 CAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAGT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 TGTTAACAATACTGGGTGCGCCTGGGATTGCAGCCGCAGCAGGTTATGATTTAGCTAATT 85
                                                                                                                                                      99;
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                                                                          TTÁGCÁAAGÁAACGTCÁGAGÁTAAATTTÁACACAAAAAAAAGCATATGAAACAGGTTTCC 79912
                                                                                                             TGAAAAACAAATTGTTATTTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCCG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTAACTGCTAAGGAGTTTGGCGGAATTACCCCAAAAAATTGGTGCTTATCAGGTGAAAA 181502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTATCATGGGTCATGTTGACCATGGTAAAACTTCGCTTTTAGACACAATTAGAAAAACTA 181442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCAAAGATTGACCAGACAGGAGATTATA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGCTAACATCCAGTTTGAAGATAGTGATGATTTATTGCAACCAAGACCACCTATTGTTA 181382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGTAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTAC 380
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                                                                                                                                                                     Score 31.8; 1
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 31.8;
Pred. No. 30;
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                                                                                                                                                      Mismatches 112;
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                                                                                                                                                                                       DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202;
                                                                                                                                                                                       Length 640681;
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                                                                                                                                                      Indels
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NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...525
SEQUENCE DESCRIPTION: SEQ ID NO: 2325:
                                                                                                                                                                           Matches
                                                                                                                                                                                    Query Match
Best Local Similarity
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GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2325;
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDENMESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Unr.1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: 1011y 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: N. 11 INFORMATION:
                           273 CTÁTÁTTGATÁTGAGTGGTGÁAÁTCAATTATGGCGÁTÁÁÁGACÁÁAÁTTGTÁC 325
                                                    330 TAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACAC 382
                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                270 TGCATATATTGATCAGGCGGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGG
                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM IS09660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80033 TAAAAACAGTTTTAAAAATTTCATCTTATGT 80063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79973 TATTTŤÍAÅÁŤTTTGAÁATTCTCŤŤGCŤAÁÁTTŤGAAÁAŤGÁACTATGŤŤCŤĊÁAŤŤÁČ 80032
                                                                                     TĠAĀTTATCTĠĀTĀĀĠĠĊĠAAAGAAĞAAGCAĞTTĠĊĊĀTŦĀŤŦŤĊTTCĀĠĠGATTAGTĠA
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELEFAX:
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCAGGGAGGCTCAAAACTTTTGGCGGTTGT 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                  525 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (781) 893-8277
                                                                                                                                                         6.9%; Score 31.4; DB 4; 54.9%; Pred. No. 1.2; ative 0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FARCIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                         51;
                                                                                                                                                                                    Length 525;
                                                                                                                                                     Indels 0;
                                                                                                                                                  Gaps
                                                                                        272
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RESULT 9
US-09-801-861-3
; Sequence 3, Application US/09801861
; Patent No. 6492154
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US-08-956-171E-133
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Sest Local Similarity 49.7%; Pred. No. 2.8;

Matches 80; Conservative 0; Mismatches 81;
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US-08-956-171E-133/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (240) 314
TELEPAX: (301) 309-8
INFORMATION FOR SEQ ID NO: 133
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 133, Applicat Patent No. 6593114
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRILING DATE: 20-0ct-1997

PRICA FILING DATE: 20-0ct-1997

PRICA APPLICATION (NUMBER: US/08/956,171E

PRICA APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 60/009,861.

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

PILING DATE: January 3, 1997

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE JOCKET NUMBER: PB248P1

TELECOMMUNICATION IPPORMATION:

TELECOMMUNICATION IPPORMATION:

TELECOMMUNICATION IPPORMATION:
                                                                                                                                                 2531 CAATTAATCAAGCAGATATCATTTCTGAACCGGTTGCTCTTGGTAGTGTTCAGGTACCAA 2472
                                                                                                            185 AGGGAGGCTCAAAACTTTTGGCGGTTGTTGGGGCAAGAAGGTAGTAGCAACCGGGCAAAGA 244
                                                                                                                                                                                         125 CATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGGTCAGTTACGGC 184
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 133:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diske
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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Gil H. Choi
TTGCAACTGTÁTGCAÁATTTGÁTCTGCCÁAÁGTTAGCACÁG 2371
                                     TTGACCAGACAGGAGATTATAACCTTGCATATATTGATÇAG 285
                                                                      ATGATGGTCAÁCCTATTATTCTGCTTAATGATAÁACÁÁACGÁTAGGTGGTTATACCÁÁAÁ 2412
                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 2785 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.50 inch, 1
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MEDOS Version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
R OF SEQUENCES: 5256
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                                                                                                                                                                                                                                                 81;
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US-09-596-002-32/c
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TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 32, Application US/09596002 Patent No. 6632636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: CLOC
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Best Local :
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NAME/KEY: misc feature

OTHER INFORMATION: Incyte template ID No. 6632636 32

PUBLICATION INFORMATION:

-09-596-002-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Patterson,
APPLICANT: Berg, Kim,
TITLE OF INVENTION: NU
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/801,861
CURRENT FILING DATE: 2001-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 62909
TYPE: DNA
ORGANISM: M. catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                  Loca1
 7909
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                                                                                                                                        8029 AATTGATTAACAACCATATGGAGTATGTTATGAAAAGATTATCTTTAATTGCATTATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8632 TGTTATGAGTATTCAACAAGAATATGTATATAAAGCACTTATCACAGAGTCAGTTTTTCA
                                                                                                      281 ATCAGGCGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGA 340
                                                                                                                                                                            221 AAGGTAGTAGCAACCGGGCAAAGATTGACCAGACAGGAGATTATAACCTTGCATATATTG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 AAAAACGGCAATTGTAGTGCA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 ТӨСӨАТӨАТТАТССАӨАААӨӨТТСТӨӨТААТАААӨСАААТАТТАСАСАӨТАТӨӨТАСТСА 395
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50; Conserv
                                                                                                                                                                                                                                6.9%;
Similarity 49.7%;
GTTTTAGCATTGACCATTTTGGCACCTCAACCAATGTGGCA 7869
                                                                       CGGTGGCAGGTTTTGCTAACGCAGCGACTTATGAGCTTGATCCTTATCACACCAATGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FastSEQ for Windows Version 4.0
                                 TGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACA 381
                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robert, E
                                                                                                                                                                                                             Score 31.4; Di
Pred. No. 14;
O.; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 31.4; D; Pred. No. 12; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF MORAXELLA CATARRHALIS GENOME
                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 53332;
                                                                                                                                                                                                                                               Length 62909;
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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RESULT 11

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US-09-134-001C-398
(Sequence 398, Application US/09134001C
(Sequence 398, Application US/09134001C
(Sequence 398, Application US/09134001C
(Seneral Information:
(Seneral Information:
(Sequence 398, Application US/09134001C
(Sequence 398, Application UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCCCUS
(SETILE OF INVENTION: BETIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
(SEQUENCE: GTC-007
(SEQUENCE: GTC-007
(SEQUENCE: GTC-007
(SEQUENCE: GTC-008-13
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US-09-540-236-1518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-540-236-1518
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SEQ ID NO 398
LENGTH: 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 1518
LENGTH: 606
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                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 78; Conserv
                                                                                                                                                                                                                                                                                  1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 GCGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 AGTAGCAACCGGGCAAAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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AAGATAATGCAA 1210
                                                                  AAAAAACGGCAA 406
                                                                                                                                         CAACTAATAATAACGATAATGTAGCCAATAATAACTCAAATTATACAAACCAAAATCAAC 1198
                                                                                                                                                                                                    CTGCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTATGGTACTC
                                                                                                                                                                                                                                                                                  ATTCTGATAAGAACGCAGATGACTCTGATAATAGTTCCTCAAATCCTAACGCTACTT 1138
                                                                                                                                                                                                                                                                                                                                                         ATATTGATCAGGCGGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATA 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGGTTTTGCTAACGCAGCGACTTATGAGCTTGATCCTTATCACACCAATGCGCGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.3%;
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Pred. No. 1.5;
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US-09-059-584-50

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RESULT 14
US-08-916-421B-1/c
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GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: pB275
CURRENT APPLICATION NUMBER: US/08/916,421B
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Best Local Similarity
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TILEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 2139 has Type
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: BatentIn Release #1.0,
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 50, Application US/09059584 Patent No. 6440701
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REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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RILING DATE: 14-APR-1998
CLASSIFICATION: DATA:
PRIOR APPLICATION NUMBER: US 08/778,570
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ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE Sim & McBurney
CORRESPONDENCE SIM & M
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APPLICANT:
TITLE OF IN
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 ТАРАССАРАТАТТАСАСАСТАТССТАС 392
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Loosmore, Sheena M.
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, Michel H
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Robin E
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Pred. No. 3.3;
0; Mismatches 35; Indels
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LOCATION: (191989)...(191989)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
LOCATION: (191995)...(191995)
OTHER INFORMATION: n equals a, t
                   NAME/KEY: misc feature
LOCATION: (309398) ..(309398)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (309418) ..(309418)
  LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals
                                                                      NAME/KEY: misc feature
LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a,
                                                                                                           NAME/KEY: misc feature
LOCATION: (234220)...(234220)
OTHER INFORMATION: n equals a,
                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (234187)...(234187)
OTHER INFORMATION: n equals a,
                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a,
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LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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OCATION: (163385)..(163385)
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LOCATION: (103998) . (103998)
OTHER_INFORMATION: n equals a,
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LOCATION: (98343) .. (98343)
OTHER INFORMATION: n equals a,
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LOCATION: (98266) . (98266)
OTHER INFORMATION: n equals
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LOCATION: (98239)...(98239)
OTHER INFORMATION: n equals a,
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
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LOCATION: (84773)...(84773)
OTHER INFORMATION: n equals
NAME/KEY: misc feature
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OTHER INFORMATION: n equals
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ORGANISM: Methanococcus jannaschii
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LOCATION: (1313224)..(1313224)
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LOCATION: (1310988)..(1310988)
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LOCATION: (855539)..(855539)
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LOCATION: (312993)...(312993)
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OCATION: (871619)..(871619)

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SEQ ID NO 2813
LENGTH: 832
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Best Local :
                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and
FILE REFERENCE: GENSET.054PR2
                                                                                                                                                                                                                                                                                                                                                                                                                                           PENERAL INFORMATION:
APPLICANT: Dumas milne Edwards,
APPLICANT: JObert, S.
APPLICANT: Giordano, J.Y.
                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1664854)..(1664855)
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LOCATION: (1470091)..(1470091)
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100 AMWTRTWTGYAYYRSMMYWWRYRCWKKKAYYRKTTCYSSKGWTWWKRWKKAWTTWWWKKT 159
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                                                               WRRKKKKAMWKYWKTWTWWYWRYAMWGTYKKKAMCRTKTKKKKKKGYMWMWYWGWRRSYM 99
                              TATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAGTCTTCATTT 129
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Search completed: March 16, 2004, 04:37:01 Job time: 53.6647 secs

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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries
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456
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                6/ptodata/2/pubpna/US09A PUBCOMB seq:*

6/ptodata/2/pubpna/US09B PUBCOMB seq:*

6/ptodata/2/pubpna/US09C PUBCOMB seq:*

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6/ptodata/2/pubpna/US10A PUBCOMB seq:*

6/ptodata/2/pubpna/US10B PUBCOMB seq:*

6/ptodata/2/pubpna/US10C PUBCOMB seq:*
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6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
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/pubpna/US06_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIE

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33		33	33	33	33	33	33.2	33.6	33.8	33.8	33.8	34.4	36	36	Score
ı ,	7.2	7.2	7.2	7.2	7.2	7.2	7.3	7.4	7.4	7.4	7.4	7.5	7.9	7.9	Query
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116-10-037-633-14907	US-10-398-221-2058	US-10-398-221-7	US-10-282-122A-35601	US-10-282-122A-35991	US-10-369-493-32803	US-10-424-599-104721	US-10-282-122A-17259	US-10-282-122A-36109	US-10-282-122A-6441	US-09-912-020-139	US-10-424-599-43422	US-10-247-671-55	US-10-184-634-156	US-10-184-644-156	ID
	Sequence 2058, Ap	Sequence 7, Appli	Sequence 35601, A	Sequence 35991, A	Sequence 32803, A	Sequence 104721,	Sequence 17259, A	Sequence 36109, A	Sequence 6441, Ap	Sequence 139, App	Sequence 43422, A	Sequence 55, Appl	Sequence 156, App	Sequence 156, App	Description

## ALIGNMENTS

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Prior Application removed - See File Wrapper or Palm; NUMBER OF SEQ ID NOS: 612; SEQ ID NO 156; LENGTH: 413; TYPE: PRT ORGANISM: Homo Sapien
US-10-184-644-156
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; Sequence 156, Application US/10184644
; Publication No. US:0030044930A1
                                                                                                                                   Query Match 7.9%; Score 36; DB 14; Length 413; Best Local Similarity 11.6%; Pred. No. 2; Matches 28; Conservative 93; Mismatches 121; Indels
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: P3430R1C227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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                                                                                       147 TGGTCAAGCTGGGACTAATAATAGTGCTCAGTTACGGCAGGGAGGCTCAAAACTTTTGGC 206
  207 GGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCAAAGATTGACCAGACAGGAGATTATAA 266
                                           172 HDGKDYVKGSKKLRVGLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGGR 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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Watanabe, Colin K.
Wood, William I.
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Godowski, Paul
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RESULT 3
US-10-247-671-55/c
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US-10-184-634-156
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Best Local Similarity 11.6
Matches 28; Conservative
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SEQ ID NO 156
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Coddard, Audrey
APPLICANT: Godowski, Paul
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TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 156, Application US/10184634
Publication No. US20030068684A1
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
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ITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                      412 YG 413
                                                                                                                   387 TG 388
                                                                                                                          352 LRLKDPDKKNWKRKIIAVYSGHQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCA 411
                                                                                                                                                        327 TGGTAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTA 386
                                                                                                                                                                                       292 ELGISPTIKKWPGGWIHFSGFDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTGSGVY 351
                                                                                                                                                                                                                    267 CCTTGCATATATTGATCAGGCGGGCAGTGCCAAÇGATGCCAGTATTTÇGCAAGGTGCTTA 326
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                                                                                                                                                                                                                                                                                                            207
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                                                                                                                                                                                                                                                                                                                                            147 ТӨӨТСААӨСТӨӨӨАСТААПАЛТАӨТӨСТСАӨТТАСӨӨСАӨӨӨАӨӨСТСААААСТТТТӨӨС 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 TGGTAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATAAAGGAAATATTACACAGTA 386
                                                                                                                                                                                                                                                                               GGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCAAAGATTGACCAGACAGGAGATTATAA 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 ELGISPTIKKMPGGMIHFSGFDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTGSGVY 351
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Watanabe, Colin K.
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Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                             7.9%; Score 36; DB 14; Length 41: 11.6%; Pred. No. 2; ative 93; Mismatches 121; Indels
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GENERAL INFORMATION:

APPLICANT: Mikita, Thomas

APPLICANT: Mikita, Thomas

APPLICANT: Mikita, Thomas

APPLICANT: Miffman, Dov

APPLICANT: Kaser, Matthew R.

ITILE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS

CURRENT APPLICATION NUMBER: US/10/247,671

FRILE REFERENCE: PA-0050 US

CURRENT APPLICATION NUMBER: US/10/247,671

FRING APPLICATION NUMBER: 60/323,784

NUMBER OF SEQ ID NOS: 186

SOFTWARE: PERL Program

SEQ ID NO 55

LENGTH: 5184

TYPE: DNA

ORGANISM: Homo sapiens

FRATORE:
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US-10-424-599-43422/c
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Best Local Similarity 58.4%;
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Best Local Similarity 52. >>,
Best Local Similarity
Conservative
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; OTHER INFORMATION: Incyte ID No. US20030194721A1 5185743CB1
US-10-247-671-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 43422, Application US/10424599 Publication No. US20040031072A1
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max FEATURE:
354 AGGTTCTGGTAATAAAGCAAATATTACACAGTATGGTACTC
                                                                            640 récadacagricos arginaricas de Grandas de Constantiva de Constantiva de 1810 de 181
                                                                                                                          294 TGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGGATGATTATCCAGAA 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 GATTGCAGCCGCAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGA 110
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52.9%;
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Pred. No. 15;
0; Mismatches
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                                                                                                                                                                                                                                                                             DB 12;
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580 AGATTCTTGTGTTAAGTCTGCAGTTACAGCTAATGGTAGTC 540

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; ORGANISM: E. Coli
US-09-912-020-139
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Publication No. US20040029129A1
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Best Local :
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TILL OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITEA.034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR APPLICATION NUMBER: 60/207,727 PRIOR APPLICATION NUMBER: 60/207,727
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REPERRNCE: ELITRA.001DV1
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CURRENT FILING DATE: 2001-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
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APPLICANT: Ohlsen, Kari L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 7.4%;
Local Similarity 56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319 GGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATA 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Conservative
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                                                                                                                                                                                                                  Yamamoto, R
Forsyth, R.
                                                                                                                                                                                                                                                            Carr, Grant
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Malone, Cheryl
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                                                                                                                                                                                                                                          Robert
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; Pred. No. 16;
0; Mismatches
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SEQ ID NO 6441
LENGTH: 1149
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                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
                                                                                                                                              PRIOR APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential FILE REFERENCE: ELITRA 034A
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PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
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PRIOR FILING DATE: 2000-10-23
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ORGANISM: Escherichia coli
                                                                                    FILING DATE:
                                                                                                   APPLICATION NUMBER: 60/230,347
                     APPLICATION NUMBER: 60/253,625
                                                                APPLICATION NUMBER:
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Yamamoto, Robert
Forsyth, R.
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Malone, Cheryl
Haselbeck, Robert
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Trawick, John
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lio, Carlos
2000-11-27
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56.9%;
                                                            60/242,578
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Pred. No. 16;
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SEQ ID NO 17259
LENGTH: 1371
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: US/10/282,122A
PRIOR APPLICATION NUMBER: 05/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                           Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
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Publication No. US20040029129A1
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APPLICANT:
APPLICANT:
TITLE OF IN
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APPLICANT:
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TYPE: DNA
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PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                  PatentIn version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 ACCGTCAAATTACAAATTATAAAACTTATGGTACGC
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Wall
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Trawick, John
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59.48;
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; Pred. No. 19;
0; Mismatches
                                                                                                                                        See File Wrapper or PALM
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                                                                                      GENERAL INFORMATION:
                                                                                                  Sequence 32803, Application US/10369493
Publication No. US20030233675A1
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
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RESULT 10
US-10-369-493-32803/c
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US-10-424-599-104721
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APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Cap vinhua
APPLICANT: Cap vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
: NUMBER OF SEQ ID NO.104721
ISROTH: 312
TYPE: DNA
COCCURRENT APPLICATION NUMBER: US/503-04-28
: SEQ ID NO.104721
ISROTH: 312
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Best Local S
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US-10-424-599-104721
US-10-424-599-104721, Application US/10424599
Publication No. US20040031072A1
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Clostridium difficile
US-10-282-122A-17259
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                                                                          249
                                                                                           387 ГССТАСТСАРАРАРССС 403
                                                                                                      189 AAAAÁÁAÁAAAAAGGGGÁTTGGCCÁTÁCGAGTCATGGTÁÁCCÁÁGAGAGACATGATGÁGCÁ 248
                                                                                                                                  327 TGGTAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTA 386
                                                                                                                                                                      129 CCATGCTTTGAATGÁTAÁAACTTACCGTGCCGTGCTGCAGGATGGTTTTTCCCCAÁGCGGCAAÁ 188
                                                                                                                                                                                                      267 CCTTGCATATATTGATCAGGGGGGGGGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTA 326
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                                                                                                                                                                                                                                               h 7.2%; Score 33; DB 12; Length 312; Similarity 52.6%; Pred. No. 13; 72; Conservative 0; Mismatches 65; Indels
                                                      CĠATAAAĊGÁTATĀĊTĠ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 TATAACCTTGCATATATT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  586 GÍRAGAAAARCÍRAGGITCÁCÁÁGAGGGÍRÁTITTGARAGGÁÁÁGÁÍGGÁGAITACITCÁRÁC 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     526 TATTÍAÓTGGÁTATAĞTAÁAİCCTÁÁAAİTTĞCAGTCATÁTCĞAÁTATAĞGAİTÁTCÁCAİ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 ATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTACGGCAGGGAGGCTCAAAACTT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     466 AATAAAGAACATGAGTGTGCTGTAATAGAGATGGGTATGTCTGGATTCAATGAAATAAAA 525
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95; Conservative
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Pred. No. 26;
0; Mismatches
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 32803
LENGTH: 1194
TYPE: DNA
ORGANISM: Chloroflexus aurantiacus
US-10-369-493-32803
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Matches
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Publication No. US20040029129A1
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APPLICANT:
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                                                                                                                                                                                                                                          FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION UMMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENERAL
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TITLE OF INVENTION: Identification of Essential Genes
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
PILE REFERENCE: 38-10(52052)B
                                 OR APPLICATION NUMBER: 60/191,078
OR FILING DATE: 2000-03-21
OR APPLICATION NUMBER: 60/206,848
OR FILING DATE: 2000-05-23
OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/230,335
OR FILING DATE: 2000-09-06
OR APPLICATION NUMBER: 60/230,347
OR FILING DATE: 2000-09-09
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/242,578
OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 ATAGTGCTCAGTTACGGCAGGGAGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90;
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                                                                                                                                                                                                                                                                                                                                                                                  Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Wall, Daniel
Trawick, John
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Zyskind, Judith
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Malone, Cheryl
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Pred. No. 28;
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; TYPE: DNA
; ORGANISM: Streptococcus mutans
US-10-282-122A-35991
                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,337
PRIOR APPLICATION NUMBER: 60/230,347
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: ELITRA.034A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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Local Similarity 49.2%;
les 87; Conservation
                   APPLICATION NUMBER: 60/269,308 FILING DATE: 2001-02-16
                                                                                                                   APPLICATION NUMBER: 60/257,931
                                                                                                                                                            APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                       APPLICATION NUMBER: 60/242,578
                                                                               APPLICATION NUMBER: 60/267,636
                                                                                                      FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 GTTCTGGTAATAAAGCAAATATTACACAGTATGGTACTCAAAAAAACGGCAATTGTAG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 GGGCAAAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTG 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAG 355
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Zyskind, Jud
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Malone, Cheryl
Haselbeck, Robert
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                                                              2001-02-09
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  data removed
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Pred. No.
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29;
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File Wrapper or
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SOFTWARE: Pate SEQ ID NO 35601

PatentIn version

ENGTH:

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Best Local Similarity
Watches 72; Conserva
                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (1). (end)
OTHER INFORWATION: n can be any nucleotide: a, g,
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Best Local Similarity 47.00,
watches 96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: FR 00/12 697 PRIOR FILING DATE: 2000-10-04 NUMBER OF SEQ ID NOS: 4025
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PRIOR FILING DATE: 2001-10-04
                                                                                                                                                                                                                                                                                                                                             ORGANISM: Listeria innocua
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                          285263 TĠĊTAATATTTCAAAAT 285247
                                                                  285323 TATTTCAAAACTATTGTATGATAATTCGGCTATTAAAGTCAAGTTATTTTGAAATATAGG 285264
                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 319630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-398-221-7/c
                                                                                                                           285383 CCCTTCACGAGTTCATAGCCTTTCGTATTTCGATATATAGTTTTGAAATATAAATCACCA 285324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Staphylococcus haemolyticus
                                                        369 AGCAAATATTACACAGT 385
                                                                                               309 ȚAȚTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATAA 368
                                                                                                                                                        249 CCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCGACGATGCCAG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1629 CTAGTCATATTGGTGCTCAAA 1649
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Pred. No. 5.5e+02;
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Pred. No. 35;
0; Mismatches 105; Indels
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; ORGANISM: Human
US-10-027-632-14807
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PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PRILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                             SOFTWARE: Fast:
SEQ ID NO 14807
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                                                                                                                            PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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APPLICANT: GLASER, Philippe
ITITLE OF INVENTION: Listeria innocua, genome and applications
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-04
VNUMBER OF SEQ ID NOS: 4025
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                                                                                                                 NUMBER OF SEQ ID NOS:
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US-10-398-221-2058
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Publication No. US20030204075A9
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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Best Local S
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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SEQ ID NO 2058
LENGTH: 3011208
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Publication No. US20040018514A1
GENERAL INFORMATION:
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                                                                                                                   AUTHORS
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Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.

1 (bases 1 to 220)
Clifton,S. Johnson,S.L., Blumberg,B., Song,J., Hillier,L.,
Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y.,
Person,B., Glbbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
Unpublished (1999)
Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                             d926906.yl Xenopus laevis gastrula non normalized Xenopus laevis cond clone IMAGE:3749963 5' similar to SW:CSGB_ECOLI p39828 MINOR CURLIN SUBUNIT PRECURSOR.;, mRNA sequence.
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BI311207 EST531295
BM815787 EST531295
BM8453027 BX453027
BM540315 BB49115
BB49135 BB49115
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BB49131 G109 G10
AL716706 AL716706
AQ308392 CITBI-E1-
AQ779365 HS 3207
BB6125943 EST471589
CA855727 PEEST0329
AL7063921 Dr0s0pbil
AL551649 AL551649
BBG125943 EST471589
CA855727 PEEST0363
BJ433259 BJ433259
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BM652363 K-EST0134
CG950664 HBEH026TF
AL187164 Tetracdon
BZ794472 PUFFRISTD
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Genes expressed in microfilaria of Onchocerca volvulus
Unpublished (1999)
Contact: Steven A. Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 ATTATAACCITGCATATATTGATCAGGCGGCAGTGC 296
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                                                                                                                         Williams, S.A.
                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Onchocercidae; Onchocerca.

1 (bases 1 to 207)
                                                                                                                                                                                                                             Onchocerca volvulus
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207 bp mRNA linear EST 11-JAN-19:
SMOVMfCAR04G09SK Onchocerca volvulus microfilaria cDNA
(SAW98MLW-CVME) Onchocerca volvulus cDNA clone SWOVMfCAR04G09 5',
                                                                                                                                                                                                                                                           Onchocerca volvulus
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Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Source lab clone id . 3749863
Trace considered overall poor quality This clone is available
(image@image.llnl.gov) for further information.
Seq primer: -40Rp from Gibco
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/note="Westor: pBluescript SK-; Site 1: EcoRI; Site 2:
/note="Westor: pBluescript SK-; Site 1: EcoRI; Site 2:
/note="Westor: pBluescript SK-; Site 1: EcoRI; Site 2:
/note="Westor: pBluescript SK-; Site 1: EcoRI; Site 2:
/note="Westor: pBluescript Sk-; Site 1: EcoRI; Site 2:
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/mol_type="mRNA"
/db xref="taxon:8355"
/clone="IMAGE:3749963"
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96.8%; Pred. No. 4.7e-51;
tive 0; Mismatches 7;
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                                                                                                                                                                   Spirurida; Filarioidea;
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION AI368352/c LOCUS RESULT 2 뭐 ş 밁 ş 밁 Ş 망 Ś

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FEATURES
http://xenopus.nibb.ac.jp,
Location/Qualifiers
                                                                                                         Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
                                                                                                                                                                                                        Contact: Tadasu Shin-i
                                                                                                                                                                                                                            Expressed genes in X. laevis embryo Unpublished (2001)
                                                                                                                                                                                                                                                                          Kitayama, A., Terasaka, C., Mochii, M., Ueno, N.,
                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BJ618688
BJ618688 NIBB Mochii normalized Xenopus early gastrula library Xenopus laevis cDNA clone XL186b22 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
1 (bases 1 to 680)
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Xenopus laevis
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                                                             il: tshini@genes.nig.ac.jp
information of this clone
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Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 4135853786
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|mol type="mRNA"
|db_xref="taxon:6282"
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/lab_host="XL1-Blue MRF'"
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Pred. No. 3.9e-06;
0; Mismatches 3
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                                         available through the following
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, (Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                          Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                     Submitted (12-APR-2000) Genoscope - Centre National BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.
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129D18 of library G fro
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                                  /clone_lib="G"
/note="Genoscope sequence
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/mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                           /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="whole embryo"
/dev_stage="stage 10.5"
/clone_lib="NIBB Mochii normalized Xenopus early
                                                                              /clone="129D18"
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Pred. No.
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                                                                                                Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,B.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira
and Hayashizaki,Y.
                                  RIKEN integrated sequence sequencing pipeline with 38 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group,
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayateu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB703456 RIKEN full-length enriched, in vitro fer musculus cDNA clone 7420452F19 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                        1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
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Mammalia; Eutheria; Rodentia;
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(bases 1 to 533)
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                    Fukunishi,Y.,
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46.6%;
nishi,Y., Shibata,K.,
Hayashizaki,Y.
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                                                            384 multicapillary
                                                                                   analysis (RISA)
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1, in vitro fertilized eggs Mus
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                  Itoh,M.,
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y sequencer. Genome
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source

St.

Paul,

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306 CAGTATTTCGCAAGGTGCTTA 326
                                                                             Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 TGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAACGATGC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 GGGAGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCAAAGAT 245
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EST669415 MTUS Medicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             further details
e mouse tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone lib="RIKEN full-length enriched, in vitro
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49.3%;
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/dev_stage="egg"
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/clone="7420452F19"
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/strain="C57BL/6J"
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Pred. No. 2.8;
0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                    562 bp mRNA linear EST 21-JUL-2003 truncatula cDNA clone MTUS-11C11, mRNA
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                                                      COMMENT
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                                                                                                                                                                Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Medicago truncatula
Medicago truncatula
Medicago truncatula
Medicago truncatula
Medicago truncatula
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermarophyta; Magnoliophyta; Embryophyta;
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Spermarophyta; Magnoliophyta; Magnoliophyta; Magnoliophyta;
Spermarophyta; Magnoliophyta; Mag
                                                                                1 (bases 1 to 671)

Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 AAATCAGCAAGGAGAAAGTTGATGAATGTTATAATGCGATTCTTCATCTTACAAATACAA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 ATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCTG 361
                                                            ESTs from developing reproductive tissues of Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  242 AGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCCAACG 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: kvandenb@cbs.umn.edu
TIGR sequence name: mTUSK35TK Alias Clone name:pGESD10A6 More
information is available at: www.medicago.org
Seq primer: Skmod (CTA gAA CTA gtg gAT CC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Minnesota
220 BioSci Center, 1445 Gortner Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 612 624 2755
Fax: 612 625 1738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VandenBosch,K., Endre,G., Silverstein,K., Town,C.D., Van Aken,S., Utterback,T., Cheung,F. and Fraser,C.M.
The Medicago truncatula 6K unigene set: cDNA clones selected and re-arrayed from various libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
Michael A. Grusak
Children's Nutrition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="MTTUS"
//clone_lib="MTTUS"
//note="Vector: pBluescript SK-, Site_1: EcoRI, Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
stratested and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-'ap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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/dev_stage="various stages"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Medicago truncatula"
/mol_type="mRNA"
/multivar="A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="MTUS-11C11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               truncatula
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linear

EST 20-JUL-2001 010A6 5' end,

ORIGIN

Matches Query Match Best Local ;

REFERENCE

Research

ACCESSION VERSION

KEYWORDS

ORGANISM

RESULT 6 CF068694 LOCUS

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DEFINITION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
Plant Nematode Genetics Group
North Carolina State University
Box 7616, Raleigh, NC 27695, USA
                                                          nematode Meloidogyne incognita
Unpublished (2002)
Contact: Bird, DM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76;
                                                                                                              Bird,D., Koltai,H., Samac,D., Town,C.D., Van Aken,S., Utterback Cheung,F., Tsai,J. and Fraser,C.M.
ESTs from roots of Medicago truncatula after infection with the
                                                                                                                                                                                                                  Medicago truncatula/Meloidogyne incognita mixed Medicago truncatula/Meloidogyne incognita mixed
                                                                                                                                                                                                                                                                                                                    EST593881 BNIR Medicago truncatula/Meloidogyme incognita mixed library cDNA clone pBNIR-28N9, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baylor College of Medicine 1100 Bates Street, Houston, Tel: 713-798-7044
                                                                                                                                                                                                   Eukaryota; mixed EST libraries.
                                                                                                                                                                                                                                                                                 BM815787.1 GI:19151801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAATTATGGTTATAATAAAC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAATAAAGCAAATATTACAC 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGATTGAACAGAGTGATGATAATGATGTGGATTACAAAAATCAGCTTCTTAATGTTCTCA 138
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                                                                                                                                                                             (bases 1 to 756)
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primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence name: MTPAR03TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Immature seeds, collected from pods ranging in age from 11 to 19 days after pollination, were harvested fr greenhouse-grown plants. Seeds were removed and separated from pod walls and were immediately frozen in liquid nitrogen. Seeds throughout the age range were pooled for mRNA extraction. cDNA was prepared from polyenriched RNA. The cDNA was directionally ligated into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propogated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pollination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="immature seeds"
/dev_stage="Immature seeds, 11 to 19 days after
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_
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lone="pGESD10A6"
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Pred. No. 5.1;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr was not normalized. Library was constructed by Life Technologies, division of Invitrogen. This sequence belongs to sequence cluster 6669.f For more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSOBAH007ZA11NP1&cluster=6669.f. Contact: Feng Liang Email: fliang@alifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSOBAH007ZA11NP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             957 bp mRN
BX453027 Homo sapiens FETAL BRAIN Homo
CSODF012YJ13 3-PRIME, mRNA sequence
BX453077
                                                                                                                                                                                                                                                                                                        1 (bases 1 to 957)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                               Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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BX453027.1 GI:31036338
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Fax: 919 515 9500
Email: david_bird@ncsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAATCAGCAAGGAGAAAGTTGATGAATGTTATAATGCGATTCTTCATCTTACAAATACAA 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="BNIR"
//clone_lib="BNIR"
//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing CDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells. "
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EST library"
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/dev_stage="3 days after infection with Meloidogyne
incognita second_stage larvae"
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/clone="pBNIR-28N9"
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Pred. No. 5.3;
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BM540455
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Matches 106;
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Best Local
                                            S O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Balija,V., Cunnius,D., Dedhia,N.N., de la Bastide,M., Katzenberger,F., King,L., Kirchoff,K.A., Miller,B., Muller,S., Nasclmento,L.U., Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T., Expressed sequence tags from Canis familiaris (dog) (2002) Unpublished (2002)
Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bource
                                     PO Box 100, Cold of Tel: 516 367 8884 Fax: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          620 TAASGGAWATKGKGGAGKSAKGGAASASSS 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 AAACGGCAATTGTAGTGCAGAGACAGTCGC 427
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 364)
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                                                                                                                                                                                                                                                                                                                                                                                   BM540455 364 bp
qj59d01.b1 Canis cDNAs from testes
clone qj59d01 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                              Canis familiaris (dog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAÁGAÁMKÁATGÁAÁÁÁÁÁKKAAAKGAÁMTÁÁÁKGÁÁÁÁÁAAAGAÁGÁAKGKGGKKGGAÁÁÁ 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ССАТБАТТАТССАБАЛАБСТТСТББТЛАГЛАДБСАЛАТАТТАСАСДБТАТБСТСДАЛА 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGAÀAAÀAAKAAKGWKKAGAÁAAAÀKĠGAÁAAGGKAAKAÁÁKAAAAAKGĠĠGKÄKÁGKĠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGAAGGTAGTAGCAACCGGGCAAAGATTGACCAGACAGGAGATTATAACCTTGCATATA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTTATTKGÁSSSSGGRSÁAAAÁSGGKÁMKAKTKAGAÁÁÁMKAGGTGGTGAAAAATKKTA 801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 99AСТААТААТАСТ GCT CAGTTA CCGCCAGGGAGGCT CAAAACTTTTGGCGGTTGTTGCCGC 21.7
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mccombie@cshl.org
qj59 row: d column:
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/db xref="taxon:9606"
/db xref="taxon:9606"
/dlone="CSOUPD12Y13"
/tissue_Type="FETAL BRAIN"
/dev stage="fetal"
/dlone lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer: Five prime end cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
|mol_type="mRNA"
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32.1%; Pred. No. 7.5;
Tative 55; Mismatches
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cells Canis familiaris cDNA
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AZ169114
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Email: acameron@caltech.edu
Plate: 113 row: A column: 18
Seq primer: T7
Class: BAC ends
                                                                                                            Contact: Cameron, RA, Davidson, EH, Division of Biology 156-29 California Institute of Technology Pasadena California 91125, USA
                                                                                                                                                                                                              A sea urchin genome project: Sequence scan, virtual map, additional resources Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          221 TTGTTCCTATCCTAAAAGACTAACCATTTACCCCTACTCTACTGAAAAAGGGGCTGGTGT
                                                                                                                                                                                                                                                                                   Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.!
                                                                                                                                                                                                                                                                                                                                                                                   Strongylocentrotus purpuratus
Eukaryota; Metazoa; Rohinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 GÁAAACAÁÁCTTÍGTAGTCÁÍTÍTGGCTÁGGGAAAÍTGGCTTTAÁCCCCTCCTÁCTCT 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 CAGTGCCAACGATGCCAGTATTTCGCAAAGGTGCTTATGGTAATACTGCGATGATTATCCA 350
                                                                                                                                                                                                                                                                                                                                                                     Strongylocentrotidae; Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ169114 597 bp DNA linear GSS 29-AUG-: SP_0113 AZ A09 T7A Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=113 Col=18 Row=A, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 ĆCÁGGĆĠĠĠÁACCTŤŤĠÁAĆÁAGAGĠĠTCTCCÁGCÁTĊŤŤTGÁAÁŤGCŤCÁGTTĠATĠĠĠ 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 ÇAACCGGGCAAAGATTGACCAGAACAGGAGATTATAACCTTGCATATATTGATCAGGCGGG 290
                                                                                                                                                                                                       .0920195
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strongylocentrotus purpuratus
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97; Conserv
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                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 597)
                                                                                 (626) 395-8421
(626) 793-3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -21M13UnivFwd
High quality sequence stop
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/clone lib="Canis cDNAs from testes cells"
/clone lib="Canis cDNAs from testes cells"
/note="Wector: Lambda Zap II, The library was produced by Careg Hannon and Raymond Preston (Cold Spring Harbor Laboratory). This library is oligo(dT) primed using stratagene zap cDNA synthesis kit. It was made from dog testes. Please contact Greg Hannon (hannon@cshl.org) with any library related inquiries."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Canis familiaris"
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/db xref="taxon:9615"
/clone="qj59d01"
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                                                                                                                                                                                                                                                                                         Davidson, E.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 657)

S Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
Unpublished (2001)
On Jul 21, 2000 this sequence version replaced gi:9310170.
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 TAGTCATCGTCCCTTTCTTGGTCACGATGGCCATAGTCATTGTCCCTTTCTTGGTCAGCC
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                Email: genome resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Ich,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watshiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB449135 RIKEN full-length enriched, 9 days embryo Mus musculus cDNA clone D030070B09 3' similar to D38046 Mouse mRNA for typeII
                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA topoisomerase beta isoform, mRNA sequence.
BB449135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High
                                                                                                                                                                                                                                                                                                                                                 1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB449135.2 GI:16425330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCATCCTGTCTGTAGTCATCGTCCCTTTCCTGGTCAGCCTGGCCGT 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTCTGTAGTCATCGTCCCTTTCTTGGTCAGCCTGGTCGTAGTCACTGGCCATTTCCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCAAAGATTGA 248
                                                                                                                                                                                                                                                                                                                           81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 597
Location/Qualifiers
integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Strongylocentrotus purpuratus"
/mol_type="genomic DNA"
/db_xref="taxon:7668"
/clone="plate=113 Col=18 Row=A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . .597
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51.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36.4; DB 28; Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81;
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SOURCE
ORGANISM
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VERSION
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BG354883
                                                    KEYWORDS
                                                                                                                                                      DEFINITION
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Best Local 8
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                                                                                                                      BG354883
769 bp mRNA linear EST 05-MJ MBTSWLA133T7SEQ Trichinella spiralis muscle stage larvae (BC)
Trichinella spiralis cDNA clone MBTSMLA133 5', mRNA sequence.
Trichinella spiralis
Trichinella spiralis
                                                    EST
                                                                          BG354883
BG354883.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of encyclopedia: real-time sequence Res. 11 (2), 281-289 (2001) nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Alzawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prepare mouse tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAAGATACAGGGGAAAATTACTATAGGCTGCAGAAGAGGGAAGATTCACAAAAACCAACAT 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTAGCAACCGGGCAAAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAG 285
                                                                                                                                                                                                                                                                                                                   ATGTCTCTATGGTCTCTTACTAAAGAAAAAGTTGAAGAACTCATTAAACAGAGA
                                                                                                                                                                                                                                                                                                                                                         ATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTATGGTACTCAAAAA 399
                                                                                                                                                                                                                                                                                                                                                                                                                      GATGACAGTTCCTCTGATTCAGGAACTCCTTCAGGCCCCTGATTTTAATTATATTTTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clome_lib="RIKEN full-length enriched, 9 days embryo"/note="Site_1: Sal1; Site_2: BamH; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'dev_stage="9 days embryo"
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mol_type="mRNA"

db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="D030070B09"
                                                                            GI:13199069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36.4; DB 10; Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                               EST 05-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      597
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Eukaryota; Metazoa; Nematoda; Enoplea; Trichocephalida;

JOURNAL COMMENT

Daub, J., Connolly, B., Garate, T. and Blaxter, M.L.
A survey of genes expressed in the muscle stage larvae of the
parasitic nematode Trichinella spiralis
Unpublished (2001)
Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
University of Edinburgh

REFERENCE AUTHORS TITLE

Trichinellidae; Trichinella.

(bases 1 to

FEATURES

FORWARD: T7SEQ (GTAATACGACTCACTATAGGG)
BACKWARD: M13 FORWARD (CGCCAGGGTTTTCCCCAGTCACGAC)
Seq primer: T7SEQ (GTAATACGACTCACTATAGGG).

Location/Qualifiers

db\_xref="taxon:6334"

clone="MBTsMLA133" sex="mixed"

/organism="Trichinella spiralis' /mol\_type="mRNA"

Email: mark.blaxter@ed.ac.uk Tel: +44 131 650 6760 Fax: +44 131 670 5450

Ashworth Labs, King's Buildings,

West Mains Road, Edinburgh, EH9

PCR PRimers

source

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ACCESSION
VERSION
KEYWORDS
               REFERENCE
                                                                 SOURCE
ORGANISM
                                                                                                                                                                                          RESULT 15
AZ811109
LOCUS
                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                          230 АЛЛААGÁÁÁÁÁÁAGAGAAAAGAÁTAGAÁAÁGÁAÁ 262
                                                                                                                                                                                                                                                                                        390 TACTCAAAAAACGGCAATTGTAGTGCAGAGACA 422
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                                                                                                                                                                                                                                                                                                                                                                                                                   110
                                                                                                                                                                                                                                                                                                                                                                                                                                                        270
 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 532)
                                                                                                           AZ811109
532 bp DNA linear GSS 20
2M0077A09F Mouse 10kb plasmid UUGCIM library Mus musculus
clone UUGC2M0077A09 F, genomic survey sequence.
AZ811109
                                                           Mus musculus
                                                                   Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                   TĀCATGTĠĊĠÁTAGTŤCŤGGĀAĀTĀTĠGATŤĠĠŤĀTACĀĀĠAĀĀGĀĀĀAĀGĀAĀĀĀĀĀĀGĀA 229
                                                                                                                                                                                                                                                                                                                                                                                       TĠAGGĀTĀAATĀTTTTCAĠAĠĊTĠTĠTĠĀGĊĀĀAĠĠĊĀĠŢĀŦĀŢĊĠŢŢTCAŢĠŢŢŢĀGAĠ
                                                                                                                                                                                                                                                                                                                                                                                                                TGCATATATTGATCAGGCGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: .
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erry
Plate: 0077 row: A column: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Utah Genome University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ass: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA polymerase and T4 passage to the sheared with T4 DNA polymerase and T4 passage to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to electrophoresis. Vector DNA was prepared from a derivative electrophoresis. Vector DNA was prepared from a derivative inducible derivative of plasmid R1. The vector was ligated purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308,
                                                                                                         GI:12979038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD$27v, Purified genomic DNA from M. muscullus C57BL/6J (male) was obtained from the Jackson /Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="UUGC2M0077All"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomedical Polymers Research Bldg.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36.2; DE
Pred. No. 8.2;
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Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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COMMENT

JOURNAL

Mouse William Plasmid inserts
Unpublished (2000)
Unpublished Robert B. Weiss

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 491)

REFERENCE AUTHORS

SOURCE ORGANISM

Mus musculus

Mus musculus (house mouse) AZ811111.1 GI:12979042

ACCESSION VERSION

KEYWORDS

RESULT 14 AZ811111 LOCUS

В Ş ₽ Ś 밁 Ś

359

299 ACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTT 358

197

CAGTTÁTGAÁTÓGGÁTÁACÁGÁAAÁTÁTACGCGCTTÁCÁAATTTGGTTCATCGÁCTTCAÁ 137

CTGATGÁTÁÁÁGGCÁÁTÁÍTÍGTTAÁTGÁACTGÁTGAÁÁÁÁÁTCAGTÁÁTTGGÁG 251 CTGGTAATAAAGCAAATATTACACAGTATGGTACTCAAAAAAAGGGCAATTGTAG 412 TCGATGCAAGCATTGATGAAGATGATTTACCTÁTGACTTATGGATTTGAAGCTTTGGTTT 239 CAAAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCA

78

Query Match

/dev stage="muscle stage larvae"
/clone lib="Trichinella spiralis muscle stage larvae (BC)"
/note="Vector: Lambda ZipLox; Site\_1: SalI (5'end);
Site\_2: NotI (3'end); The infective L1 larva of
Trichinella spiralis is a nematode parasite of mammalian
skeletal muscle. The library was constructed using muscle
larvae of the T. spiralis isolate IS33, and was provided
by Dr Bernadette Connolly, University of Aberdeen."

Local Similarity

8.0%;

Score 36.4; DB 12; Length 769; Pred. No. 8.1;

88;

Conservative

0;

Mismatches

86;

Indels

0

Gaps

298 0

ORIGIN

DEFINITION

AZ811111
491 bp DNA linear GSS 20-FEB-200 clone UUGC2M0077A11 F, genomic survey sequence.

GSS 20-FEB-2001

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JOURNAL COMMENT
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Best Local Similarity
Matches 80; Conserv
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                                                                                                       330 TAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTATGG 389
212 AAAAAGAAAAAGAGAAAAGAATAGAAAAGAAA 244
                                                   390 TACTCAAAAACGGCAATTGTAGTGCAGAGACA 422
                                                                                                                                                                                                                                                                     270 TGCATATATTGATCAGGCGGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGG 329
                                                                                                                                                                                                                 92 TGAGGATAAATATTTTCAGAGCTGTGTCAGCAAAGGCAGTATATCGTTTCATGTTTAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0077 row: A column: 09
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Contact: Robert B.
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Utah Genome Center University of Utah
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus CSTBL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone_lib="Mouse_10kb_plasmid_UUGCIM_library"
/note="Vector: PWD42nv; Purified_genomic_DNA_from_M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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Search completed: March 16, 2004, 04:28:52 Job time : 2237.91 secs Inden Will to Joyld SHILL

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Database
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Maximum Match 100%
Listing first 45 summaries
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48
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

No	° 1;	Score	Query Match		BB	Ħ.	8
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	6	29.4	۲.	96	w	LEIGP63B	0669 Leishhmar
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## ALIGNMENTS

TITLE	REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	LEIMSP52A	RESULT 1	
and Donelson, J.E. Sequence diversity and organization of the msp gene family encoding	1 (bases 1 to 1797) Roberts, S.C., Swihart, K.G., Agey, M.W., Ramamoorthy, R., Wilson, M.B.	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.	Leishmania donovani	Leighmania donovani	glycoprotein 63: surface protein: virulence factor: zinc protease.	L19563.1 GI:308887	L19563	Leishmania donovani glycoprotein 63 (mspS2) gene, complete cds.	LEIMSP52A 1797 bp DNA			
the msp gene family encoding	Ramamoorthy,R., Wilson,M.E.	Trypanosomatidae;			lence factor; zinc protease.			nspS2) gene, complete cds.	linear INV 28-NOV-1994			

COMMENT FEATURES

8139613

3963 of Leishmania chagasi Mol. Biochem. Parasitol. 62 (2), 157-171 (1993) 94187791

source

organism="Leishmania donovani" |mol\_type="genomic DNA"

o\_species="chagasi" \_xref="taxon:5661"

\_stage="stationary stage promastigote" 1797

CDS

gene="msps2" gene="msps2" JOURNAL MEDLINE PUBMED

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Direct Submission
Submitted (12-DEC-1996) Ortiz G., Facultad de Medicina. Universidad de Murcia, Genetica Microbiologia, Campus de Espinardo, Murcia, SPAIN, 3010, Murcia, Eocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Original source text: Leishmania donovani (sub_species chagasi) stationary stage promastigote DNA.
Location/Qualifiers
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AUTHORS
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AUTHORS
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ORGANISM
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VERSION
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Best Local Similarity 76.6
Conservative
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                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leishmania donovani
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                  Mauricio, I.L., Stothard, J.R. and Miles, M.A. Genetic diversity in the Leishmania donovani complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GP63; major surface protease; mspC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leishmania donovani
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MHOM/KE/0000/Neal-R1.
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QHRCIHDAMQARVRQSVARHHTAPGAVSAVGLPYVTLDTAAAADRRPGSAPTVVRAAN
WGALRIAVSTEDL/TDPAYHCARVGOHIKRRLGGVDICTAEDILIDEKRDILVRHAAN
ALGLHTERLKVRQVQDKWKVTGMGDDVCSDFKVPPAHITDGLSNTDFVWYVASVPSEB
ARILESISVRHCDFVVPVINSTAAANIASRVDQLVTRHVTHEMAHALGFSVGFFEG
ARILESISNVRHCDFVVPVINSTAVAKAREQYGCDTLEYLEIEDGGAGSASASHIKM
RANITKWPAMFCNENEVTWRCPTSRLSLGKCGVTRHPDLPYWQYFTDDSLAGISAFKCME
CCPVVETYGDGGCAQBASGAGAPFKGFNVFSDAARCLIGARFPKTSHGIIKSYAGLCA
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/protein_id="CAD42811.1"
/db_xref="GI:21954456"
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/db_xref="SPTREMBL:QBMNZ5"
                                                                /codon_start=1
/allele="mspCLdA1"
/product="GP63"
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/note="constitutive major surface protease"
                                                                                                                                                                                               /organism="Leishmania donovani"
/mol_type="genomic_DNA"
/strain="WHOM/KE/0000/Neal-R1"
/db_xref="taxon:5661"
                                                                                                                                                 gene="mspC"
5. .1940
                                                                                                                                                                            country="Kenya"
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/product="GP63"
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76.6%;
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Pred. No. 2.8;
0; Mismatches 11;
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0,

REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE

FEATURES

/organism="Leishmania infantum"

JOURNAL

Ortiz, G

(bases 1 to 1860)

KEYWORDS SOURCE ORGANISM

283677

.1 GI:1743284

9p63 gene; protease. Leishmania infantum Leishmania infantum Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

1 (Dases I to 1860)
Ortiz,G., Martinez,P. and Segovia,M.
Characterization of GP63 of Leishmania infantum

RESULT 2 LIGP63GEN LOCUS DEFINITION ACCESSION VERSION

LIGP63GEN

infantum GP63 gene

1860 bp

DNA

linear

밁 Ş

751

1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGC 47

TACGACCAGCTGGTGACGCGTGTCGTCACGCGAGGATGGCGCGCACGC 797

ORIGIN

mat\_peptide sig\_peptide

/gene="mspS2" 97. .1794

/gene="mspS2" /product="glycoprotein 63"

Query Match Best Local Similarity

Matches

36;

Conservative

, ,

61.2%;

Score 29.4; DB: Pred. No. 2.8; 0; Mismatches

DB 3;

Length 1797;

11; Indels

0;

Gaps

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KEYWORDS
SOURCE
ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (11-JUL-2002) Mauricio I.L., Infectious and Tropical Diseases, London School of Hygiene and Trop. Med., Keppel Stre WC1E 7HT, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leishmania donovani
Leishmania donovani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leishmania donovani mspC gene
AJ495006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mauricio, I.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GP63; major surface protease; mspC gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AJ495006.1 GI:21954463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 2106)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cio, I.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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/db_xref="GI:21954464"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diversity in the Leishmania donovani complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="msvdsssthrhrsvaarlvrlaaagaaviaavahagav
qhrcihdamqarvrqsvachhtapgavsavglpyvtldtaaaadrrpgsaptvvraan
wgalriavsteditdsaavlcarvggrvnnhagaiatctaedilvkylipq
Alqlhterlkvrqovqdkmvvtdmvdelcgbfkvpqahiteffsutdfvmyvasvpsek
gvlamattcqvrsdghpavgvinipaaniasrvqqlvtrvvthemahalgfsgtffte
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ALQLHTERLKVRQVQDKWKYTDMVDBICGDFKVPPAHITDGLSNTDFVMYVASVPSEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QNITKMPAMFCNVSVDVVRCPTSRIMLGTCGIRGYSTPFSPYMQYFTNISLGGYSPFL
DYCPFVIGYGDGSCNQDASLATGFFGAENVFSDARCI IDGAFRENGRTAADGYYAGLC
ANVRCDTATRTYSVQVRGSMDYVNCTPGLRVELSTVSSAFEEGGYITCPPVEVCQA
VKGAKDFAGDSDSSSAGDAADRAAMQRWNDRMAGLATAAMVLLGMVLSLMALVVVWL
                                                                                                                                                                                                                                                                    /note="constitutive major surface protease"
                                                                                                                                                                                                                                                                                                                           14. .1939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="mspC"
132. .1823
                                                                                                                                                                                                                                                codon_start=1
                                                                                                                                                                                                                                                                                          /gene="mspC"
                                                                                                                                                                                                                                                                                                                                     /gene="mspC"
                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="MCAN/IQ/1977/Bumm3"
/db_xref="taxon:5661"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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/product="GP63"
                                                                                                                                                                                                                                                                                                                                                                                             country="Iraq"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Leishmania donovani"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type="genomic DNA"
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gene for GP63,
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strain MCAN/IQ/1977/Bumm3.
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ACCESSION VERSION

RESULT 4 LDO495006

POCUS

문 S ORIGIN

Matches

밁 Ś ORIGIN

JOURNAL REFERENCE REFERENCE AUTHORS TITLE

AUTHORS

FEATURES

gene CDS

JOURNAL

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REFERENCE
AUTHORS
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TITLE
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VERSION
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 764 TACGACCAGCTGGTGACACGTGTCGTCACGCACGAGATGGCGCACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mauricio, I.L., Stothard, J.R. and Miles, M.A. Genetic diversity in the Leishmania donovani complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AJ495007
AJ495007.1 GI:21954465
GPG3; major surface protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TATGATCAGCTGGTTACCCGTGTTGTTACCCGATGAAATGGCACATGC 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diseases, London School of WC1E 7HT, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-JUL-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mauricio, I.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mauricio, I.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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ILVVTQMMNIRGXDFNVSVINSSTAVAKARBQYGCGTLSYLEIBGQGGAGSAGSHIKM
RNAKDEHAPAAAAGYYSALTWAIFQDLGFYGADFSKABENFWGRNAGCAFLSEKCME
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RNITGWPAMFCNVSVDVVRCFTSRLMLGTCGIRGYSTFFSFYWQYFTNISLGGYSFFF
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RNAKDELMAPAAAGYYSALTMAIGODGFYQADFSKAEEMPRGNAGCAFLSEKCME
QNITKMPAMFCONVSUDVMRCTPSRLAUGTCGIRGYSTPFSFYMQYFTNISLGGYSPFL
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ANVRCDTATRTYSUQVCGSMDYVNCTPGLRVELSTVSSAFEBGGYITCPPYWFCQAN
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131. .1822
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l4._.1939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLTCPWWCCKFGGLPT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKGAKDFAGDSDSSSSAGDAADRAAMQRWNDRMAGLATAAMVLLGMVLSLMALVVVWL
                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                note="constitutive
                                                                                                                                                                                                                                                                                                                                                                                                                                      mol_type="genomic DNA"
strain="MHOM/SU/1984/Marz-Krim"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Leishmania donovani"
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76.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mauricio I.L., of Hygiene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2106 bp
                                                                                                                                                                                                                                                                                                                  major
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for GP63, strain
                                                                                                                                                                                                                                                                                                                  surface protease"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trop. Med.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Infectious and Tropical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INV 22-JUL-2002
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KEYWORDS,
SOURCE
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LDO495005
LOCUS
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     sig_peptide
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (11-JUL-2002) Mauricio I.L., Infectious and Tropical Diseases, London School of Hygiene and Trop. Med., Keppel StrewClE 7HT, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mauri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GP63; major surface protease; mspc
Leishmania donovani
Leishmania donovani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mauricio, I.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leishmania donovani mspC gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGC 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCAN/IQ/1981/Sukkar2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LD0495005
   /protein_id=_varoj
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GVLAWATTCQVESDGHPÄVGVINIPAANIASRYDQLVTRVVTHEMAHALGFSGTFFTE
RNAKDELMAPAAAAGYYSATMAAIFABVGYGCGTLEYLEIEDQGAGSAGSHIKM
QNITKWPAMFCNVSVDVVRCPTSRLMLGTCGTRGYSTPSESYMQVETNISLGGYSBFL
ANVRCDTMTRTYSVQVCGSMUYVNCTPGLRVETSDAARCIDGAFRFKNTAADGYYAGLC
VKGAKDFAGSDSSSSSAGDAADRAANQRWNDRMAGLATAAMVLLGMVLSLMALIVVVML
1.1.TCDWWCCYRGCIDGN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cio, I.L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
LLLTCPWWCCKFGGLPT"
14. .130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o,I.L., Stothard,J.R. and Miles,M.A. diversity in the Leishmania donovani complex
                                                                                                                                                                                                                                                                                note="constitutive major surface protease"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                       gene="mspC"
                                                                                                                                                                                                                                                                                                                                                                                                                               mol_type="genomic_DNA"
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'db_xref="taxon:5661"
                                                                                                                                                                                                                                                                                                                                                                                     gene="mspC"
                                                                                                                                                                                                                                                                                                                                                                                                       country="Iraq"
4. .1939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Leishmania donovani"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131. .1822
/gene="mspC"
/product="GP63"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="mspC"
131. .1822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2107
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VERSION
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LDO495003
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                                                                            mat_peptide
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Submitted (11-7UL-2002) Mauricio I.L., Infectious and Tropical Diseases, London School of Hygiene and Trop. Med., Keppel Stree WC1E 7HT, UNITED KINGDOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mauricio, I.L., Stothard, J.R. and Miles, M.A. Genetic diversity in the Leishmania donovani complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ495003
AJ495003.1 GI:21954457
GP63; major surface protease; mspC gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leishmania donovani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leishmania donovani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHOM/KE/1954/LRC-L53.
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VKGAKDFAGSBSSAGGBAADRAAMQRWNDRMAGLATAAWVLLGWVLSLMALUVVWL
III-TTDWWGTCVFFGIF DT"
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/gene="mspC"
/product="GP63"
                                                                 /gene="mspC"
132. .1823
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/allele="mspCLdA2"
/product="GP63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="constitutive major surface protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="mspC"
|5. .1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
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|db_xref="taxon:5661"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="mspC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         country="Kenya"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Leishmania donovani"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131. .1822
/gene="mspC"
/product="Gp63"
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gene for GP63,
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Query Match
Best Local Similarity 76.6
Matches 36; Conservative
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (11-JUL-2002) Mauricio I.L., Infectious and Tropical Diseases, London School of Hygiene and Trop. Med., Keppel Street, WC1E 7HT, UNITED KINGDOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GP63; major surface protease; mspC gene Leishmania donovani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mauricio, I.L.,
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mauricio, I.L
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="GOA:Q8MNZ3"
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/db_xref="SYTREMBL:Q8MNZ3"
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ANVRCDTATRTYSVQVRGSMDYVNCTPGLRVELSTVSSAFEEGGYITCPPYVEVCQGN
VQAAKDFAGDSDSSSSAGDAADRAAMQRWNDRMAGLATAAMVLLGMVLSLMALVVVWL
                                                                                                                                                            /gene="mspC"
/product="GP63"
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15. .1940
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/mal_type="genomic DNA"
/strain="MHOM/CN/0000/WangJiel"
/db_xref="taxon:5661"
                                                                                                                                                                                                                                                    gene="mspC"
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/db_xref="GI:21954460"
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                                61.2%;
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Score 29.4; DB Pred. No. 2.8; 0; Mismatches
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Gene for GP63,
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864 TACGACCAGCTGGTGACGCGTGTCGTCACGCACGAGATGGCGCACGC
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                               1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGC 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Original source text: Leishmania donovani (sub_species chagasi)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Three distinct RNAs for the surface protease gp63 are differentially expressed during development of Leishma chagasi promastigotes to an infectious form J. Biol. Chem. 267 (3), 1888-1895 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ramamoorthy, R., Donelson, J.E., Paetz, K.E., and Wilson, M.E.
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Leishmania donovani chagasi surface
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                                                                           Similarity
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/note="log glycoprotein 63"
2892
                                                                                                                                                                                                                                                                  QAAKDGGNAAAGRRGPRAAATALLVAALLAVAL"
                                                                                                                                                                                                                                                                                RNAQDELMAPAAAGYYSALTMAIFQDLGFYQADFSKAEVMPWGRNAGCAFLSEKCME
RNITKWAMFCNENETYMRCDTSRLSLGKCGYTRHPDLPFYWGYSTDIBSLAGISAFMA
CCPVVEPYGDGSCAQRASBAGAPKGENVFSDAARCIDGAFRPKTSHGIIKSYAACLA
NVRCDTATRTYSVQVHGGSGYANCTPGLRVELSTVSSAFEBGGYITCPPYVEVCQGNV
                                                                                                                                                                                                                                  gene="GP63"
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/sub_species="chagasi"
                                                                                                                                                                                                     gene="GP63"
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76.6%;
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                                                                           Score 29.4;
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se (log glycoprotein 63,
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                                                                         RESULT 11
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VERSION
KEYWORDS
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AUTHORS
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Best Local (
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LEIGP63B
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               LEIGP63A
L.chagasi major surface
                                                                                                                                1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGC
                                                                                                                                                                                        36;
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                                                                                                             racdaccaderregreacecereregreacedaceacearegreaced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Original source text: Leishmania donovani (sub_species chagasi)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   stationary glycoprotein 63; surface protease.
Leishmania donovani
Leishmania donovani
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ramamoorthy, R., Donelson, J.E., Paetz, K.E., Maybodi, M., and Wilson, M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEIGP63B 2966 bp mRNA linear INV 2 Leishimania donovani chagasi surface protease (stationary glycoprotein 63, GP63) mRNA, complete cds.
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M80669
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ilarity 76.6%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   /protein id="MAAA2233".1"
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/note="stationary glycoprotein 63"
2966
                                                                                                                                                                                                                                                                      'gene="GP63"
                                                                                                                                                                                                                                                                                                                                                      /gene="GP63"
120. .1925
                                                                                                                                                                                                                                                                                                                                   gene="GP63"
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/product="surface protease"
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|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _species="chaqasi"
                                                                                                                                                                              Score 29.4; DB Pred. No. 2.8; 0; Mismatches
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        3047 bp DNA linear INV 26-APR-1993 glycoprotein (gp63) gene, complete cds.
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                                   97388259
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(bases 1 to 3047)
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1246 TÁCGÁCCAGCTGGTGÁCGCGTGTCGTCÁCGCÁCGÁGÁTGGCGCÁCGC 1292
Cloning of the gp63 surface protease of Leishmania infantum. Differential post-translational modifications correlated with different infective forms
Biochim. Biophys. Acta 1361 (1), 92-102 (1997)
                                                                                         and Larraga,
Cloning of t
                                                                                                                  Gonzalez-Aseguinolaza, G., Almazan, F., Rodriguez, J.F., Marquet, A.
                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                                                                                                                               Leishmania
                                                                                                                                                                                                                                                                  Leishmania infantum
                                                                                                                                                                                                                                                                                                                 U48798
U48798.1 GI:1213329
                                                                                                                                                                                                                                                                                                                                                                             LIU48798 3047 bp DNA linear INV 15-JAN-1998
Leishmania infantum surface glycoprotein gp63 (gp63) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGC
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Draft entry and computer-readable sequence for [1] kindly provided by M.Parsons, 03-OCT-1989.
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Leishmania gp63 molecule
Arg-Gly-Asp sequence
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Leishmania donovani
Leishmania donovani
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496. .2295
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/mol_type="genomic DNA"
/sub_species="chagasi"
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le implicated in cellular adhesion lacks an
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Webb,J:R., Button,L.L. and McMaster,W.R.
Heterogeneity of the genes encoding the major surface glycoprotein
of Leishmania donovani
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Leishmania donovani
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M60048
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                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="msvdsssthrhrsvaarlvrlaaagaaviaavgtaaawahagav
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496. .220s
                                                                                                                                                                                                   source text: L.donovani DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNITKWPAMFCNENEVTWRCPTSRLŠLGKCGVTRHPDLPPYWQYFTDPSLAGISAFMD
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101. .1873
                                                                                                                                                                                   Location/Qualifiers
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Pred. No. 2.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ramamoorthy,R., Donelson,J.E., Paetz,K.E., Maybodi,M., Roberts,S.C. and Wilson,M.E.
Three distinct RNAs for the surface protease gp63 are differentially expressed during development of Leishmania donovani chagasi promastigotes to an infectious form J. Biol. Chem. 267 (3), 1888-1895 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constitutive glycoprotein 63;
Leishmania donovani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leishmania donovani chagasi surface protease glycoprotein 63, GP63) mRNA, complete cds.
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/tranelation="MSVDSSSTHRHRSVAARLVRLAAAGAAVIAAVGTAAAWAHAGAV
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WGALRIAVSTEDLTDPAYHCARVAGVRVNNHAGAIATCTAGFESUTDFWMYVASVPSEE
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NITKWPAMFCNENEVTMRCFTSRLMVGTCGIRGYSTPFSLTWQYFTWASLGLAAFDDV
CPFVIGYSDGSCNQDASLAAGFFSAFNVFSDAARCIDGAFRFKNTAAMGYYAGLCAN
VRCDTATRTSSVQVRGSMDYNCTPGLKVELSTVSSAFEEGGYITCPPYVEVQANVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source text: Leishmania donovani (sub_species chagasi)
                                                                                                                                                                                                                              /protein_id="AAA29237.1"
/db_xref="GI:159327"
/transla+;-- ""
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VRQVQDKWKVTGMGNBICGHFKVPPAHITDGLSNTDEWMYVASYDSBGDVLAWATTCQ
VFSDGHPAVGVINIPAARIASRYQDLVTRVVTHEMAHALGFSVVPFRDAFILESISUV
RHKDFDVPVINSTAVAKAREQYGCGTLEYLEMEDQGGAGSAGSHIKMRNAQDELMAP
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CNENEVTMRCHTGRLSLGVCGLSSSDIPLPPYWQYFTDPLLAGISAFMDYCPVVVPFG
DGSCAQRASEAGAPFKGFNVFSDAARCIDGAFRPKTTETVTNSYAGLCANVRCDTATR
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                                                                                                                                                                                                                                                                                                 /codon_start=1
/product="surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sub_species="chagasi"
/db_xref="taxon:5661"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (11-JUL-2002) Mauricio I.L., Infectious and Tropical
Diseases, London School of Hygiene and Trop. Med., Keppel Street,
WC1E 7HT, UNITED KINGDOM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ495010
AJ495010.1 GI:21954471
GP63; major surface protease; mspC gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mauricio,I.L., Stothard,J.R. and Miles,M.A. Genetic diversity in the Leishmania donovani complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leishmania turanica
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MRHO/SU/1983/MARZ-051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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15. .131
/gene="mspC"
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/allele="mspCLtuAl"
/product="GP63"
                                                                                                                                                                                                                                                                                                                                                                                                    /gene="mspC"
/note="constitutive major surface protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Leishmania turanica"
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/strain="MRHO/SU/1983/MARZ-051"
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/note="constitutive glycoprotein 63"
2621
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.

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## ALIGNMENTS

Leishmania major PT3 epitope DNA sequence SEQ ID NO:9.

AAC64621;

26-FEB-2001

(first entry)

AAC64621 standard; DNA; 48

RESULT 1
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XX V WPI; 2000-672631/65. P-PSDB; AAB36345. Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen; ds. White AP, Doran JL, 05-APR-1999; 05-APR-2000; 2000WO-CA000356. 12-OCT-2000. WO200060102-A2. Leishmania major. (UYVI-) UNIV VICTORIA. 99US-0127888P Collison SK, Kay WW

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 135; 139pp; English.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmontella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombinantion of a recombinant gene homologous species; (3) directing recombinantion of a recombinant gene back into the chromosome of the homologous species, replacing the native

AgfA

for

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or the expression of recombinant MagfA protein which is useful for the expression of recombinant MagfA protein which is useful for the expression of recombinant MagfA protein which is useful for coliting an immune response in an animal. In a fimbrial presentation communogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong communogens, which may be important for directing an immune response consequence in the inserted epitope, and hybrid fimbriae are usually strong consequence which may be important for an efficient live against the inserted epitope, and hybrid fimbriae are usually strong consequence the present of the present sequence is given in the exemplification of the present invention
      The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: assembly system of strains of Salmonella, Escheriohia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria submitts, respectively; (2)
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mune response; immunogen; PCR primer; ss.
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Pred. No. 8.4.
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thes 0;
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RESULT 3
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AC 4610
AC 64610
AC 6
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Best Local (
                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                               (UYVI-) UNIV VICTORIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2000
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26-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000WO-CA000356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant agfA::PT3a generating PCR primer 17-C.
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ilarity 100.0%;
Conservative c
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA;
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                                                                                                                                                                                                                                                                                                                                           SK,
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Pred. No. 9.5
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The present invention describes a recombinant agfA gene (I) segment of the gene has been replaced by a segment of a fore sequence which encodes a foreign epitope or antigen. Also de (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation assembly system of strains of Salmonella, Escherichia coli e

(I) where a foreign DNA

are:

Example 2; Page 61; 139pp; English.

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protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for cellciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbria protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and cinexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention. (Updated on 06-AUG-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Escherichia coli.
                                                                                                                                                                           WPI; 2000-672631/65.
P-PSDB; AAB36352.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccine; immune response; immunogen; ds
                                                                                                                                                                                                                                         White AP,
                                                                                                                                                                                                                                                                                    (UYVI-) UNIV VICTORIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA. CagA and AgfA-homologue fimbrin subunits, respectively; (2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TATGATCAGCTGGTTACCCGTGTTACCCCATGAAATGGCACATGCA
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                                                                                                                                                                                                                                         Doran JL,
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100.0%; S
tive 0;
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                                                                                                                                                                                                                                       Kay WW;
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Disclosure;

Page 137; 139pp; English

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

The present invention describes a recombinant agfA gene (I) where

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
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                                                                                                                                                                                       WPI; 2000-672631/65.
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                                                                                                                                                         P-PSDB;
                                                                                                                                                                                                                                                   White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                   (UYVI-) UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella;
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Similarity 100.0%;
48; Conservative C
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mune response; immunogen; ds.
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                                                                                                                                                                                                                                                   Collison
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Pred. No. 1.5e-09;
; Mismatches 0;
                                                                                                                                                                                                                                                   SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                   Kay WW
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Disclosure; Page 135;

139pp; English

 $x_{3}$ 

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA (1) use of thin aggregative fimbriae (SEFI/T/RAF) nucleation described are: assembly system of strains of Salmonella, Bscherichia coli and AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) after recombinant of a recombinant gene into the chromosome of the homologue of the chromosome of the chromosome of the homologue of the chromosome of the ch

homologous species; (3) directing recombination of a recombinant

CC back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, cc comprising separating an amino acid polymer comprising a recombinant AgfA acid sequence or sequences grown on a Salmonella, E. coli or coling the expression of recombinant AgfA cc Enterobacteriaceae host cell, from the host cell and introducing the cuseful for the enhand in colinction with a carrier or diluent. (1) is cc lost the grown of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for cc system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live creaminogens, which may be important for directing an immune response cc inexpensive to purify in large amount. The present sequence is given in the exercited epitope, and hybrid fimbriae are usually strong cc inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention

Sequence 456 BP; 121 A; 112 C; 118 G; 105 T; 0 U; 0 Other;

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AAC64626
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence
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Best Local 9
                                                                                                                                                                                          White AP,
                                                                                                     P-PSDB; AAB36350
                                                                                                                                 WPI; 2000-672631/65.
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Escherichia coli.
Synthetic.
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                                                                                                                                                                                    Doran JL,
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                                                                                                                                                                             Collison
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1.5e-09;
les 0;
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RESULT 7
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XX VACC
XX Salm
XX VACC
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Best Local :
WPI; 2000-672631/65
                                                          White AP,
                                                                                                                        (-IVYU)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agfa::PT3#9 DNA sequence SEQ ID NO:27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(I) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 137; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 ratigaticadorieditacoccióriditatoccaridadaticación 243
                                                                                                               UNIV VICTORIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
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                                                    Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                          Collison SK,
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Pred. No. 1.5e-09;
0; Mismatches 0;
                                          Kay WW;
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P-PSDB;

AAB36354

are:

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RESULT 8
AAC64629
ID AAC6
XX AAC6
XX AAC6
XX AAC6
XX AGFA
XX AGFA
XX AGFA
XX AGFA
XX VACC
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XX XX YX YX
PA (UYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of a recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC eliciting an immune response in an animal. (I) is CC useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for segment or presented in high numbers (up to S0),000 copies/cell), the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live combinant and the carrier fimbrial presentation of immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                  05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                 WO200060102-A2
                                                                                                                                                                                                                                                                Salmonella enteritidis
                                                                                                                                                                                                                                                                                                      Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is the exemplification of the present invention
                     (UYVI-) UNIV VICTORIA
                                                           05-APR-1999;
                                                                                                                                            12-OCT-2000
                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                    AgfA::PT3#8 DNA sequence SEQ ID NO:25
                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC64629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC64629 standard; DNA; 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mmunogens, which may be important for directing an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity
48; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 115 A; 116 C; 118 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                             (first entry
                                                           99US-0127888₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Pred. No. 1.5e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 456;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                           Salmonella enteritidis. Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          assembly system of strains of Salmonella, Bscherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
    05-APR-1999;
                                                                                                                                                                                                                                                       Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                     26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                AAC64625 standard; DNA; 456 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 456 BP; 114 A; 108 C; 123 G; 111 T; 0 U; 0 Other;
                                      05-APR-2000; 2000WO-CA000356
                                                                               12-OCT-2000
                                                                                                                                                                                                                                     vaccine; immune response; immunogen;
                                                                                                                                                                                                                                                                                              AgfA::PT3#4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described a continuous of thin aggregative fimbriae (SEF17/TAF) nucleation depended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA
                                                                                                                    WO200060102-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            White AP, Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATGATCAGCTGGTTACCCGTGTTACCCATGAAATGGCACATGCA 219
                                                                                                                                                                                                                                                                                            DNA sequence SEQ ID NO:17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                     (first entry)
    99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 456;
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RESULT 10
AAC64631
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                                                                                                                                                                                                                                                                                                                                                                                  CC Agfa, CsgA and Agfa-homologue fighbrin subunits, respectively; (2)
CC directing recombination of a recombinant gene into the chromosome of the CC homologous species; (3) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombinative comprising separating and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant Agfa acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the CC eliciting an immune response in an animal in conjunction with a carrier or diluent. (1) is CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to CC immunogenicity and adhesion properties relevant for an efficient live carrier fimbrial subunit protein possesses both the carrier fimbrial subunit proteins are usually strong CC against the inserted epitope, and hybrid fimbriae are easy and the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                      Matches
                             12-OCT-2000
                                                                                 Salmonella enteritidis
Escherichia coli.
                                                                                                                    Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                  WO200060102-A2
                                                                          Synthetic
                                                                                                                                                         AgfA::PT3#10
                                                                                                                                                                                26-FEB-2001
                                                                                                                                                                                                                       AAC64631 standard; DNA; 456 BP
                                                                                                                                                                                                                                                                                                                                                                      Sequence 456 BP; 120 A; 110 C; 122 G; 104 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: a seembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 136; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                                                                                                         1 TATGATCAGCTGGTTACCCGTGTTGTTACCCGATGAAATGGCACATGCA 48
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DB; AAB36349.
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                                                                                                                                                  DNA sequence SEQ ID NO:29.
                                                                                                                                                                                                                                                                                                                                 100.0%; ilarity 100.0%; Conservative 0;
                                                                                                                                                                            (first entry)
                                                                                                                   response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collison
                                                                                                                  immunogen;
                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                          Score 48; DB 3; I
Pred. No. 1.5e-09;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                               Length 456;
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assembly system of strains of Salmontale, Becherichia coli and CC AgfA, CsgA and AgfA, homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologues species; (3) directing recombinant gene into the chromosome of the back into the chromosome of the homologues species; (3) directing recombination of a recombination of a recombination of a recombination of a recombination of the chromosome of the copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant of gene comprising a replacement segment or sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the cuseful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for colisting an immune response in an animal. In a fimbrial presentation constitution which is useful for compinative and adhesion properties relevant for an efficient live carrier fimbrial subunit protein possesses both the carrier fimbrial subunit proteins are usually strong companist the inserted epitope, and hybrid fimbria are usually strong constituted in high constitution of the present of the present sequence is given in the exemplification of the present invention.
                                                                                                    Query Match
                                                                                                                               Sequence 456 BP; 113 A; 110 C; 124 G; 109 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a recombinant agfA gene (I) segment of the gene has been replaced by a segment of a fore sequence which encodes a foreign epitope or antigen. Also de assembly system of strains of Salmonella, Escherichia coll a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-672631/65.
P-PSDB; AAB36355.
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               100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0127888P
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Score 48; DB 3;
Pred. No. 1.5e-09;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SK,
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RESULT 11
AAC64623
      Salmonella enteritidis.
Escherichia coli.
                                       Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen; ds.
Synthetic
                                                                                                     AgfA::PT3#2
                                                                                                                                    26-FEB-2001
                                                                                                                                                                  AAC64623;
                                                                                                                                                                                        AAC64623 standard; DNA; 456
                                                                                           DNA sequence SEQ ID NO:13.
                                                                                                                              (first entry)
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Similarity

48;

0,

Length 456; Indels

0,

Gaps

0

307 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 48

354

WO200060102-A2

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RESULT 12
AAC64627
ID AAC64
XX
AC AAC64
XX
DT 26-FE
XX
DE AgfA:
XX
Salmo
KW Vacci
XX
Salmo
OS Salmo
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Best Local Similarity
Salmonella enteritidis
Escherichia coli.
                                                                                                                       Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 456
                                                                                            vaccine; immune response;
                                                                                                                                                                                         AgfA::PT3#6
                                                                                                                                                                                                                                                        26-FEB-2001
                                                                                                                                                                                                                                                                                                                       AAC64627;
                                                                                                                                                                                                                                                                                                                                                                                   AAC64627 standard; DNA; 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA segment of the gene has been replaced by a segment of the gene has been replaced by a segment of the described segmence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended to the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segment of the segme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATGATCAGCTGGTTACCCGTGTTACCCCATGAAATGGCACATGCA 399
                                                                                                                                                                                         DNA sequence SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                  (first entry)
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                                                                                            immunogen;
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Pred. No. 1.5e-09;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 456;
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Also described
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement esgment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for . CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live CC vaccine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response CC against the inserted epitope, and hybrid fimbriae are usually strong CC inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen; ds.
                                                             AgfA::PT3#3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                    26-FEB-2001
                                                                                                                                                                                     AAC64624 standard; DNA; 456 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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P-PSDB; AAB36351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 137; 139pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                         262
                                                                                                                                                                                                                                                                                                                                                                        48;
                                                                                                                                                                                                                                                                                                                         1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 48
                                                                                                                                                                                                                                                                                         TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     456 BP; 112 A; 113 C; 125 G; 106 T; 0 U; 0 Other;
                                                           DNA sequence SEQ ID NO:15.
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                    (first entry)
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Pred. No. 1.5e-09;
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Salmonella enteritidis. Escherichia coli. Synthetic.

WO200060102-A2

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RESULT 14
AAC64616
ID AAC64
XX
AC AAC64
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DT 06-AU
DT 26-FE
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Best Local
                      06-AUG-2003
26-FEB-2001
                                                                                                                 AAC64616;
                                                                                                                                                        AAC64616 standard; DNA; 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 456 BP; 118 A; 112 C; 115 G; 111 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
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(first entry)
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100.0%; Pred. No. 1.
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RESULT 15

AAC64606;

AAC64606 standard; DNA; 78

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1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 48

TATGATCAGCTCGTTACACGTGTTGTTACACATGAAATGGCACATGCA

48

Matches Query Match Best Local

45; Similarity

Conservative

0,

Score 43.2; DB 3; Pred. No. 7.6e-08; 0; Mismatches 3;

Length Indels

0;

0

90.0%;

Sequence 48

BP; 14 A; 10 C; 10

G; 14 T; 0 U; 0 Other;

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CC Segment of the gene has been replaced by a segment of a foreign DNA CC segment of the gene has been replaced by a segment of a foreign DNA CC (1) use of thin aggregative fimbriae (SER17/TAF) nucleation described are: CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA-homologue fimbriae isomprising recombinant CC directing recombination of a recombinant gene into the chromosome of the brooklogues species, (3) directing recombination of a recombination of a recombinant gene into the chromosome of the copy of that gene, and (4) eliciting an immune response in an animal. CC acid sequence or sequences grown on a Salmonella, Escoli or polymer into the animal in conjunction with a carrier or diluent. (1) is cliciting an immune response in an animal. (2) cuseful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for the expression properties releant which is useful for the chromosome of recombinant AgfA protein which is useful for comples/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong capainst the inserted epitope, and hybrid fimbria are usually strong capainst the inserted epitope, and hybrid fimbria are usually strong capainst the inserted epitope, and hybrid fimbriae are easy and carrier to S field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-672631/65.
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                                                                              Matches
                                                                                                Query Match
Best Local
                                                                                                                                                                                            system the heterologous antigens are presented in high numbers (up to $90,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention. (Updated on 06-AUG-2003 correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                       Sequence 78 BP; 16 A; 16 C;
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<u> </u>	Query Match Best Local ( Matches 3	PF AI	STREET: 9410 Key West CITY: Rockville STATE: Maryland COUNTRY: USA ZIP: 20850 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, COMPUTER: HP Vectra 48 OPERATING SYSTEM: MSDC SOFTWARE: ASCII Text CURRENT APPLICATION NUMBER: US FILING DATE:	SSULT 1 3-08-961-527-78/c Sequence 78, Applicat Patent No. 6420135 GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADD ADDRESSEE: Huma	4444443333333322 4444443335 543276533322
6 TQ	C 0,	CLASSIFICATION: 424 APPLICATION NUMBER: FILING DATE: FILING DATE: TORNEY/AGENT INFORMAT NAME: Brookes, A. An REGISTRATION NUMBER: REFERENCE/DOCKET	STREET: 941 STREET: 941 STATE: Mary STATE: Mary COUNTRY: US ZIP: 20850 AMPUTER READA MEDIUM TYPE: COMPUTER: H OPERATING SY SOFTWARE: A PELICATION APPLICATION APPL	78, App lo. 64201 INFORMA INFORMA CANT: C CONT: C S OF INVE S PONDENC SPONDENC	OOOOOOOOOOOOOOOO
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ATTORNATION:
ATTORNAY AGENT INFORMATION:
NAME: BTOOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
""""T.FPHONE: (301) 309-8504
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APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of forestry plant devel
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                                                                                                              SEQUENCE CHARACTERISTICS:
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APPLICANT: Charles Kunso
TITLE OF INVENTION: Str
NUMBER OF SEQUENCES; 39:
CORRESPONDENCE ADDRESS:
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Patent No. 6451604
                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quence 166, Application US/08961527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/325,932A
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Pinus radiata
                                                                 LENGTH: 5406 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                        COPOLOGY:
                                                                                                                                                                                                                                                                                                                                         COMPUTER: HP Vect
OPERATING SYSTEM:
DECLI 7
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                                                        linear
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NENTION: Streptococcus pneumoniae Polynucleotides and Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                      ASCII Text
                                                                                                                                                                                                                                                                                                                                                               E: Diskette, 3.50 inch, 1.4Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Genome Sciences,
                                                                double
          45.8%;
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      Score 22;
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      DB
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Length 5406;
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                                                                                                                   US-09-252-991A-11586
                                    Query Match
Best Local Similarity 71...
28; Conservative
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; Sequence 11586, Application US/09252991A
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                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 11586
LENGTH: 648
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GENERAL INFORMATION:
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                                                                                                                                                                                                            APPLICANT: MAIG J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTMARE: FastSEQ for Windows vers
SEQ ID NO 3
LENGTH: 7754
TYPE: DNA
ORGANISM: Lactobacillus rhamnosus
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US-09-634-238-3/c
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Best Local
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                                                                                                                   TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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APPLICANT: Reid, Julian R.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polymucleotides,
TITLE OF INVENTION: them and methods
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4 GATCAGCTGGTTACCCCGTGTTGTTACCCCATGAAATGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
29; Conserv
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Bloksberg, Leonard, N.
Lubbers, Mark W.
Dekker, James
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                                                                44.6%;
71.8%;
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70.7%;
                                              0; Mismatches
                                                             Score 21.4;
Pred. No. 14
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Pred. No. 20;
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0; Mismatches
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                                          Indels
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RESULT 8
US-09-453-702B-36/c
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11794
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US-09-252-991A-11645/c
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                Sequence 36, Application Patent No. 6365723
GENERAL INFORMATION:
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
SEQ ID NO 11794
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: Marc J. Rubenfield et al.
ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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               APPLICANT: Blattner, Frederick R.
                                                                                                                                                                  681 GATCGCCTCGATCCTGGTGTTTTCCCATGCACTGGAA 719
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                                                                        Application US/09453702B
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Burland,
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1998-07-27
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71.8%;
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Pred. No. 1
                                                                                                                                                                                                                                                        Score 21.4;
Pred. No. 16;
                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Thomps
APPLICANT: Yaver,
                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           372
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Welch, Rod
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Best Local Similarity 66.0 Matches 31; Conservative
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TITLE OF INVENTION: ASP
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (608) 251-9
INFORMATION FOR SEQ ID NO: 36:
             COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                           STREET: 405 Lexi
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORD PERFECT 8.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 960296.95017 TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ATGATCAGCTGGTTACCCGTGTTACCCATGAAATGGCACATGCA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGATCAATTGGACCAACTTTTGGTTACCCGTGAAATTCAAGATGAA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08317401E
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                          405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                                                                   Thompson,
                                                                                                                                                                                                                                                                 No. 59225610 No. 5922561disk of No.
                                                                                                                                                                                                                                                                                                                                                                              Debbie Sue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.6%;
                                                                                                                                                                                                                                                                                                                                  GENES ENCODING SIGNAL RECOGNITION PARTICLE OF ASPERGILLUS NIGER
                                                                                                                                                                                                                                                                                                                                                                                                     Sheryl Ann
US/08/317,401E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 21.4;
Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
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                                                                                                                                                                                                                                                                   5922561th America, Inc
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TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

STRANDEDNESS: ENGTH:

0,

TELECOMMUNICATION INFORMATION: TELEPHONE: 212 867 0123

FILING DATE: 03-October-ATTORNEY/AGENT INFORMATION:

03-October-1994

EGISTRATION NUMBER:

James J. IR: 38,711

DOCKET NUMBER:

4248.000-US

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US-08-317-401E-1
                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2877 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-08-317-401E-1
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                                             TOPOLOGY: line
MOLECULE TYPE: D
ORIGINAL SOURCE:
ORGANISM: Aspe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-317-401E-3
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
APPLICATION DATA:
APPLICATION MUMBER: US/08/317,401E
ATTORNEY/AGENT INFORMATION:

ATTORNEY/AGENT INFORMATION:
                                       FEATURE
                                              TYPE: "STRANDEDNESS: "COPOLOGY: linear "OPE: DNA (genomic)
                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 quence 1, Applatent No. 5922561
TENERAL INFORMATION:
                                                                                                                                                                                            NAME: Harrington, James J.
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 42
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
ORGANISM: Asp
                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                         DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 ĠATGAĠĊŢĠĠŢŢŢĊĊĊŢĠĠŢŢĠAŢĊĊĊĀŢĠ 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 GATCAGCTGGTTACCCCGTGTTGTTACCCATG 34
                                                                                                                                                                                                                                                                                                                                                                  New York
Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08317401E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1: 2166 base pairs nucleic acid DEDNESS: double
join (126..203, 253..1776)
                                       Aspergillus niger
                                                                                                                                                                                                                                                                                                                                                                                     E: No. 59225610 No. 5922561disk of No. 5922561th America,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yaver, Debbie Sue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thompson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aspergillus niger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sheryl Ann
                                                                                                                                                                                            4248.000-US
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US-09-543-681A-3167

Sequence 3167, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION: DIAGNOSTICS AND THERAPBUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION UNMBER: US/09/543,681A

TITLE OF INVENTION: DIAGNOSTICS AND THERAPBUTICS

CURRENT APPLICATION UNMBER: US/09/543,681A
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                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.8
Conservative
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US-08-961-527-132/c
/ Sequence 132, Application US/08961527
                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 132:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                맑
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 9541 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 941.
STREET: P41.
CITY: Rockville
CTATE: Maryland
TTSA
                                                                                                                                                                                                                                                                                                                                             COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
                                                                                                                                                                                                              6099 CAGTTGATTAGCCGTGGGGCTATCAATAAAATGGGAAAT 6061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                    7 CAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              418 GATGAGCTGGTTTCCCCTGGTTGATCCCCATG 448
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                                                                                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                               (301)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                    44.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.6%;
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                                                                                                                                                                                                                                                                 i Score 21.4; DE
i Pred. No. 31;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PB340P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 21.4;
Pred. No. 22;
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                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                  11;
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                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                      Length 9541;
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                                                                                                                                                                                                                                                           Gaps
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; PRIOR FILING DATE: 1999-04-09; NUMBER OF SEQ ID NOS: 8344; SEQ ID NO 3167; LENGTH: 597; TYPE: DNA; ORGANISM: Proteus mirabilis US-09-543-681A-3167
                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-879-337-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: variation
; LOCATION: (1)...(2975)
; OTHER INFORMATION: N can be any nucleotide.
US-08-879-337-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-08-879-337-10
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Best Local Similarity 73.0
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/088793378 Patent No. 6639130
                                                                                                                      SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/088793378 Patent No. 6639130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                       TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF FILE REFERENCE: 00786/338001
CURRENT APPLICATION NUMBER: US/08/879,337B
CURRENT FILING DATE: 1997-06-20
EARLIER APPLICATION NUMBER: 60/022,086
EARLIER FILING DATE: 1996-06-21
RUMBER OF SEO ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jang, Jyan-Chyun
APPLICANT: Sheen, Jen
TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
FILE REFERENCE: 00786/338001
CURRENT APPLICATION NUMBER: US/08/879,337B
CURRENT FILING DATE: 1997-06-20
EARLIER APPLICATION NUMBER: 60/022,086
EARLIER FILING DATE: 1996-06-21.
                                                                                                                                                                                                                                                                                                 APPLICANT: Jang, Jyan-Chyun APPLICANT: Sheen, Jen
                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
FEATURE:
NAME/KEY: variation
LOCATION: (1)...(6587)
                                                         LENGTH: 6587
TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             310 TTTTATCAGATGGCTCTCAACTTCGTTACCGATGCAATGGTATAT 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 GGTTGGAACTGTTGCTACACTTGAAATGACACAAGCA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 GGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.8%; ilarity 66.7%; Conservative
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73.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Pred. No. 21;
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Search completed: March 16, 2004, 04:37:03 Job time : 7.01734 secs

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RESULT 15
US-09-596-002-39
; Sequence 39, Application US/09596002
; Patent No. 6632636
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                                                                                                                      US-09-596-002-39
                                                                                                                                                                                                                                          SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 30; Conserv
                                                          Matches
                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
                                                                                                                                 ORGANISM: M. catarrhalis
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte template ID
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                           LENGTH: 100848
TYPE: DNA
                                                          Local Similarity 66.
73642 GATGTGCTATTGACACATACATTTATCCATCAAATGGCACAAGAA 73686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3664 TTTTATCAGATGGCTCTCAACTTCGTTACCGATGCAATGGTATAT 3708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TATGATCAGCTGGTTACCCGTGTTACCCCATGAAATGGCACAT 45
                             GATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 48
                                                                                                                                                                                                                                                                                                                                                                             Patterson,
Berg, Kim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                 PM-0008-4 US
                                                                                                                                                                                                                                                                                                                                                                                                             Lagace,
                                                                        43.8%;
                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.8%;
                                                                                                                                                                                                                                                                                                                                                                                             Chandra
                                                                                                                                                                                                                                                                                                                                                                                                             Robert,
                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                        Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21; DB
Pred. No. 40;
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                  No.
                                                                        86;
                                                                                                                                                  6632636
                                                                                      4; Length 100848;
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                                                           15;
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                                                           Indels
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                                                        Gaps
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Database
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                              Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

15: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

16: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptodata/2/pubpna/US10B_PUB.seq:*

19: /cgn2_6/ptodata/2/pubpna/US10B_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US10B_PUB.seq:*
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48
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Copyright (c) 1993 - 2004 Compugen Ltd.
SUMMARIES
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14	c 10	0 0 9 8 7 6	00	Result No.
22. 22. 24.	22.6	2222	27.8 24.6 24.6 24 23.2	Score
46.7	47.9 47.1	47.9 47.9 47.9 47.9	57.9 51.3 51.3 50.0 48.3	Query Match
1925 1925 912	301120 1767 3984	420 420 436 116302	2547 1 2547 1 3636 1 409 1 720 1	Query  Query  Match Length DB
9 14	15 21.	15 10 10	12212	
US-10-219-220-217 US-10-219-220-217 US-09-738-626-2582	US-10-398-221-2058 US-10-282-122A-25322 US-10-369-493-42554	US-10-398-221-318 US-10-398-221-2306 US-09-918-995-26274 US-10-398-221-10	US-10-282-122A-36154 US-10-282-122A-37710 US-10-158-844-78 US-10-424-599-119735 US-10-425-114-6010	ID
Sequence 15, Appl Sequence 217, App Sequence 2582, Ap	Sequence 2058, Ap Sequence 25322, A Sequence 42554, A	Sequence 318, App Sequence 2306, Ap Sequence 26274, A Sequence 10, Appl	Sequence 36154, A Sequence 37710, A Sequence 78, Appl Sequence 119735, Sequence 6010, Ap	Description

C 44	4.	42	c 41	c 40	39	38	c 37	36	35		c 33		31	30	29	28	27		c 25									
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US-09-769-744A-119 US-10-114-170-36	US-10-282-122A-30293			US-10-067-514-1	C		US-10-425-114-21821	US-10-627-476-367	US-09-738-626-1352	US-09-917-800A-1050	US-10-108-605-356	US-10-264-213-3	US-10-425-114-34623	US-10-425-114-32979	US-10-425-114-31422	US-10-425-114-36154	US-10-424-599-56999	US-10-158-844-166	US-09-822-830A-241	US-09-864-761-7925	US-10-226-956-320	US-09-864-761-24629	US-09-738-626-1	US-10-227-195A-2	US-10-227-195A-1	US-10-369-493-34295	US-10-369-493-44598	US-10-369-493-32121
Sequence 119, App Sequence 36, Appl		Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 13682, A	Sequence 578, App	Sequence 21821, A	Seguence 367, App	Sequence 1352, Ap	1050	Sequence 356, App				Sequence 31422, A	3615	LO.		Sequence 241, App	Sequence 7925, Ap	Sequence 320, App	Sequence 24629, A	Sequence 1, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 34295, A	Sequence 44598, A	Sequence 32121, A

## ALIGNMENTS

RESULT 1
US-10-282-122A-36154
US-10-282-122A-36154
Sequence 36154, Application US/10282122A
PUBLICATION:
PUBLICANT: Wang, Liangsu
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Mang, Liangsu
APPLICANT: Mang, Liangsu
APPLICANT: Mang, Liangsu
APPLICANT: Zyakind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Yanamoto, Robert
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APPLICANT: NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/291,078
PRIOR APPLICATION NUMBER: 60/297,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,576
PRIOR APPLICATION NUMBER: 60/242,576
PRIOR PRIOR APPLICATION NUMBER: 60/242,576
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PRIOR APPLICATION NUMBER: 60/242,576
PRIOR PRIOR APPLICATION NUMBER: 60/242,576
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/253,625
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PRIOR APPLICATION NUMBER: 60/253,625
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBE

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; ORGANISM: Streptococcus pneumoniae US-10-282-122A-37710
   Query Match
Best Local Similarity
                                                                                                                  SEQ ID NO 37710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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; ORGANISM: Streptococcus mutans
US-10-282-122A-36154
                                                                                                                       Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                          PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 37710, Application US/10282122A Publication No. US20040029129A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patcentin version 3.1
SEQ ID NO 36154
                                                                                                                                                                                      APPLICATION NUMBER: 60/267,636
FILING DATE: 2001-02-09
APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                         FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/230,347
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                    2547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zamudio, Caric
Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trawick,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haselbeck, Robert
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     51.3%;
76.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.9%;
82.1%;
Score 24.6;
Pred. No. 6;
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Pred. No. 0.27
0; Mismatches
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                                                                                                                                               See File Wrapper or PALM
           DB 12;
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          Length 2547;
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US-10-424-599-119735/c

; Sequence 119735, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION;
; APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Plants and Uses Thereof
; FILE REFERENCE: 38-21(5323)B
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                     RESULT 4
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Matches
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US-10-158-844-78/c
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB:
INFORMATION FOR SEQ ID NO: 78:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                    2806 TCAACAAGTTGCCCTTGTTGTGGCCCATGAATTGGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/029,960 FILING DATE: 1996-10-31 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude Pentium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                             6 TCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kunsch et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 849 TCAACAAGTTGCCCTTGTTGTGGCCCCATGAATTGGCTCA 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/158,844
FILING DATE: 03-Jun-2002
CLASSIFICATION: «Unknown»
IOR APPLICATION DATA:
APPLICATION NUMBER: US 08/961,527
FILING DATE: 1997-10-30
                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3636 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 TCAGCTGGTTACCCGTGTTGTTACCCGATGAAATGGCACA 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/10158844
No. US20040029118A1
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                                                                                                                                                                                                                                                                                                                                     Score 24.6; DB Pred. No. 6.6; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٥,
                                                              Molecules and Other Molecules Associated With Thereof for Plant Improvement
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                                                                                                                                                                                                                                                                                                                                                                                                                        78:
                                                                                                                                                                                                                                                                                                                                                                    DB 12;
                                                                                                                                                                                                                                                                                                                                     9
                                                         Plant Improvement
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; TYPE: DNA
; ORGANISM: Listeria innocua
US-10-398-221-318
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; OTHER INFORMATION: Clone ID: 700550972_FLI
US-10-425-114-6010
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US-10-425-114-6010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 6010
LENCTH: 720
TYPE: DNA
ORGANISM: Zea maya
                                                                              SEQ ID NO 318
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Best Local S
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LENGTH: 409
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Best Local Similarity
                                                                                          APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: Patentin version 3.0
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CURRENT FILING DATE: 2003-04-28
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APPLICANT: Zhou, Yihua
                                                         LENGTH: 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 70.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 ATGITCAGCIGGTICCCGATCTTTTCCCCATTGAGAAAGCCCAT 328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ATGATCAGCTGGTTACCCGTGTTACCCCATGAAATGGCACAT 45
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Screen, Steven E
Tabaska, Jack E
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Pred. No. 16;
0; Mismatches
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Pred. No. 6.2;
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, NAME/KEY: misc_feature

; LOCATION: (1)...(436)

; OTHER INFORMATION: n = A,T,C or G

US-09-918-995-26274
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; LENGTH: 420
; TYPE: DNA
; ORCANISM: Listeria innocua
US-10-398-221-2306
                                                                                                                                                                                                                                                                                                    APPLICANT: Hyseq, inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OB:
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
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US-10-398-221-2306
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Publication No. US20030073623A1
GENERAL INFORMATION:
                                                           Matches
                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                    SEQ ID NO 26274
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Listeria innocua, genome FILE REFERENCE: 344 702 - US CURRENT APPLICATION NUMBER: US/10/398,221 CURRENT FILING DATE: 2003-03-27 PRIOR APPLICATION NUMBER: PCT/FR 01/03 061 PRIOR PILING DATE: 2001-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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SOFTWARE: PatentIn version 3.0
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APPLICANT: GLASER, Philippe
                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                    ENGTH: 436
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2 ATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 48
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                                                           Conservative
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68.1%;
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Pred. No. 16;
0; Mismatches 15; Indels
                                                       Score 23; DB 10; Length 436; Pred. No. 16; O; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
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.0-398-221-10/c

347 ACGATCACCTGGTTATCTGGGTGGTTGACAGTGAAGTAGCCCACACA 301

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US-10-282-122A-25322
                           RESULT 11
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Best Local Similarity
Matches 32; Conserva
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, ORGANISM: Listeria innocua
US-10-398-221-2058
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Best Local Similarity
Matches 32; Conserva
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: LOCATION: (1). Tend)
: OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
US-10-398-221-10
                                                                                                                                                                                                                                                                               SEQ ID NO 2058
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
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Publication No. US20040018514A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILB REFERENCE: 344 702 - US
                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
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                                            1249014 TCTGATTATCAGGTTAAGTATGTAGTTGCTCATGAACTAGGGCATGC 1248968
                                                                                                                                                                                                                                                        ENGTH: 3011208
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Publication No. US20040018514A1
GENERAL INFORMATION:
APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
MTTT COT TATTEMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Listeria innocua, genome and applications CIURRENT APPLICATION NUMBER: US/10/398,221 PRIOR APPLICATION NUMBER: US/10/398,221 PRIOR APPLICATION NUMBER: PCT/FR 01/03 061 PRIOR PILING DATE: 2003-03-27 PRIOR PILING DATE: 2001-0-04 PRIOR FILING DATE: 2001-0-04 PRIOR FILING DATE: 2001-10-04                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 4025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                        1. TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGC 47
                                                                                                                                                                                                                                                                                  PatentIn version 3.0
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                                                                                                                     47.9%; Score 23; DB 68.1%; Pred. No. 2.1e tive 0; Mismatches
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68.1%;
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Pred. No. 1.7e+02;
0; Mismatches 15
                                                                                                                                       le+02;
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                                                                                                                                                Length 3011208;
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 25322
LENGTH: 1767
TYPE: DNA
ORGANISM: Legionella pneumophila
US-10-282-122A-25322
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US-10-369-493-42554
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                                                                                         TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 47.1%;
Best Local Similarity 68.9%;
Matches 31; Conservative
                                                                  CURRENT APPLICATION NUMBER: US/10/369,493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/267,636
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
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PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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PRIOR FILING DATE: 2000-03-21
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CURRENT FILING DATE: 2003-02-20
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APPLICATION NUMBER: US 60/360,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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FILING DATE: 2000-11-27
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Malone, Cheryl
Haselbeck, Robert
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Yamamoto, Robert
Forsyth, R.
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Pred. No. 37;
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                                                                                                                                        IN PLANTS FOR PRODUCTION OF
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; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 42554
; LENGTH: 3984
; TYPE: DNA
; ORGANISM: Anabaena PCC7120
US-10-369-493-42554
                                                                         ; LENGTH: 1925
; TYPE: DNA
; ORGANISM: Pinus radiata
US-10-219-220-217
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US-10-219-220-217
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US-10-219-220-15
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                                                                                                                                                 PRIOR APPLICATION NUMBER: U.S. NO. US20030082724A1 09/325,932 PRIOR FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 290 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 217
                                                                                                                                                                                                                                                                                                                                                                          Sequence 217, Applic Publication No. US20 GENERAL INFORMATION:
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Best Local Similarity 75.7
Matches 28; Conservative
   Query Match 46. Best Local Similarity 66. Matches 32; Conservative
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Best Local Similarity 66.7%;
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Publication No.
                                                                                                                                                                                                                              APPLICANT: Flinn, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
CURRENT FILING DATE: 2002-08-14
CURRENT FILING DATE: 2002-08-14
CURRENT FILING DATE: 2002-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Plin, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: death and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
CURRENT APPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
PRIOR FILING DATE: 1999-06-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Pinus radiata
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10. US20030082724A1
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o. US20030082724A1
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                     46.7%;
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75.7%;
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Score 22.4; DB 14;
Pred. No. 46;
0; Mismatches 16;
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Pred. No. 47;
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   Indels
                                    Length 1925;
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Search completed: March 17, 2004, 08:15:38 Job time: 54.3775 secs

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                                                                                                                                    ; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-2582
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US-09-738-626-2582
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SEQ ID NO 2582
LENGTH: 912
                                                                                   Query Match
Best Local Similarity
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                                                                    Matches
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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180 TGATGCGCTGGTCAAGCGTGGTGGTCGATGAGAAGGCACGT 222
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                           3 TGATCAGCTGGTTACCCGTGTTACCCCATGAAATGGCACAT 45
                                                                    30;
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OZAKI, AKIO
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YOKOI, HARUHIKO
TATEISHI, NAOKO
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                                                                   46.2%;
nilarity 69.8%;
Conservative
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                                                                 Score 22.2; DI
Pred. No. 44;
0; Mismatches
                                                                   0;
                                                                                                   DB 9;
                                                                   13;
                                                                                                   Length 912;
                                                                   Indels
                                                                   <u>0</u>
                                                                   Gaps
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                   US-09-543-407-9
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
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gb_est2:*
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Result

Score

Length DB

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SUMMARIES

Query Match

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25.2 25.2 24.8 24.6

52.5 52.1 51.7 51.3

878 894 273 1201

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CC001571 BU147350 BB435111 AL576676

CC001571 PUDIE23TD BU147350 AGENCOURT BB435111 BB435111 AL576676 AL576676

Description

RESULT 1 CC001571 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	0 0 000 00 0 0 00000000 0 0 0 0 0 0 0
CCC001571 genomic (CC001571) genomic (CC001571) GSC	2222 24.4.4.2 24.4.4.2 24.4.4.2 24.4.4.2 24.4.4.2 24.4.4.2 24.4.4.2 24.4.4.2 24.4.4.2 24.4.4.2 24.4.4.2 24.4.2 25.0 26.0 26.0 26.0 26.0 26.0 26.0 26.0 26
M 0.6_1.0_KB Z  vey sequence.  GI:29380131  viridiplantae; tta; Magnolioph coideae; Andro to 878 A., Quackenbus Fraser,C.M., ics Consortium [(2003) thy Whitelaw thy Whitelaw thy Whitelaw thy Conter Drive 8-5843 8-0208 elaw@tigr.org TF	446 9 AU29 539 28 AZ0 903 29 CNS 176 10 AW8 300 12 BF3 176 13 BU21 786 13 BU22 786 14 CB4 610 9 AL58 812 13 BU22 786 10 BB4 1016 29 CC6 10
878 bp DNA line ea mays genomic clone ea mays genomic clone Streptophyta; Embryop Streptophyta; Embryopyta; Liliopsida; Poale pogoneae; Zea. h.J., Van Aken,S., Utt Yuan,Y., San Miguel,P.	9906 56038 00568 01XVV 37303 34108 34108 34108 9140 02575 52476 52476 52476 52477 73707 73707 73707 73707 73707 64019 6401
near GSS 31-MAR-2003  EMMBTa217C21,  phyta; Tracheophyta;  les; Poaceae; PACCAD  terback,T.,  ,, Ma,J. and  ,, USA	AU299906 AU299906 AZ056038 RPCI-23-4 CB200568 AGENCOURT AL172228 Tetracdon AW837303 QV2-LT003 BF634308 NF082C02D BJ102563 BJ102563 BU252275 60349436 BU252275 60349436 BU324056 60349436 BU324056 60349436 BU252275 60415238 AA224363 zx14b09.8 AA224363 zx14b09.8 BU32657 50415238 AU373707 QV4-BT053 CB017485 pgn1c.pk0 BU25054 603321055 BE443880 WHE1124-F CB891544 EST1648513 CD0452770 WHE1124-F CC600714 ZMMBBC040 BU250554 B0343592 BB443592 BB443592 CF245156 3530-1-8 BB43592 BB435592 CF245156 3530-1-8 BB43592 BB43592 BB436405 BB436405 BB436405 BB436405 BB4379062 MEST573-G BQ744659 946106F04 BG947566 IP1-6 B09 CD204019 HS1-3-C07 BI076448 IP1-26 B0 AI711846 605064607 BG17768 IP1-26 B0 AI711846 605064607 BG103593 RHIZ2 38 BM318096 PN1 78 D1 BE363335 PI1-26-B1 CF049562 QCL38bb9. CD527595 3529-1-12

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ORIGIN
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Best Local Similarity
                                                                             Matches
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BU147350
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2 ATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCA 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BU147350
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894 bp mRNA linear EST 03-SEP-2002
AGENCOURT_8070809 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6089930
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                                                                   Conservative
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                                                                                                                                       /tissue_type="melanotic melanoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 112"
/note="Organ: skin, Vector: pOTB7; Site 1: XhoI; Site 2:
into EcoRI/XhoI sites using the following 5 adaptor:
into EcoRI/XhoI sites using the following 5 adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   b_xref="taxon:9606"
lone="IMAGE:6089930"
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/clone lib="ZM 0.6_1.0 KB"
/note="Vector: DCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
                                                                                   52.1%;
75.6%;
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mol_type="genomic DNA"
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71.7%;
                                                      Score 25; DB 13; Length 894;
Pred. No. 1e+02;
0; Mismatches 10; Indels
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Pred. No. 87;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nashiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramattsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA, Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramattsu,M.,
Automated filtration-based high-throughput plasmid preparation
System. Genome Res. 9 (5), 43-470 (1999)
High-efficio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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High-efficiency full-length cl
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/note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                         Islet cells"
                                                                                                                                                                                                 /clone_
                                                                                                                                                                                                                               /tissue_type="pancreas"
/cell_type="Islet_cells"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                            Clone="C820011N02"
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                                                                                                                                                                      lib="RIKEN full-length enriched, adult pancreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA cloning. Methods Enzymol. 303,
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1201 bp mRNA linear EST 01-JUN-200.
AL576676 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens cDNA clone CS0DI080YF21 3-PRIME, mRNA sequence.
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 9106 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1179.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                    cgi-bin/cluster.cgi?seq=CSODIO8OCC11NP1&cluster=1179.f. Contact Feng Liang Email: filang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSODIO8OCC11NP1.
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1 (bases 1 to 1201)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACAT 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feb 16, 2001 this sequence version replaced gi:12939053
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                     /tissue_type="PLACENTA COT 25-NORMALIZED" /clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo(dT) /note="Type prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primed with a primer [5' GAGAGAGAGAGAGATCCAAGAGCT
                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI080YF21"
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72.7%;
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Pred. No. 1.6e+02;
1; Mismatches 10;
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Pred. No. 84;
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                                                                                          Length 1201;
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REFERENCE AUTHORS

TITLE

JOURNAL

KEYWORDS

ORGANISM

VERSION ACCESSION

COMMENT

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ORIGIN

Query Match Best Local Matches

24;

FEATURES

Bource

RESULT 4 AL576676/c

DEFINITION

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147

N 32; ORIGIN

Matches Best Local Query Match

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RESULT 6
AZ056038/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville
                                                        Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-413M16.TV
Contact: Shaying Zhao
                                                                                                                                      Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S.
Akinret,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., F
Jong,P. and Fraser,C.M.
                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 539)
                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                SSD
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RPCI-23-413M16, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bio-resources Technology Division
Forestry and Forest Products Research Institute
Matsunosato 1, Kukizaki, Ibaraki 305-8687, Japan
Tel: 81-298-73-371(ex.444)
Fax: 81-298-73-3795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cryptomeria japonica (Japanese cedar)
Cryptomeria japonica
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Coniferopsida, Coniferales, Cupressaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AU299906 Cryptomeria japonica developing female japonica cDNA clone CF0701 5', mRNA sequence. AU299906
                                                                                                                                                                                                                                                                                                                 AZ056038.1 GI:7347274
                                                                                                                                                                                                                                                                                                                                                                                              AZ056038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: udino@ffpri.affrc.go.jp;
URL:http://www.ffpri.affrc.go.jp/labs/cjgenome/database/cjdatae.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Tokuko Ujino-Ihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU299906.1 GI:32947357
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                                                                                                                                                                                                                                                                          musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Cryptomeria
/mol_type="mRNA"
/db_xref="taxon:3369"
/clone="CF0701"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="developing female cone"
/clone_lib="Cryptomeria japonica deve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Pred. No. 1.7e+02;
0; Mismatches 13;
    Rockville,
                                                                                                                                                                                                                                                                                                                                                                                              539 bp
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Best Local Similarity
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                                                               source
                                                                                           CDNA Library Preparation: CLONTECH
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Colone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
plate: LLCM3111 row: h column: 16
                                                                                                                                                                                                                                            Unpublished (1997)
On Feb 4, 2003 this sequence version replaced gi:28233219.
Contact: Robert Strausberg, Ph.D.
Email: Cgapbs-remail.nih.gov
Tissue Procurement: Drs. Donald Brown and Liquan Cai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      493
                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Verrebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB200568.2 GI:29147154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGENCOURT 11271837 NICHD XGC Tad2 IMAGE:6875681 5', mRNA sequence.
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Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
AC (pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
com reiman.com; M column: 16
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                                                                   quality sequence stop: 104.
Location/Qualifiers
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/organism="Xenopus laevis"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1: ECORI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
                                                          . 903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lab_host="DH10B"
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'clone="RPCI-23-413M16"
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71.1%;
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Pred. No. 1.8e+02;
0; Mismatches 13; Indels 0
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Xenopus laevis cDNA
                                                                                                                                                          information can be
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                                                                                                        Direct Submission
Submitted (12-ABR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
                                                                                                                                                                                                                                                                                                                                                                                Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                    Genoscope
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AL172228
AL172228 1 GI:7810285
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fish Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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Tetraodon nigroviridis genome surv.
217C04 of library G from Tetraodon
sequence.
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/dlone="IMAGE:6875681"
/dev_stage="metamorphosis stage 62"
/dlone_lib="NICHD xGC Tad2"
/clone_lib="NICHD xGC Tad2"
/note="Organ: Developing Tadpole; Vector: pDNR-LIB;
Site 1: Sfil; Site 2: Sfil; 5' and 3' adaptors were used
5'-CACGGCCATIATGGCC-3' and 3' adaptor sequence:
5'-ATTCTACAGGCCGACGCGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.7 kb
PCR. This library was enriched for full-length clones and
was constructed by "lantach taboratories" (bal) alto all."
/organisme"Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db xrefs"ttaxon:99883"
/clone="217C04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was constructed by Clontech Laboratories (Palo Alto,
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71.1%;
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Pred. No. 2.1e+02;
0; Mismatches 13;
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AW837303
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                                                                                                                  ORIGIN
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                                        33;
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Dlass Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                                                                                                                                                         Seg primer: puc 18 forward
High quality sequence star
High quality sequence stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conteact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=QV2-LT0038-180300-079-d01&t3=2000-03-18&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QV2-LT0038-180300-079-d01 LT0038 Homo sapiens cDNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simpson, A.J.
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                                                                                                        /clone_lib="LT0038"
/clone_Tip="LT0038"
/note="Torgan: leiomios; Vector: puc18; Site_1: SmaI;
/note="Torgan: leiomios; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="LT0038"
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/note="Genoscope
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71.1%;
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                                                                          Length 176;
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                                                                                                                                                                                     BJ102563 unpublished oligo-capped Caenorhabditis elegans cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                 Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                   Caenorhabditis elegans
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                                                                                                                                                        BJ102563
BJ102563.2 GI:31238878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: gdmay@noble.org
Insert Length: 300 Std Error: 0.0
Plate: 082 row: C column: 02
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580 221 7391
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C. Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                Kohara, Y., Shin-i, T.,
                                                                                                                       Caenorhabditis elegans
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complementary view of the C.elegans genome
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                                                (bases 1 to 600)
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                Sugano, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Plantlets"
/dev stage="Pooled timepoints"
/clone lib="Drought"
/note="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       timepoints.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Medicago truncatula"
/mol_type="mRNA"
/db xref="taxon:3880"
/clone="NF082C02DT"
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Pred. No. 1.7e+02;
                                Thierry-Mieg, J.,
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                                Thierry-Mieg, D.,
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FEATURES
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AL589140/c
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                                                                                                                                                                                                                                                                                  Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
GCGGCCGCTTTTTTTTTTTTTTTTT 3' pol
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                                                                                                                                                                                                                                                             Seq primer: T7.
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                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                     BP Chicken Brain Library
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Gallus gallus
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On Jan 18, 2002 this sequence version replaced gi:18245233.
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCA 48
/organism="Gallus gallus"
/organism="Gallus gallus"
/mol_type="mRNA"
/mol_type="mRNA"
/do_xref="taxon:9031"
/clone="RoSo83H01"
/tissue_type="Brain"
/dev_stage="trnknown"
/dev_stage="trnknown"
/lab_host="PH108"
/clone_lib="Bp_Chicken_Brain_Library"
/note="Tyector: pSPORT1; Site_1: Not1; Site_2: Sall; Cloned_5: TCACCTCGAG_3:, 3', adaptor_sequence: 5'
GCGGCCGCTTTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from
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tissue_type="whole animal"
dev_stage="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:6239"
clone="yk1040a11"
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Pred. No. 2.2e+02
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                                                                                                                                                                                                                                                                      Poly A RNA purchased from Clonetech
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1 TATGATCAGCTGGTTACCCGTGTTGTTACCCGATGAAATGGCACATGCA 48

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BU294276/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PO Box 88, Manchester, M60 1QD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 766)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 01612008930
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603606963F1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACAATGATCTGTTATCTGTGTTTACAGTAAAATAGCCCACACA 350
                                                                                                                                               /note="forgan: kidney + adrenal; Vector: pBluescript II
KS(+); Site 1: EcoRI; Site 2: Not1; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an olige (dT) primer;
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al. pNAS
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                                                                                      (1996): 791, except that a signific reannealing hybridization was used
                                                                                        rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                        dev_stage="adult"
|lab_host="DH10B"
|clone_lib="CSEQCHN55"
                                                                                                                                                                                                                                                                                                                                                                                                                 'sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="ChEST590n16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="Compton Line 151"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mol_type="mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Gallus gallus"
                           50.0%;
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CSEQCHN55 Gallus
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Score 24; DB 13; Length 766;
Pred. No. 2.4e+02;
0; Mismatches 15; Indels
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Pred. No. 2.2e+02;
0; Mismatches 15;
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gallus cDNA clone ChEST590n16 5', mRNA
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TACAATGATCTGGTTATCTGTGTTTTACAGTAAAATAGCCCACACA 136

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sequence.
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603493436F1 CSEQCHN63 Gallus
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Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.
A Comprehensive Collection of Chicken CDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biomolecular Sciences University of Manchester Institute of Science
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EST.
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                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="CSEQCHN38" /clone libs="CSEQCHN38" /clone libs="CSEQCHN38" /clones limbs; Vector: pBluescript II KS(+); Site_1: /note="Forgan: limbs; Vector: pBluescript II KS(+); Site_1: /corea. limbs; Vector: pBluescript II KS(+); Site_1: /corea. libs="Corea" /corea. libs="Corea" /corea. libs="Corea" /corea. libs="Corea" /corea. libs="Corea" /corea. libs="Corea" /corea. libs="Corea" /corea. ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9212 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simon.Hubbard@umist.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="36"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Gallus gallus"
GI:25832057
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                                                                                                                                                                                                                                                                                                            50.0%;
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Pred. No. 2.4e+02;
0; Mismatches 15
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                                                              mRNA linear EST 28-NOV-2002
s cDNA clone ChEST399g10 5', mRNA
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Search completed: March 16, 2004, 04:29:00 Job time: 242.832 secs

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REFERENCE
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                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., I
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.
P. Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archosauria; Aves; Chordata; Craniata; Vertebrata; Euteleostomi; Phasianinae; Gallus.

1 (bases 1 to 791)

Boardman.pr
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Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simon Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PO Box 88, Manchester, M60 1QD, UK
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                            TATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCA 48
TACAATGATCTGGTTATCTGTGTTGTTTACAGTAAAATAGCCCACACA 322
                                                                                            Conservative
                                                                                                                                                                                                  /note=Torgan: heads; Vector: pBluescript II KS(+); Site_1: ECORI; Site_2: Not1; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with ECORI, size-selected, and cloned into the NotI and ECORI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994). 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simon.Hubbard@umist.ac.uk.
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain="White Leghorn, Hisex"
| db_xref="taxon:9031"
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                                                                                     Score 24; DB 13, --
Pred. No. 2.4e+02;
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OLESHI WANTER JOYE SHILL

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Maximum DB seq length: 2000000000
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2: gb_htg:
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456
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result No. a a a a ი 00000 ņ Score 36 35 Match 9.8 2000 8.6 2000 8.6 669 7.9 1425 7.9 302156 7.9 302156 7.9 302154 7.7 290029 7.5 1511828 7.5 183711 7.5 211981 7.5 183711 7.5 183711 7.5 183711 7.5 183711 7.5 183711 7.5 183711 7.5 183711 7.5 183716 648 306358 1711 10190 327773 327773 1 2883 10370 10370 292504 437 Length 230 4680 10346 15047 BB SEU43280 STBAJ2301 ABCO08749 AL627269 AL627269 AL627269 AL627269 AC016840 STAGFBA I44908 CCFR515701 SEU53207 ECCSGABDG AE016759 AE016759 AE016759 AE016759 AE016759 AE015131 AE016981 AE015131 AE015131 AE015131 AE015131 AE016981 ij **I44909** AX814811 Sequence L04979 Escherichia AE016759 Escherich AF275733 Escherich AF275733 Escherich AF002554 Escherich AJ015702 Enterobac AE015131 Shigella AF237726 Shigella AF237726 Shigella AF237726 Escherich D90742 Escherichia AJ131756 Escherich D90742 Escherichia AJ131756 Escherichia AJ131756 Escherichia AJ131756 Escherichia AJ131756 Escherichia AJ131756 Escherichia AJ131756 Escherichia AJ131756 Escherichia AJ131756 Escherichia AX814798 Sequence AX655393 Sequence AX655393 Sequence AX655393 Danio rer AF343445 Lactobaci AC116977 Dictyoste AC016009 Pan trogl AE0167038 Bacillus AF523644 Gavia imm AL627269 Salmonell AE016840 Salmonell AJ000514 Salmonell I44908 Sequence 56 AJ515700 Citrobact AJ515701 Citrobact U53207 Salmonella X90754 E.coli csgG AE000205 Escherich D90741 Escherichia AC146008 AP001445 AJ002301 Salmonell AE008749 Salmonell U43280 Description Sequence 58 Salmonella 8 Pan trogl 5 Homo sapi 6 Homo sapi 3 Orientia 9 Plasmodiu 1 Plasmodiu 1 Plasmodiu 1 Plasmodiu 1 Homo sapi 7 Homo sapi 8 Oryza sat

ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	I44909	RESULT 1
Salmonella Patent: US 5635617-A 58 03-JUN-1997;	Methods and compositions comprising the agfA gene for detection of	Doran, J.L., Kay, W.W., Collinson, S.Karen. and Clouthier, S.C.	1 (bases 1 to 456)	Unclassified.	Unknown.	Unknown.		I44909.1 GI:2469622	I44909	Sequence 58 from patent US 5635617.	I44909 456 bp DNA linear PAT 07-OCT-1997		

Kay, W.W

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JOURNAL
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AUTHORS
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Salmonella enteritidis
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales,
Enterobacteriaceae; Salmonella.

1 (bases 1 to 2067)
Doran, J.L., Collinson, S.K., Burian, J., Sarlos, G., Todd, E.C.,
Munro, C.K., Kay, C.M., Banser, P.A., Peterkin, P.I. and Kay, W.W.
DNA-based diagnostic tests for Salmonella species targeting agfa,
the structural gene for thin, aggregative fimbriae
J. Clin. Microbiol. 31 (9), 2263-2273 (1993)
                                                                                                                                                                                                     Salmonella enteritidis agfBAC operon encoding
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Collinson, S.K., Clouthier, S.C.,
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2067 bp DNA linear BCT 14-
Salmonella enteritidis agfBAC operon: fimbrin-like protein
precursor (agfB), thin aggregative fimbriae precursor (agf)
AgfC (agfC) genes, complete cds
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WPPSAQ"
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1352. .1645
/gene="agfA"
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.710. .2036
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IOQMNARNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNATANQY"
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/db_xref=-ng:11184713"
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SISQSAYGNSAAIIQKGSGNKANITQYGTQKTAVVVQKQSHMAIRVTQR"
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|193. .1648
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|strain="27655-3b"
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bunit of thin aggregative fimbriae precursor"
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Salmonella typhimurium
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                                                                                                                                                                                                       Submitted (29-OCT-1997) Romling U.,
Karolinska Institute, MTC, Box 280,
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhimurium
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Enterobacteriaceae; Salmonella.
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:8gG, csgF,
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S-17177, SWEDEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene; csgF gene;
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                                                                                           complement (2869.
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                                                                                                                                                                                                                                                                                                                                                                           gene="csgD"
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                                                                                                                                                                                                                                                                                                                                        gene="csgD"
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transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          xref="SWISS-PROT:054291"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function="nucleator"
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1469. .3924
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The Salmonella typhimurium Genome Sequencing Project Direct Submission .
Submitted (29-MAR-2001) Genome Sequencing Center, Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4206
                                                                                                                                                     McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W.,
Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M., Du, F.,
Hou, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes, A.,
Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Miller, W.,
Stoneking, T., Nhan, M., Waterston, R. and Wilson, R.K.
Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG 420
                                                                                                                                                                                                                                                                      Salmonella typhimurium LT2
Salmonella typhimurium LT2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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                                                                                                                                  21534948
                                                                                                                                           Nature 413 (6858),
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AE008749 AE006468
AE008749.1 GI:16419641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GGCGTCGTTCCACAATGGGGCGGCGGCGGCAATAATCATAACGGCGGCGGCAATAGTTCCGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419;
                                                                                           (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCÁCCÁTCGÁCCÁGTGGÁÁCGCTÁAAAÁCTCCGÁTÁTTÁCTGTCGGTCÁÁTÁCGGCGGT 4325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCGÁTGCCCGTAAAATCTGAAACGACCATTACCCCAGAGGCGGTTATGGTAACGGCGCCGAT 4205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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/translation="MSVIKKNIPAIGLCICAFFIHSAVGQQTVQGGVIHFRGAIVEPL
CDISTHAENI"
                                                                                           22411)
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91.9%;
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Pred. No. 1.3e-101
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CDS

gene

mat\_peptide sig\_peptide

gene

BCT 23-APR-2003

gene CDS		gene RBS	FEATURES BOUTCE		COMMENT
COMPLEMENT VINGULTYCOLPRGVRSGLSUALERFEEDEMVGLVHFNKDDCVRSALC QRTLHAYS"  COMPLEMENT (14142303)  /gene="STM1127"  Complement (14142295)  /gene="STM1127"  Complement (14142295)  /gene="STM1127"  /pene="STM1127"  /note="similar to E. coli orf, hypothetical protein (AAC75480.1); Blastp hit to AAC75480.1 (285 aa), 29%  identity in aa 15 - 264"  /codon_start=1  /trans[_table=11  /product="putative transcriptional regulator"  /product="putative transcriptional regulator"  /product="putative transcriptional regulator"  /product="putative transcriptional regulator"  /protein_id="AAL20058.1"  /db_xref="gutative transcriptional regulator"  /protein_id="AAL20058.1"  /db_xref="gutative transcriptional regulator"  /protein_id="AAL20058.1"  /stanslation="mepoperuptational regulator"  /translation="mepoperuptational regulator"  /translation="mepoperuptational regulator"  /translation="mepoperuptational regulator"  /ktanslation="mepoperuptational regulator"  /ktanslation="mepoperuptati	/gene="phoH" /note="similar to E. coli PhoB-dependent, ATP-binding pho regulon component; may be helicase; induced by P starvation (AAC74105.1); Blastp hit to AAC74105.1 (354 aa), 92% identity in aa 71 - 354" /codon start=1 /transI_table=11 /product="PhoB-dependent ATP-binding pho regulon component" /protein_id="AAL20057.1" /db_xref="GI:16419642" /translation="MCAHRYQENAGDVYLQLKVLSMGRQKAVIKARREAKRVLRRDS RSHKQREESETVSLVQMGGVEAIGMARDSRDTSPVKARNEAQAHYLNAIDSKQLIFAT GEAGCGKTWISAAKAAEALIHKUVERIIVTRPVLQADEDLGFLDGILBKFARVERPV VDVLLKRLGASEMQYCLREIGKVELAFFAYWGRTERNAVILDEAQANVTAAAQMKMF TTALTANTINGTICTORIANTICTICTORIANT	/note="LT2" 434 . 1308 /gene="phoH" /note="Bynonym: STM1126" 434439 /gene="phoH" /note="putative RBS for phoH; RegulonDB:STMS1H001398" /554 . 1308	This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.  Location/Qualifiers 122411 /organism="Salmonella typhimurium LT2" /mol type="genomic DNA" /mol type="genomic DNA" /mol type="genomic DNA" /db_xref="taxon:99287"	Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tlgr.org/sofflab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/  EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EccCyc; http://ecccyc.PangeaSystems.com/ecccyc/  The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and ReguonDB; http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset	Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 AI43283
gene RBS	RBS gene CDS		RBS gene CDS	gene CDS	RBS

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NAKLVAVIPVFFFAIGSALFYYYQQHFDQLDAGFNTGGILPLFVVTTDSIEGILIIA
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6793. .6798
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AFDASFRSRPVDIDSILTRIKHGLLAMADCSTVNEGISCHQKGIEFIGTTLSGYTGP
AFDASFRSRPVDIDSILTRIKHGLLAMADCSTVNEGISCHQKGIEFIGTTLSGYTGP
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/gene="STM1129"
/note="similar to E. co
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/gene="STM1129"
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Blastp hit to AAC76255.1 (229 aa), 70% identity in aa 1 -
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/gene="STM1128"
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QARESKLRTMNALDMTK"
                                                                                                                                                                            #QYMGKMKQPLGYGVSVSYGDEVFLIGGENAKGKPVSSVTSFTMRDGNLLIK"
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                                                                                                           /gene="STM1131"
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(AAC76702.1); Blastp hit to AAC76702.1 (571 aa), 22%
identity in aa 7 - 478"
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RBS for STM1131; RegulonDB:STMS1H001402"

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RESULT 5
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      AL627269
Salmonella enterica serovar Typhi
complete chromosome; segment 5/20,
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AL627269.1 GI:16502231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Cranslation="MKINKYLLGWVSFIAFSSYLQAATLDYRHEYADRTRINKDRIAI
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DELKLEYNFTWMDSDQIKFDNKKTNYEHNVALAWKLNKSFTPYVEVGNVAVRNNTDER
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/transl_table=
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91.9%;
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Pred. No. 1.3e-
0; Mismatches
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                                          DNA lir
(Salmonella
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) strain CT18,
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                 gene="STY1078"
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Salmonella enterica subsp. enterica serovar Typhi
Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
CE 1 (bases 1 to 254050)
RS Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D.,
Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T.,
Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T.,
Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N.,
Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P.,
Jagels, K., Whitehead, S. and Barrell, B.G.
Complete genome sequence of a multiple drug resistant Salmonella
Nature 413 (6858), 848-852 (2001)
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Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 1SA, UK E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Details of S. typhi sequencing on the World Wide Web.
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AQDGSGYQFLYEMITDLNSRNPQVASRLIEPLIRLKRYDDKRQEKWRAALEQLKGELEN

T.SCRIVFKTMALA."
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Orthologue of E. coli pepN (AMPN ECOLI); Fasta h
to AMPN_ECOLI (869 aa), 94% identity in 869 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="CT18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="synonym: pepN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Salmonella enterica subsp. enterica serovar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="dihydroorotate dehydrogenase"
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                                                                                                                                                                                                                                                                                                                                                 complement(4716. .5825)
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/note="Orthologue of E. coli P75863; Fasta hit
/note="Orthologue of E. a coli P75863; Fasta hit
(369 aa), 86% identity in 367 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (4716. .5825)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="STY1080"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="STY1079"
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Dihydroorotate dehydrogenase, score 563.50, E-value
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EIIRRLSLELKGQLPIIGVGGIDSVIAAREKIAAGATLVQIYSGFIFKGPPLIKEIVT
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/transl_table=
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to PYRD_ECOLI (336 aa), 95% identity in 336 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="PS00142 Neutral zinc metallopeptidases, zinc-binding region signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="STY1079"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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.4955)
                                                                                                                                                                                                                                                                                                                                               367 aa overlap"
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da overlap. N
l start site."
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                        241
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Query Match
Best Local Similarity
GTAGGCCAGGGTGCGGATAACAGTACTATTGAACTGACTCAGAATGGTTTCAGAAACAAT 89205
                                                                                                                                                                                                                                                                              CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                         GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 88965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
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                                                                                                                    AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 89145
                                                                                                                                                                                                                                              CCGGATTCCACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                                                                                                                                                                                     GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGG 89025
                                                                                                                                                                                    AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db xref="Springly:Q82786"
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MOFGGMULSLFSASPDLLGSLGCRADKQFKAKWGPLDCVQKNYHTAETTADSKFATVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Pfam match to entry PF01170 UPF0020, Uncharacterized protein family UPF0020, scc E-value 3.7e-231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Similar to Haemophilus influenzae hypothetical protein hi0116 H10116 SW:YCBY HAEIN (P44524; P43945) fasts scores: E(): 0, 60.3% id in 710 aa Orthologue of E. coli YCBY ECOLI; Fasta hit to YCBY_ECOLI (702 aa), 92% identity in 702 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8045. .9952
/gene="STY1083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8045. .9952
/gene="STY1083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fasta hit to YJJK_ECOLI (554 aa), 34% identity in 524 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein id="CAD08187.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="PS01261 Uncharacterized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="STY1082"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.7%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 395.2; DB 1;
Pred. No. 3.9e-101;
0; Mismatches 38;
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Deng, W., Liou, S.-R., Plunkett, G. III,
Burland, V., Kodoylanni, V., Schwartz, D.
Direct Submission
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Salmonella enterica subsp. enterica serovar Typhi Ty2
Bacteria, Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Yphi Ty2"
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Salmonella typhi CT18"
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Salmonella typhi CT18"
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complement(1812. .3473)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STY1221 from Accession AL513382:
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Query Match
Best Local Similarity
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                                              /codon_start=1
/transT_table=11
/transT_table=11
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                                                                                                                                                                                                                                                                                                            /translation="MDHAIYTAMGAASQTLNQQAVTASNLANASTPGFRAQLNALRAV PVDGLSLATRTLVTASTPGADMTQGQLDYTSRPLDVALQQDGMLVVQQADGAEGYTRN GNIQVGPTGQLTIQGPGPITVPEGSEITIAADGTISALNPGDPPNTVAPVGR LKLVKAEGNEVQRSDGLFRLTAEAQAERGAVLAADPSIRIMSGYLEGSNVKPVEAMT DMIANARRFEMQMKYITSVDENEGRANQLLSMS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MISSLWIAKTGLDAQQTINMDVIANNLANVSTNGFKRQRAVFEDL
LYQTIRQPGAQSSEQTTLPSGLQIGTGVRPVATERLHSQGNLSQTNNSKDVATKGQGF
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QOGQNAPVQVGQLNLTTFMNDTGLESIGENLYIETQSSGAPNESTPGLNGAGLLYQGY
VETSNVNVABELVNMIQVQRAYEINSKAVSTTDQMLQKLTQL"
Complement (7146...7901)
                                                                                                                                                                       /locus_tag="t1743"
/note="corresponds to STY1216
Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVANGSIFQSAQPINYGYQPLFEDRRPRNIGDTLTIVLQENVSASKSSSANASRDGKT
SFGFDTVPRYLQGLFGNSRADMEASGGNSFNGKGGANASNTFSGTLTVTVDQVLANGN
LHVVGEKQIAINQGTEFIRFSGVVNPRTISGSNSVPSTQVADARIEYVGNGYINEAQN
                                                                                                                                                                                                                                          complement (7922. .9133)
                                                                                                                                                                                                                                                                                              complement (7922. .9133)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="t1742"
/note="corresponds to STY1217
/nonella_typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus_tag="t1742"
complement(7146. .7901)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (6350. .7132)
/gene="flgG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (5597. .6295)
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                                                                                                                                                                                                                                                             /locus_tag="t1743"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /locus_tag="t1741"
/note="distal rod protein; corresponds to STY1218
Accession AL513382: Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (6350. .7132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGWLQRFFLNLSPM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="flagellar L-ring protein precursor"
/protein_id="AAO69364.1"
/db_xref="GI:29137803"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhi CT18"
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                                                                                                                                                                                                                             'gene="flgE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="flagellar basal-body rod protein
/protein_id="AAO69365.1"
/db_xref="GI:29137804"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MQKYALHAYPVMALMVATLTGCAWIPAKPLVQGATTAQPIPGPV/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="corresponds to STY1219 from Accession AL513382:
   86.7%;
91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tag="t1740"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _tag="t1740"
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   Score 395.2; DB 1;
Pred. No. 3.9e-101;
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                  Length 301983,
                                                                                                                                                                                           Accession
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                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
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STAGFBA
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DEFINITION
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KEYWORDS
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                                                                                                                   gene
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                                                                                                                                                                                                                                                                                                                                                  Infect.
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AJ000514.1 GI:2275119
agfA gene; agfB gene.
Salmonella typhimurium
salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sukupolvi,S., Lorenz,R.G., Gordon,J.I., Bian,Z., Pfeifer,J.D., Normark,S.J. and Rhen,M.
Expression of thin aggregative fimbriae promotes interaction of Salmonella typhimurium SR-11 with mouse small intestinal epithelial
                                                                                                                                                                                                                                                                                                                            Submitted (14-JUL-1997) Sukupolvi S.S., University of Turku, Kiinanmyllynkatu,
                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 1048)
Sukupolvi, S.S.
                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98053981
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AJ000514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCACCATCGACCAGTGGAACGCTAAAAAACTCCGATATTACTGTCGGTCAATACGGCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAGGCCAGGGTGCGGATAACAGTACTATTGAACTGACTCAGAATGGTTTCAGAAACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGGATTCCACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immun.
/gene="agfB"
/codon start=1
/transT_table=11
/product="AgfB protein"
/protein_id="CAA04150.1"
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                               db_xref="taxon:602"
                                                                                                                                  gene="agfB"
4. .553
                                                                                                                                                                                                                                                     organism="Salmonella typhimurium
                                                                                                                                                                                                                                                                                    . .1048
                                                                                                                                                                                                                                _type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 (12),
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Doran, J.L., Kay, W.W., Collinson, S. Karen,
Methods and compositions comprising the a
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Sequence 56 from patent US 5635617.
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Pred. No. 1.7e-99;
0; Mismatches 41
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Direct Submission
Submitted (11-NOV-2002) Romling U., Micro
Center, Karolinska Institute, Box 280, S.
Location/Qualifiers
2889
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Production of Cellulose and Curli Fimbriae by Members of the Family
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract
Infect. Immun. 72 (7), 4151-4158 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Citrobacter sp. Fec2
Citrobacter sp. Fec2
Bacteria, Proteobacteria, Gammaproteobacteria,
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component of curlin monomers;
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Citrobacter sp. Fec2 csgB gene,
AJ515700
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/function="necessary operon"
                                                                     complement (212. .862)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                        /isolation_source="faeces"
/specific_host="Homo sapiens"
/db_xref="taxon:213763"
                                                    /gene="csgD"
                                                                                                     /gene="csgD"
                                                                                                                               complement (212.
                                                                                                                                                    country="Germany"
                                                                                                                                                                                                                                                                  /isolate="Fec2"
                                                                                                                                                                                                                                                                                 /organism="Citrobacter sp.
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:31790491
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/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 csgD gene; curlin-csgA protein; nucleation
pnomers; regulatory protein.
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Pred. No. 2.1
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     for transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        csgA
                                                                                                                                                                                                                                                                                                              Fec2
                                                                                                                                                                                                                                                                                                                                                                     Microbiology and Tumorbiology
80, S-17177 Stockholm, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
3A gene
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and csgD
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of the csgBA
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303 240

180 243 120 183 60

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REFERENCE AUTHORS

TITLE

JOURNAL

codon\_start=1

KEYWORDS SOURCE

ORGANISM

RESULT 8 I44908

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ORIGIN
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                         GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                       AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCGATGAAATG 420
                                                                                                                                                                                  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATACGGCGGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
GGTTTTGGCAACAACGCCACCGCTAACCAGTACTAA 2571
                                                                           CATAACGCCGCACTGGTGAACCAGACTGCGTCCGATTCCAGCGTTCTGGTGCATCAGGTT 2535
                                                                                                                                                           GCCACCATCGATCAGTGGAACGGCAAAAAATTCGGACATTACTGTGAGCCAGTATGGTGGA
                                                                                                                                                                                                                                         GTGGGCCAGGGCTCAGATAACAGCACCATCGATCTGACTCAAAACGGCTTCAAAAACAAC 2415
                                                                                                                                                                                                                                                                                                                       AGCGACGCTCGTAAATCTGATACGACCATTCATCAGAATGGCTTTGGTAACGGCGCAGAC 2355
                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                             GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                                                                                                                                                                                                                                                             AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                    CCGGAATCGACCCTGAGCATTTATCAGTCAGGAGTCAATAACGCCGCGCTTGCGCTGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mknkllfmmltvlgapglasatsyplahseynfavnelskssfn
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2119. .2571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mkilqvaafaaivvsgsalagsvpqwggggggggggsssgpestl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mfnefhsihghtlllitkpslQatallQhlkQslalsgklhniQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="nucleation component
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/transl_table=11
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/transl_table=11
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/function="nucleator'
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Pred. No. 4.9e-67;
0; Mismatches 103;
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ORGANISM
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VERSION
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CFR515701
LOCUS
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component of curlin monomers;
Citrobacter freundii
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2123. .2572
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/function="curli
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/transl_table=11
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transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                  function="nucleator"
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ક 문 S 밁 ક 밁 8 무 ঠ 밁 र् 밁 श 8 ঠ

ORIGIN Submitted (12-NOV-2002) Romling U., Mic Center, Karolinska Institute, Box 280, Zogaj, X., Bokranz, W., Nimtz, M. and Romling, U. Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract Infect. Immun. 72 (7), 4151-4158 (2003) CFRS15701 2920 bp DNA linear BCT Citrobacter freundii csgB gene, csgA gene and csgD gene AJ515701 Enterobacteriaceae; Citrobacter Bacteria; Proteobacteria; Gammaproteobacteria; QWNAKNADISVTQFGGRNGALVNQTASDSNVLIQQVGFGNNATANQH" /codon\_start=1 /transT\_table=11 /product="curlin-csgA\_protein" /protein\_id="CAD56675.1" /db\_xref="GI:31790498" NQAAIIGQVGTANSANTRQGGSKLLSVISQEGSGNRAKTDQTGSYNFAYIDQTGSSND ASIKQGSYGNTAVIIQKGSGNKANITQYGTQKTAVVVQRQSQMAIRVTQR" /translation:"Menevhsihghtllitkpslqatallqhlkqslaltgklhniq RSLDD185G1VLlbMMeadkKLihtWqDnlsrknnniktlllmtpddypyrdienwe HINGVFYATeDeQRVVSGLOGVLRGECYFSQKLASYLITHSGNYXYNSTESALLTHRE KEILNKLRIGASNIEIARSLFISENTVKTHLYNLFKKIAVKNRTQAVSWANDNLRR" 'transT table=11

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Query Match 51.0
Best Local Similarity 71.1
Matches 324; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2537
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                                                                                                                                                                                                                                      2 (bases 1 to 230)
2 (bases 1 to 230)
COx, J.M., Eglezos, S. and Woolcock, J.B.
Direct Submission
Submitted (01-APR-1996) J.M. Cox, Food Science and Technology,
University of New South Wales, Sydney, NSW 2052, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2297
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salmonella enteritidis
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Cox,J.M., Eglezos,S. and Woolcock,J.B.

Virulence of Salmonella enteritidis in chickens correlates with colony morphology and expression of SEF17 fimbriae
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Salmonella enteritidis SEF17
U53207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCACCATCGACCAGTGGAACGCTAAAAACTCCCGATATTACTGTCGGCCAATACGGCGGT 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AĞTĞĀTĞCĞCĞTAAATCAĞATGTCACCATCACACAACAĞĞGCGTĞĞCCAACĞĞAĞCTĞTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAGACTOTTOACTGAGTATOTACCAATATGGGTOAAACAACTGTGCAAATGCTCTGCAA 2296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTGTTGTŤCCGCÁÁŤGGGGCGGC-----ÀÁŤCÁŤCÁTGGTGGTĞGTÁGTÁAŤŤATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGAĀĀCTTTRĀĀĀĀGTĠĠĊĀĠCĀTTCĠĊĀĠĊĀĀTĊĠTĀGTTTĊTĠĠĊĀĠTĠĊTĊTĠĠĊT 2182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAAACTTTTAAAAGTGGCAGCAGTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.0%;
71.1%;
                                  fimbrin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No. 7.3e-55;
0; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp DNA linear BCT 01-MAY-1996
fimbrin (agfA) gene, partial cds.
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PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
TITLE
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ORGANISM
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ACCESSION
VERSION
KEYWORDS
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ECCSGABDG
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Best Local Similarity
                                                                                                                                                                                                                                                                                          Hammar,M.

Direct Submission
Submitted (11-AUG-1995) M. Hammar, Karolinska Institutet,
Microbiology and Tumorbiology Center, Box 280, S-171 77 Stockholm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 ATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCCACGATGGACCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 ATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCCAGGGTGCGGATAATAGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hammar,M., Arnqvist,A., Bian,Z., Olsen,A. and Normark,S. Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli
Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X90754.1 GI:1147558
C89A gene; C89B gene; C89D gene;
orfC gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                            96414468
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E.coli csgG, csgF, csgE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TÁCGGTTCCGCTAACGCTGCCCTTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACC
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Pred. No. 6.7e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4680
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~ກ, csgB,
                                                                                              coli"
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|B, csgA,
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gene,

317

180

120 207 60 147 0,

٥,

Gaps

FEATURES Source

gene

JOURNAL

JOURNAL REFERENCE AUTHORS TITLE

REFERENCE AUTHORS TITLE

SOURCE ORGANISM ACCESSION VERSION KEYWORDS DEFINITION

RESULT 11 SEU53207 LOCUS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / t-abia at i on="morlfllvavmlisgcltapergbarptimpragsykdlthlpa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (1828. .2478)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQTEEALNRRQINQALLSTGDLAHDEF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="csgF"
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                                                                                                                                                                                                                                                                                                                                                                                                                    note="necessary for transcription of the csgBA operon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="SWISS-PROT: P52103"
                                                                                                                                                                                                                                                                                                                                                                                    table=11
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       4149
                                       421
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4243. .4575

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transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    db_xref="GOA: P28307"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xref="SWISS-PROT:P28307"
     <u>,</u>
Score 217.6; DB 1;
Pred. No. 1.2e-50;
0; Mismatches 149;
                                                     Length
     Indels
                                                       4680;
     0;
     Gaps
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ATGAAACTTTTAAAAGTAGCAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCTCTGGCA 3788 GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456 GGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT 4148 AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATG 420 GCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGTGGT GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360 GTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCCAACGTGGCTTCGGTAACAGC 4028 GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300 ACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGCAGAT 396 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240 CCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAA 3908 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCCTCTGCAA 180 GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC 3848 egcercerrecacaareegecegecegeraarearaacegecegecaaraerrecege ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 4088 120 60

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FEATURES
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AUTHORS
TITLE
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AUTHORS
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ORGANISM
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AE000205
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                                                                                                                                                                          JORS Plumhett, G. III.

B Direct Submission

What Submitted (13-OCT-1998) Laboratory of Genetics, University of Misconsin, 445 Henry Mall, Madison, WI 53706, USA

Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

University of Wisconsin-Madison (Frederick R. Blattner, director). Project and NCHGR) The entire sequence was independently frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, have been correlated with genetic loci are being annotated with CG Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible ongoing task whose goal is to make the genome sequence more useful appreciated. Updated information will be available at the E. coli (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and sequence changes. Annotation updates: updated gene lead the sequence changes. Annotation updates: updated gene identifications are periodically updated; this is version M54. No and products; all new functional assignments courtesy of Monica sequences described in reference 1. The unique numeric identifiers RNA.encoding) are now designated as gene synonyms instead of names.

Location of the man of the man of the period of the service of manes of the searched for in Entrez as gene
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Submitted (02-8EP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
608-263-7459
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Escherichia coli K12
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Escherichia coli K12 MG1655 section 95 of 400 of the complete
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/organism="Escherichia coli K12"
/mol_type="genomic DNA"
                                                                                                                               Location/Qualifiers
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SITRYVLLSVCISTVVNLTTISPLRNSTTINGFT
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SITRYVLLSVCISTVVNLTTISPLRNSTT
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SITRYVLLSVCISTVVNLTT
SITRYVLSVCISTVVNLTT
SITRYVLSVCIST
                                                                                                                                                                                                                                                                               /function="orf; Unknown"
(note="083; This 83 aa ORF is 25 pct identical (7 gaps)
1081 residues of an approx. 616 aa protein ALBU_RABIT S
                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="b1030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLRFSKRYAFLGRLFLQEIDLFFSSENALSTFFAKFLWLRLFILLVIEVMWITLVSVL
ATLVEWRIWFEAYFLLCYVPCLIYYFFYCRFLWHNDFMMACDMYFRWGHFNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="b1030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="factor Sigma70; predicted +1 start at 1096049"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="No predicted promoter"
bound_moiety="DeoR predicted"
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/function="orf; Unknown"
/note="0328; This 328 aa ORF is 19 pct identical (4 gaps)
to 191 residues of an approx. 288 aa protein Y320_MYCGE
SW: P47562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="synonym: b1029"
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/function="orf; Unknown"
/note="o107; This 107 aa ORF is 27 pct identical (0 gaps)
to 58 residues of an approx. 1888 aa protein FAS2_CANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (<1.
/note="IS3"
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                          121
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CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                            GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC
                                                                                                GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGC
                                                                                                                                      ATGAAACTTTTAAAAAGTAGCAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCTCTGGCA
                                                                                                                                                                            ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
                                                                                                                                                                                                                47.7%;
ilarity 67.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MRINFAQRESGVSMDIIFYHPTFDTQWWIEALRKAIPQARVRAW KSGNNSADYALVWHPPVEMLAGRDLKAVFALGAGVDSILSKLQAHPEWLNESVPLFR LEDTGMGEQWDEYAVGVULHWFRRFDDYRIQQNSSHWOPLEKLPHREDFIGIGAGTVL GSKYAQSLQTWRPPLLGWSRTREKSWFGVQSFAGREELSAFLSQCRVLINLLPMTPETV GIINQQLLEKLPDGAYLLNLARGVHVVEDDLLAALDSGKVKGAMLDVFNREPLPPESP GINQQLEKLPDVAAITRPAEAVEYISRTIAQLEKGERVCGQVDRARGY"
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/note="factor Sigma70; predicted +1
3396. .3423
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2355. .2383
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/note="0137; This 137 aa ORF is 27 pct identical (1 gap)
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.513. .1926
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Pred. No. 1.2e-50;
0; Mismatches 149;
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                                                                                                                                                                      Submitted (29-JUL-1996) Hirotada Mori, and Technology, Res. & Edu. Center for Takayama, Tkoma, Nara 630-01, Japan (E-mail:hmori@gtc.aist-nara.ac.jp, Tel:
                                                                                                                                                                                                                                                                                                     Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Horiuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S., Ithh,T., Kanai,K., Kasai,H., Kashimoto,K., Kim,S., Kimura,S., Kitagawa,M., Kitakawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T., Saito,N., Sampel,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamamoto,Y. and Yano,M.

The systematic sequencing of the Escherichia coli genome in Japan Unpublished
                                                                                                                                      Fax:81-7437-2-5669)
Collaboration Information:
                                                                                                                                                                                                                                                      Direct Submission
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Escherichia coli Kl2 genomic
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Oshima,T., Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Ikemoto,K., Inada,T., Itoh,T., Kajihara,M., Kanai,K., Kashimoto, Kimura,S., Kitagawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nashimoto,H., Nishio,Y., Saito,N., Sampei,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamamoto,Y., Yano,M. and Horiuchi,T.
A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map DNA Res. 3 (3), 137-155 (1996) D90741 AB001340
D90741.1 GI:1651509
D90741.1 GI:1651509
Complete and shotgun sequencing; csgG; csgF; cs csgA; ycdE; cls; nov; mdoG.
Escherichia coli K12
Escherichia coli K12
Bacteria; Proteobacteria; Gammaproteobacteria; Honjo, A., ., Kashimoto, K.,

sequencing

project

Tel:81-7437-2-5660,

NARA Institute of Science Genetic Info.; 8916-5

The Japan E.coli genome DNA sequencing group Members: (1995.4 - 1996.3)
Aiba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Horiuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono Isono,

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The Japan E. coli genome database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Information operator:
Name: Hirotada Mori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Address: NARA Institute of Science
_____Ikoma, 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Address: National Institute
E-mail: kishori@nibb.ac.jp
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PLRCWSRTRKSWFGVQSEAGREELSAFLSQCRVLINLLPNTPETVGIIMQQLLEKLPD
GAYLLNLARGYHVVEDDLLAALDSGKVKGAMLDVFNREPLPPESPLWQHPRVTITPHV
AAITRPAEAVEYISRTIAQLEKGERVCGQVDRARGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2145. .2882
                                                                                                                                                                                                                                                                                                                                                              /protein_id="BAA35824.1"
/db_xref="GI:4062607"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="unnamed protein product; ORF_ID:o231#2"
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similar to SwissProt Accession Number P45637"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="BAA35823.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="Hypothetical 33.0 kd protein in proB-proA
intergenic region."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="Kohara clone #231"
/note="Nucleotide position 1097101-1112147 from the initiation site of ThrA (0 min.).~This clone is from Kohara lambda miniset library."
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                                                                                                                              _table=11
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                                                                                    protein."
                                                                                                                                                                                                                                         /gene="csgD"
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db_xref="GI:4062613"
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                                                                                                                                      'codon_start=1
'transl_table≈
                                                                                                                                                                                                                                                                                             complement (5812.
                                                                                                                                                                                                                                                                                                                                                                                                                                 CsgE precursor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similar to SwissProt Accession Number P52105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (5418. .5807)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MRVKHAVVLLMLISPLSWAGTWTFQFRNPNFGGNPNNGAFLLNSAQAQNSYKDFSYNDDFGIFTPSALDNFTQAIQSQILGGLLSNINTGKFGRMVTNDYIVDIANRDGQLQLNVTDRKTGQTSTIQVSGLQNNSTDF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="Curli production
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/transl_table=11
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IGADTQYQLDQIAVNLRVNNVSTGBILSSVNTSKTILSYEVQAGVFRFIDYQRLLEGG
VGYTSNEPVMLCLMSAIETGVIFLINDGIDRGLWDLQNKAERQNDILVKYKHMSVPPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="Curli production assembly/transport component
sgF precursor."
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CsgG precursor."

CsgG precursor."
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IVAFLMCIQAKGLLLSFVPGTFIGACATFAGQGDWKLVLPSLALGLIFGYAMKNSGLW
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REFERENCE
AUTHORS
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DEFINITION
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                                                                                                                                                                                                                                                                                                                      Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Sequence 15 from Patent WOO3064446.
AX814811 GI:39104001
                                                                                                                                                                                                             Patent: WO 03064446-A 15 07-AUG-2003;
Hansa Medical Research Aktiebolag (SE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                   Bjoerck, L., Olsen, A., Wikstroem, M. and
                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                      Peptides
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                                                                                                        note="unnamed protein product"
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Pred. No. 1.2e-50;
0; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                     Herwald, H.
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ORIGIN

Search completed: March 15, 2004, 22:50:01 Job time : 1964.17 secs

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## ALIGNMENTS

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AAC64622 standard; DNA;

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escheribhia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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P-PSDB; AAB36346.
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CC homologous species; (3) directing recombination of a recombinant gene CC back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC protein containing an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid segment or sequences grown on a Salmonella, E. coli or polymer into the animal in conjunction with a carrier or diluent. (1) is CC useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for CC system the heterologous antigens are presented in high numbers (up to CC system the heterologous antigens are presented in high numbers (up to CC immunogenicity and adhesion properties relevant for an efficient live cagainst the inserted epitope, and hybrid fimbria are usually strong CC immunogens, which may be important for directing an immune response consensive to purify in large amount. The present sequence is given in XX to the exemplification of the present invention
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Best Local
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                     GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                            AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG
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Pred. No. 1.1e-120;
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ies 32;
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RESULT 2
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XX AAQR
AC AAQR
AC AAQR
DT 25-M
DT 26-J
XX
XX
DE AgfA
XX
XX
Salr
XX
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Salr 25-MAR-2003 26-JUN-1995 Salmonella Salmonella; AgfA; vaccine; genetic AgfA sequence. AAQ87467; AAQ87467 standard; DNA; (revised)
(first entry) 456 BP. immunization;

RESULT 3 AAT74142

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Matches 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Col 19-112; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 456
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P-PSDB; AAW23570.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enteritidis 27655-3b agfA gene
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                                                                          AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
                                                                                                                                                                          CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                           GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC 120
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                                              AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
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Pred. No. 1.1e-120;
Pred. No. 1.2e-120;
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back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid gequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the Nathernation and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live
                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of finbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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DB; AAB36341.
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WPI; 2000-672631/65. P-PSDB; AAB36347.

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RESULT 5
AAAC64623
AID AAC6
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Best Local
    White AP,
                                                                              05-APR-2000; 2000WO-CA000356
                                                                                                                                                                    Salmonella enteritidis
Escherichia coli.
                                                                                                                               WO200060102-A2
                                                                                                                                                                                                                         Salmonella;
                           (UYVI-) UNIV VICTORIA.
                                                                                                        12-0CT-2000
                                                                                                                                                                                                             vaccine;
                                                                                                                                                                                                                                               AgfA::PT3#2 DNA sequence SEQ ID
                                                                                                                                                                                                                                                                              26-FEB-2001
                                                                                                                                                                                                                                                                                                                            AAC64623 standard; DNA; 456 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine, the carrier fimbrial subunit proteins are usually stroimmunogens, which may be important for directing an immune respanse the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is the exemplification of the present invention
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  Doran JL,
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                                                  99US-0127888P
                                                                                                                                                                                                          response;
                                                                                                                                                                                                                   chromosomal gene replacement; fimbrin; epitope;
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                                                                                                                                                                                                          immunogen; ds.
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Pred. No. 1.1e-120;
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Sequence 456 BP; 118 A; 109

C; 121 G; 108 T; 0 U; 0 Other;

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Agfa, CSgA and Agfa-homologue finbrin subunits, respectively, (2)
CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of the chromosome of the homologous species, replacing the native CC copy of that gene, and (4) eliciting an immune response in an animal, cC comprising separating an amino acid polymer comprising a recombinant Agfa CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CR acid sequence or sequences grown on a Salmonella, E. coli or CR polymer into the animal in conjunction with a carrier or diluent. (1) is CR useful for the expression of recombinant Agfa protein which is useful for CR coliciting an immune response in an animal. In a fimbrial presentation CR system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein sare usually strong creating the inserted epitope, and hybrid fimbriae are usually strong creating the inserted epitope, and hybrid fimbriae are easy and cinexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising are combinant of the production of strains of salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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5 밁 Ş 뮍 Ş 뮹 Ş 밁 Ş 밁 Ş 밁 S Query Match Best Local S Matches 406 361 301 241 241 181 181 121 121 406; 61 61 GCACATGCAAACAACGCCACGGCTAACCAGTATTAA Similarity AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT CTGGTTACCCGTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA ĠĊĊĀĊĊĀŤĊĠĀĊĊĀĠŤĠĠĀĀĊĠĊŤĀĀĀĀĀĊŤĊĊĠĀŤĀŤŤĀĊŤĠŤĊĠĠĊĊĀĀŤĀŤĠĀTCAG GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT AGCGATGCCCGTAAATCTGAAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT GGCGTCGTTCCACAATGGGGCGGCGGCGGCAATACTTCCGGC GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC ATGAAACTTTTAAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT Conservative 82.5%; 89.0%; Score 376; DB 3; Pred. No. 2.4e-111; 0; Mismatches 50; Length 456; Indels 0, 360 300 180 420 300 240 240 180 120 120 60 0

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421

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CC Agfa, Cega and Agfa, chomologue finbrin subunits, respectively; (2) cdirecting recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene combinant gene comprising a recombinant agfa grown of the box combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene grown on a Salmonella, E. coli or combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant gene combinant 
Query Match
Best Local Similarity
Matches 397; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                Sequence
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                                                                                                                                                 exemplification of the present invention
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DB; AAB36350.
                                                                                                  456 BP;
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 137; 139pp; English.
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                                                                                             116 A; 111 C; 120 G; 109 T; 0 U;
                       79.3%;
87.1%;
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Score 361.6; DB 3;
Pred. No. 1.1e-106;
0; Mismatches 59;
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                                                                                                0 Other;
Indels
                                            Length 456;
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Gaps
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RESULT 7
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                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA seqwhich encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC64625;
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                                                                                                                                                                                                                                                                                                      White AP,
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The present invention describes a recombinant agfA gene (I) where a

Disclosure; Page 136; 139pp; English

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cc segment of the gene has been replaced by a segment of a foreign DNA CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) cc homologues species; (3) directing recombinant on of a recombinant open into the chromosome of the comprising separating an amino acid polymer comprising are mative protein containing a replacement segment or segments of foreign amino acid polymer comprising are manimo acid polymer comprising are manimo acid polymer comprising are manimo acid polymer comprising are manimo acid polymer comprising are protein containing a replacement segment or segments of foreign amino CC enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is cystem the heterologous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to vaccine, the carrier fimbrial subunit proteins are usually strong consequence to putify in large amount. The present seguence is given in expensive to purify in large amount. The present seguence is given in
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Best Local (
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                                                             ĠGTTTŤĠGCAAĊAAĊĠĊĊAĊĠĠĊŤAAĊĊAĠŤAŤŤAA 456
                                                                                                             AATAACGCCGCGCGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                                                                              AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTGACCCGTGTTGTTACCCCATGAAATG 420
                                                                                                                                                                                    GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
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DNA;
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86.2%; Pred. No. 1.3e
tive 0; Mismatches
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Best Local S
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Escherichia coli.
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           The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEP17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombination of the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene back into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of the native copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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P-PSDB; AAB36353.
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Synthetic.

Escherichia

coli.

WO200060102-A2

Salmonella enteritidis.

Salmonella; agf/ vaccine; immune

agfA;

chromosomal gene replacement; fimbrin; epitope;

response;

AgfA::PT3#3 26-FEB-2001

DNA sequence SEQ

ID NO:15

(first entry)

AAC64624

standard; DNA; 456

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a recombinant agfA gene (I) where a CC sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEP17/TAP) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA. CsgA and AgfA-homologue fimbriae (SEP17/TAP) nucleation depended CC AgfA. CsgA and AgfA-homologue fimbria subunits, respectively; (2) the chromologue species; (3) directing recombinant gene into the chromosome of the back into the chromosome of the homologues species, replacing the native comprising separating an amino acid polymer comprising a recombinant of a recombinant of a recombinant or protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or polymer into the expression of recombinant hafA protein which is useful for the expression of recombinant hafA protein which is useful for setul, then the homologues and introducing the cliciting an immune response in an animal. To a fimbrial presentation of setulation of setulation with a carrier or diluent. (I) is cliciting an immune response in an animal. In a fimbrial presentation of setulations are presented in high numbers (up to combine the heterologous antigens are presented in high numbers (up to combine the carrier fimbrial subunit protein sare usually strong companist the inserted epitope, and hybrid fimbriae are usually strong consequence in a present sequence in segment or sequence in the exemplification of the present invention
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85.7%;
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Pred. No. 1.5e-103
0; Mismatches 65
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CC The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC (1) use of thin aggregative fimbriae (SEF17/TAP) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) firecting recombination of a recombinant gene into the chromosome of the back into the chromosome of the homologous species, (3) directing recombinant gene into the chromosome of the back into the chromosome of the homologus species, replacing the native comprising separating an amino acid polymer comprising a recombinant of a recombinant agene CC comprising separating an amino acid polymer comprising a recombinant of segment or segments of foreign amino CC Enterobacteriaceae host cell, from the host cell and introducing the CC acid sequence or sequences grown on a Salmonella, E. coli or CC polymer into the animal in conjunction with a carrier or diluent. (I) is CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to 100,000 copies/cell), the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live immunogens, which may be important for directing an immune response
                                RESULT 11
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RESULT 12
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Escherichia coli.
  WPI; 2000-672631/65
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                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
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                                                 White AP,
                                                                                                        (UYVI-) UNIV VICTORIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCGATGCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
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                                              Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence SEQ ID NO:21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                         99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.8%;
85.5%;
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                                                    Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0:
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Pred. No. 4.8e-103;
0; Mismatches 66;
                                                 SK,
                                                 Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456
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P-PSDB; AAB36351

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Page 137; 139pp; English.

CC The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) CC directing recombination of a recombination of a recombination of a recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC comprising a replacement segment or segments of foreign amino CC comprising a replacement segment or segments of foreign amino CC comprising an animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for System the heterologous antigens are presented in high numbers (up to CC system the heterologous antigens are presented in high numbers (up to CC system the heterologous antigens are presented in high numbers (up to CC system the heterologous antigens are presented in high numbers (up to CC system the heterologous antigens are presented in high numbers (up to CC system the heterologous antigens are presented in high numbers (up to CC system the heterologous antigens are presented in high numbers (up to CC system the heterologous antigens).

Sequence 456 BP; 112 A; 113 C; 125 G; 106 T; 0 U; 0 Other;

Ş 밁 S 멍 5 밁 δ 문 ð 밁 Ş 밁 Ś S 밁 Matches Query Match Best Local Similarity 361 301 301 241 241 181 181 121 121 390; 61 61 ۲ GCACATGCAAACCAACGCCACGGCTAACCAGTATTAA 456 AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120 GCACATGCAGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT GTAGGCCAGGGTGCGGATAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT Conservative 76.8**%**; 85.5**%**; 0 Score 350.4; DB 3; Pred. No. 4.8e-103; Mismatches Indels 456; <u>,</u> 420 420 360 300 240 180 120 60

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RESULT 13

ADC64631

ID AC640

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XX AC640

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XX WO200

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XX O5-AP

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PR WPI;

PR WPI;

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                                                                                                                                                                                                                                                                                                                                    CC Agfa, CsgA and Agfa-homologue fimbrin subunits, respectively; (2)
Cd directing recombination of a recombinant gene into the chromosome of the CC back into the chromosome of the CC back into the chromosome of the CC copy of that gene; and (4) eliciting recombination of a recombinant gene CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant Agfa acid sequence or sequences grown on a salmonella, E. coli or polymer into the animal in conjunction with a carrier or diluent. (I) is CC polymer into the expression of recombinant Agfa protein which is useful for the expression of recombinant Agfa protein which is useful for System the heterologous antigens are presented in high numbers (up to 1900,000 copies/cell), the hybrid fimbrin protein possesses both the CC vaccine, the carrier fimbrial subunit proteins are usually strong communacens. Which may be important for directing an immune response
                                                                                                         Matches
                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                       Sequence 456 BP; 113 A; 110 C; 124 G; 109 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                     immunogens, which may be important for directing an immune ragainst the inserted epitope, and hybrid fimbriae are easy a inexpensive to purify in large amount. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 138; 139pp; English.
                                                                                                                                 Local
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Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella; agfA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC64631 standard; DNA; 456
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                                                                                                                                                                                                                                                         exemplification of the present
                                                                                                                        Similarity
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                                                                                             Conservative
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85.1%;
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                                                                                          0;
                                                                              Score 347.2; DB 3;
Pred. No. 5.3e-102;
0; Mismatches 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID NO:29.
                                                                                                                                                                                                                                                      invention
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                                                                                                                                                                                                                                                                                                directing an immune response id fimbriae are easy and
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1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60

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26-JUN-1995
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                                                                                                                                                                   note= "TAF6 primer
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                                                                                                                                                                                                                                                         note= "TAF5 primer (pair with TAF6)"
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/note= "AgfA"
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                                                                                                                "TAF4 primer (pair with TAF3)"
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Best Local
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(KING/)
                  primer_bind
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30-SEP-1997
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                                                                                                Enteropathogenic bacteria;
                                                                                                                                                                     AAT74141;
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                                                                                                                  enteritidis 27655-3b TnphoA mutant agfA gene fragment
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(first en
               /label= agfA_gene_fragment
16. 60
/label= Primer_TAF5
                                                          Location/Qualifiers
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The present sequence represents an isolated agfA gene fragment derived from Salmonella enteritidis 27655-3b TnphoA mutant strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can nucleic acid sequence can be used to provide probes or primers which can selficially hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 361 BP; 94 A; 93 C; 94 G; 80 T; 0 U; 0 Other;
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                                                                                ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAAT
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Result
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

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                    Sequence 58, Appl
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US-09-103-840A-1 US-09-103-840A-1 US-09-103-840A-1 US-09-134-000C-1704 US-09-489-039A-2162 US-09-489-039A-2162 US-09-252-991A-4506 US-09-252-991A-473 US-08-565-386-1 US-09-252-991A-4473 US-09-252-991A-4473 US-07-751-891B-24 US-07-751-891B-23 US-07-751-891B-23 US-07-751-891B-23 US-07-751-891B-23 US-07-751-891B-23 US-07-751-891B-23

ALIGNMENTS

## ; NAME/KEY: ; LOCATION: US-08-233-788A-58 RESULT 1 US-08-233-788A-58 STREET: 6300 Columbia Center, 701 Fifth Aver CITY: Seattle STATE: Washington COUNTRY: U.S.A. ZIP: 98104-7092 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1. CURRENT APPLICATION NATA: APPLICATION NUMBER: US/08/233,788A FILING DATE: 26-APR-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: King, Joshua REGISTRATION NUMBER: 35,570 REFERENCE/DOCKET NUMBER: 920043.403C2 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: Sequence 58, Application Patent No. 5635617 TELEPHONE: (206) 622-4900 TELEFAX: (206) 682-6031 TELEX: 3723936 SEEDANBERRY INFORMATION FOR SEQ ID NO: 58: GENERAL INFORMATION: SEQUENCE CHARACTERISTICS: LENGTH: 456 base pairs TYPE: nucleic acid STRANDEDNESS: single FEATURE: CORRESPONDENCE ADDRESS: ADDRESSEE: Seed and Berry STREET: 6300 Columbia Center, 701 Fifth Avenue APPLICANT: Doran, James L. APPLICANT: Kay, William W. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Clouthier, Sharon C. TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION TITLE OF INVENTION: OF SALMONELLA NUMBER OF SEQUENCES: 61 TOPOLOGY: linear US/08233788A #1.25

Query Match Best Local Similarity Matches 424; Conserv

Conservative

0

Score 404.8; DB 1; Pred. No. 4.5e-131; 0; Mismatches 32;

Indels Length 456;

0;

Gaps

0

88.8**%**; 93.0**%**;

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61

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENT Release #1.0, Version #1.
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 920043.403C2
TELECOMPUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: 37.23836 SEEDANBERRY
SEQUENCE TARACTERISTICS: 56:
LENGTH: 31 base Paice.
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GENERAL INFORMATION:
APPLICANT: DOTAN, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION INTERESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 56, Application US/08233788A Patent No. 5635617
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US-09-120-927-1/c
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,108
FILING DATE: 06-AUG-1977
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1581
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09120927
Patent No. 6262018
GENERAL INFORMATION:
APPLICANT: Kim, Jihyun Francis
APPLICANT: Beer, Steven V.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR FROM NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 69.1%;
Best Local Similarity 99.1%;
Matches 317; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: P.O. Box 1051, Clinton Square CITY: Rochester STATE: New York COUNTRY: U.S.A.
ZIP. 1460.
                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: CDS
LOCATION: 1..357
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 AACGCCGCGCTGGTTAATTA 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GÁTGCCCGTAÁATCTGAAÁCGACCATTÁCCCAGÁGCGTTÁTGGTÁÁCGGCGCCGÁTGTÁ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC 183
                                                                                                                                                                                                                                                                                                                                       14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GICGTICCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTICCGGCCCG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAAT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ĠŔĊŦĊŔŔĊĠŦŤĠŔĠĊŔŦŤŦŔŤĊŔĠŦŔĊĠĠŦŦĊĊĠĊŤŔŔĊĠĊŤĠĊĠĊŤŦĠĊŦĊŦĠĊŔĸŔĠĊ
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Pred. No. 6.5e-100;
0; Mismatches 3;
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RESULT 2 US-08-233-788A-56

STATE: W STREET: 6300 (CITY: Seattle

Washington Y: U.S.A.

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RESULT 5
US-09-125-619-3
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; ORGANISM: Erwinia amylovora
US-09-431-614-5
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Matches
Sequence 3, Application US/09125619
Patent No. 6437116
GENERAL INFORMATION:
APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 5
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Best Local Similarity 54.9%;
Matches 67; Conservative
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APPLICANT: Schading, Richard L.
APPLICANT: Schading, Richard L.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
TITLE OF INVENTION: RESISTANCE
FILE REFERENCE: 21829/41 (EBC-003)
CURRENT APPLICATION NUMBER: US/09/431,614
CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 60/107,243
EARLIER FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (716) 263-1600 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 1344
                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 7.5%;
Local Similarity 54.9%;
les 67; Conservative
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STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
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                                                                                                                                                                                                                                                                                                                                                209 GCTCCGGTTGCCGCATTACCTGATTGTGGCGATAGCAGTGACTTTAACAGTTCCGCCAAT 150
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                                                                                                                                                                                                                                                                      149 AATTGAGCCATTTGCTCAATGGTTTGCCGATCGATGGGTTGTTGCCCCAACGCAGAATTT
                                                                                                                                                                                                                                                                                                        112 AGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149 AATTGAGCCATTTGCTCAATGGTTTGCCGATCGATGGGTTGTTGCCCCCAACGCAGAATTT
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                                                                                                                                                                                     89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
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Pred. No. 0.13;
0; Mismatches
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; ORGANISM: Homo sapiens
US-09-220-132-30
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                                                                                                                                                                                                                                  SOFTWARE: Fast
SEQ ID NO 30
LENGTH: 14770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWALL SEQ ID NO 3
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APPLICANT: WEINSTOCK, GEORGE M.

TITLE OF INVENTION: WPP-LIKE SEQUENCES OF PATHOGENIC BORRELIA FILE REFERENCE: UTSH:234

CURRENT APPLICATION NUMBER: US/09/125,619

CURRENT FILING DATE: 1999-01-27

NUMBER OF SEQ ID NOS: 48

SOFTWARE: Patentin Vary

SEO TN NO.
                                                                                 Query Match 7.3%;
Best Local Similarity 48.7%;
Matches 91; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/220,132
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Borrelia burgdorferi
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 47.4%;
10282 GGATCTGGAAAAGATAATGAATTTGGCCTTGGCCTTGATTCACCTCAGAATGAAATTGCC 10341
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                                        220 GGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 GCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTGCTGTGAAGAGTAATGATGGTGAGAAAG 4642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09220132
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                                                                                 Score 33.4; DB 4; Length 14770;
Pred. No. 0.8;
0; Mismatches 96; Indels 0;
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OF PROSTATE CANCE
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280 CAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAAACTCCGATATT 339

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RESULT 8
5486473-3/c
;Patent No. 5486473
; Patent No. 5486473
; APPLICANT: FUKITA, HIROYUKI;YOSHIDA,
;MANABE, SADAO;FUKAI, KONOSUKE
; TITLE OF INVENTION: A DNA CODING FO.
; NUMBER OF SEQUENCES; 16
; CURRENT APPLICATION DATA;
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                                                                                                                                               5486473-3
                                                                                               Query Match
Best Local S
                                                                                                                                                                              SEQ ID NO:3:
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Best Local Similarity 61.2%;
Matches 52; Conservative
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LENGTH: 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/(FILING DATE: 09-FEB-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709_2004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                             LENGTH: 1491
                                                                                                                                                                                                APPLICATION NUMBER: 279,685
FILING DATE: 05-DEC-1988
APPLICATION NUMBER: 932,419
                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                            APPLICATION NUMBER: 809,255 FILING DATE: 18-DEC-1991
                        178 CAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1007 AGCACCGGACCGATAAACAGGCCGATCATGCCGAAGGCGATCAGGCCGCCAATGACGCCG
                                                                                   78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      947 GTGAĞĞATAAGGATCATTGĞÇAĞĞT 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 CGCTGGTTAATTATGATCAGCTGGT 395
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                                                                           Similarity 50.0
78; Conservative
CAAGTCACTGACCGAAGCTAAGTAACAGTAACTGCGCACATCTGCGAGGTTGGCTGCTTC 145
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                                                                                                                                                                                      19-NOV-1986
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                                                                                        50.0%;
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                                                                   Score 31.2; DB Pred. No. 1.3; 0; Mismatches
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Pred. No. 0.49;
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                                                                                                  DB 6;
                                                                78;
                                                                                             Length 1491;
                                                                 Indels
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Score Pred.

31.2; No. 11;

DB 4;

Length 65792;

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US-09-596-002-31
                                                                                                                                                         SOFTWARE:
SEQ ID NO 31
LENGTH: 65792
Query Match
Best Local Similarity
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Sequence 492, Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR!

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-540-236-492
                                                          NAME/KEY: misc feature
OTHER INFORMATION: Incyte
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   Sequence 31, Application US/09596002
Patent No. 6632636
                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 88
                                                                                                                                                                                           PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-(
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                 FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
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                                                                                                                     ORGANISM: M. catarrhalis
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: N
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                                                                                                                                            TYPE: DNA
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SEQ ID NO 492
LENGTH: 2436
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CURRENT FILING DATE: 2000-04-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269 TTGA---ACTGACTCAGAATGGTTTCAGAAATBATGCCACCATCGACCAGTGGAACGCTA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 TTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
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                                                                                                                                                                                                                                                                                                                 Patterson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 53.7
88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
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                                                                                                                                                                                PERL Program
                                                                                                                                                                                                                                                                                                                                   Lagace,
                                                                                                                                                                                                                1999-06-18
                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
6.8%;
53.7%;
                                                                                                                                                                                                                                                                                                                  Chandra
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53.7%;
                                                                       template ID No.
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                                                                      6632636
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US-08-508-761B-1
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Query Match
Best Local Similarity
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Patent No. 6027
                                                                                                                                                                                                                                           TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2547 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/508,761
FILING DATE: 31-UUL-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: FR 91/09652
FILING DATE: 29-UUL-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P58525NA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FR 9
FILING DATE: 02-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                   FEATURE:
                                                                                                                                 ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                              MOLECULE TYPE:
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                                                                NAME/KEY:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                  ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                               NAME: Player, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                  Corynebacterium Melassecola
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 6.8%;
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   Score 30.8; DB Pred. No. 2.4;
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               Length 2547;
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US-09-103-840A-1/c
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US-09-103-840A-2/c
                        CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VA-
TEO IT NO
                                                                                                                                                                                                                                              Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
                  SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Patent No. 6294328
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                                                                                                            APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
                                                                                                                                                                                                          APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
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SOFTWARE: Patentin Ver
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CURRENT APPLICATION NUMBER: US/09/103,840A
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TITLE OF INVENTION: DNA SEQUENCES
TITLE OF INVENTION: TUBERCULOSIS
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APPLICANT: WHITE, OWER R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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4411529
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                                                                                                                                                                                                        WHITE, Owen R.
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Pred. No. 95;
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RESULT 15
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                                                                                                                    Sequence 10904, Appl
Patent No. 6551795
GENERAL INFORMATION:
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Matches
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Best Local Similarity
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09350756 Patent No. 6495143
                                                          APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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APPLICANT: Michael F. Smith
APPLICANT: Wark T. Dertzbaugh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                             390 GCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAACAACGCCACGGCTAAC 447
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nilarity 53.4%;
Conservative (
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Pred. No. 95;
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Search completed: March 16, 2004, 04:37:19 Job time: 63.6647 secs
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-10904
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LENGTH: 1008
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PRIOR TILING DATE: 198-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                             Local
                                                                                                        101
                                                                                                                                     141 TGTATGCCTGGTCGGTGACCGAGGGCGTGCAGCGCCTGGGCTTCGGCGGCGAGCCGCTGG
                                                                   201 GCGGGGAGGAGCCGCGACCCGGTCGCGCGTTGCGCTTGATCAAGCACGAT 253
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61; Conserv
                                                                                                    GCGGCGGCAATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGT
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54.0%;
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Pred. No. 3
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     Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NBW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NBW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NBW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

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18: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

17: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*

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US-10-441-736-5
9 US-09-801-368-131
15 US-10-398-221-3563
14 US-10-292-798-1569
12 US-10-222-566-3
14 US-10-222-162-3
14 US-10-222-162-3
15 US-10-232-367C-230
15 US-10-045-674-593
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US-09-835-684-6
US-09-880-371-6
US-09-879-248-5
Sequence 88945, A
Sequence 6, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 131, App
Sequence 131, App
Sequence 1913, Ap
Sequence 1563, Ap
Sequence 1563, Ap
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 30, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 330, App
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654 829 1203	1024 1601042	392 992	75216	2301	1164	2699	725 2050	715	525	2394	1245	840	6003	52101	24081	978	1776	4830	1110	972	568	9025608	1662
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US-10-425-114-28546 US-10-027-632-164999 US-09-738-626-3184	US-10-323-069A-111 US-10-027-632-59064	US-10-282-122A-25231 US-10-425-114-31747	US-10-080-170-646	US-09-815-242-4844	US-10-282-122A-13500	US-10-260-238-418	US-09-919-580-878	US-10-424-599-10132	US-09-918-995-32144	US-10-282-122A-26837	US-10-369-493-40803	US-10-282-122A-31900	US-10-010-901-9	US-10-132-134-1	US-10-132-134-13	US-10-369-493-24265	US-10-282-122A-24385	US-10-282-122A-27869	US-10-282-122A-23637	US-10-333-631-4	US-10-333-631-1	US-10-156-761-1	US-10-156-761-3483
Sequence 28546, A Sequence 164999, Sequence 3184, Ap	w	31747	Sequence 546, App	Sequence 4844, Ap		Sequence 418, App	Sequence 878, App	Sequence 10132, A	32144,		Sequence 40803, A		9	۳			24385,		23	4.	Sequence 1, Appli	Sequence 1, Appli	Sequence 3483, Ap

## ALIGNMENTS

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RESULT 1
US-10-424-599-88945/c
US-10-424-599-88945/c
Sequence 88945, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NO 88945
LENGTH: 616
TYPE: NUMBER
TUBER OF SEQ ID NOS: 285684
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Best Local Similarity 50.9%;
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LOCATION: (1)..(616)
OTHER INFORMATION: unsure at all n locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                              161
                                                                                                                                               101 GCGGCGGCAATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTA 160
                                                                                             GGGCCCACAAGGGTAACGCCCCTGAATCCACGCCGGGTCCATGTGTGGATGATGATGTTG 497
ATGATGGTGATGATGAGGATGATGAGGCATGGGAGGTGGCACCGAAGGATAGTAACCGGG
                                            ACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCG
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                         Score 34.2; DB 12; Length 616; Pred. No. 0.51; 0; Mismatches 78; Indels 0
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SEQ ID NO 6
LENGTH: 1344
TYPE: DNA
ORGANISM: Erwinia amylovora
US-09-880-371-6
                   Query Match
Best Local Similarity 54.9%;
Matches 67; Conservative
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                                                                                                                                                        APPLICANT: Wei, Zhong-Min
APPLICANT: Wei, Zhong-Min
APPLICANT: DeRocher, Jay
TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC
TITLE OF INVENTION: PLANTS
TITLE OF INVENTION: PLANTS
CURRENT EFFERICE: 21829/91
CURRENT APPLICATION NUMBER: US/09/880,371
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,585
NUMBER OF SEQ ID NOS: 16
SOFTMARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09880371 Patent No. US20020059658A1
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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US-09-835-684-6
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US-09-835-684-6/c

/ Sequence 6, Application US/09835684
/ Patent No. US20020019337A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.5%;
Best Local Similarity 54.9%;
Matches 67; Conservative
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PRIOR PLING DATE: 2000-04-16
PRIOR FLING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
LENGTH: 1344
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wei, Zhong-Min
APPLICANT: Qiu, Dewen
APPLICANT: Qiu, Dewen
APPLICANT: Remick, Dean
TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE
TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR
FILE REFERENCE: 21829/71
CURRENT APPLICATION NUMBER: US/09/835,684
CURRENT FILING DATE: 2001-04-16
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89 GC 88
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                     0,
          Score 34; DB 9;
Pred. No. 0.93;
0; Mismatches 5
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Pred. No. 0.93;
0; Mismatches 55; Indels
         55; Indels
                                      Length 1344;
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     0;
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GENERAL INFORMATION:

APPLICANT: Wei, Zhong-Min

APPLICANT: Wei, Zhong-Min

APPLICANT: Wei, Zhong-Min

APPLICANT: Leon, Ernesto

APPLICANT: Oviedo, Agustin

ITILE OF INVENTION: METHODS OF INHIBITING DESICCATION OF CUTTINGS REMOVED

FILE REFERENCE: 21829/11

CURRENT APPLICATION NUMBER: US/10/010,390

PRIOR APPLICATION NUMBER: US/10/010,390

PRIOR APPLICATION NUMBER: 60/248,169

PRIOR APPLICATION NUMBER: 60/248,169

RIOR APPLICATION NUMBER: 60/248,169

NUMBER OF SEQ ID NOS: 14

SOFTMARE: Patentin Ver. 2.1

IEMATHER: 1144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Fan, Hao
APPLICANT: Wei, Zhong-Min
ITILE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS AND USE
ITILE OF INVENTION: THEREOF
ITILE OF INVENTION: THEREOF
ITILE OF INVENTION: THEREOF
ITILE OF INVENTION: THEREOF
ITILE OF INVENTION: THEREOF
ITILE OF INVENTION: THEREOF
ITILE OF INVENTION: US/09/879,248
ITILE REFERENCE: 2.1829/91
ICURRENT FILING DATE: 2001-06-12
INUMBER OF SEQ ID NOS: 18
ISOFTWARE: PATENTIN Ver. 2.1
ISEQ ID NO 5
ILENGTH: 1344
ITYE: DNA
INCRANIESM: Erwinia amylovora
US-09-879-248-5
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-10-010-390-6/c
                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/10010390 Publication No. US20030104979A1
ORGANISM: Erwinia amylovora
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US-09-879-248-5/c
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Patent No. US20020062500A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 GC 173
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US-10-010-390-6

Matches Query Match

67;

Conservative

Local

Similarity

7.5%;

; Score 34; DB; ; Pred. No. 0.93 0; Mismatches

0.93,

55;

Indels

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150

90 171 DB 14; Length 1344;

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US-09-801-368-131
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; ORGANISM: Erwinia amylovora
US-10-441-736-5
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US-10-441-736-5/c
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                                                            APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
                                                                                                                                                             Sequence 131, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 5
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wei, Zhong-Min
APPLICANT: Wei, Zhong-Min
APPLICANT: Schading, Richard L.
APPLICANT: Schading, Richard L.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
TITLE OF INVENTION: RESISTANCE
FILE REPERENCE: 21829/203 (EBC-003)
CURRENT APPLICATION NUMBER: US/10/441,736
CURRENT APPLICATION NUMBER: 60/107,243
PRIOR APPLICATION NUMBER: 60/107,243
PRIOR APPLICATION NUMBER: 60/107,243
PRIOR PILING DATE: 1998-11-05
PRIOR PILING DATE: 1998-11-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/431,614
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     match 7.5%;
Local Similarity 54.9%;
es 67; Conservative
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                                                        Hecht, Peter
Holtzman, Doug
Madden, Kevin
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Milne, Todd
No. US20020128250Alman, Thea
                                    Maxon,
                   Mary
Todd
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Pred. No. 0.93;
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                                                                                                                                                       US-10-398-221-3563
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome an
FILE REFERENCE: 344 702 US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
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                                                                                                                                                                                                                                                                                            SEQ ID NO 3563
LENGTH: 2751
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Publication No. US20040018514A1
GENERAL INFORMATION:
                                                                            Matches
                                                                                                                Query Match
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APPLICANT:
APPLICANT:
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SOFTWARE: PatentIn version 3.0
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CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
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                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: (1)..(end)
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                                                                                                                                                                        OTHER INFORMATION: n can be any nucleotide: a,g,c
                                                                                                                                                                                                                                                      ORGANISM: Listeria monocytogenes
                                                                                                                                                                                                                                                                             TYPE: DNA
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Local Similarity 50.6%;
nes 82; Conservative
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                                     238 GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT 297
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  321 GATGTAGTGAAAGAAGCGAAAAATATTACTATCGACAAACCGTTTCCTCGTATGACATAT 380
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Silva, Jeff
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Pred. No. 1.4;
0; Mismatches
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Pred. No. 1
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US-10-292-798-1569
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                                                                                                                   Sequence 1569, Application US/10292798 Publication No. US20030235833A1 GENERAL INFORMATION:
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APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
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Best Local Similarity
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SEQ ID NO 1913
LENGTH: 3532
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Publication No. US20030143668A1
GENERAL INFORMATION:
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APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
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PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
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APPLICANT: ASAI, KIYOSI
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NAME/KEY: source
LOCATION: (1)..(3532)
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LOCATION: (201)..(437)
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RESULT 11
US-10-222-566-3
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SEQ ID NO 3
LENGTH: 7766
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US-10-292-798-1569
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                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/125,619
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234USD3
CURRENT APPLICATION NUMBER: US/10/222,566
CURRENT FILING DATE: 2002-08-16
DETON AND INVENTED CO.
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Best Local Similarity
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LOCATION: (127)
OTHER INFORMATION: R = A OR
                                  FEATURE: modified_base
                                                                 LENGTH: 7766
TYPE: DNA
ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: NORRIS,
APPLICANT: JING-R
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CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: UP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
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LOCATION: (201)..(437)
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HARDHAM, JOHN M.
HOWELL, JERRILYN K.
BARBOUR, ALAN G.
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Pred. No. 2.2;
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Best Local Similarity
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APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HARDHAM, JERRILYN K.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH:234USD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/125,619
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver: 2.1
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CURRENT FILING DATE: 2002-08-16
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ORGANISM: Borrelia burgdorferi
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                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                   217 AGCGGTTATGGTAACGGCGCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTG 276
                                                                                                                                                                                                                                                            157 GCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAG 216
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                                                                                                                                                                                                                         GTTACGGCTGCGGCTGCTGGTGAGCAGGATGGAGAGAGCCTGCAGAGGCTACAAATCCG
                                                                      AAGAAGGATGATCAGATTGCTGCTATTGCTTTGAGGGGGATGGCTAAGGATGGAAAG 4611
                                                                                                         ACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGAT 336
TTTGCTGTGAAGAGTAATGATGGTGAGAAAG 4642
                                   ATTACTGTCGGCCAATACGGCGGTAATAACG 367
                                                                                                                                                ATTGCTGCTGCTATTGGGAAGGGTAATGAGGATGGTGCGGATTTTGGTAAGGATGAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTGCTGCTGCTATTGGGAAGGGTAATGAGGATGGTGCGGATTTTGGTAAGGATGAGATG
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                                                                                                                                                                                                                                                                                                                 7.3%;
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                                                                                                                                                                                                                                                                                               Score 33.4; DB 14;
Pred. No. 4;
0; Mismatches 111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.4;
Pred. No. 4;
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RESULT 13

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US-09-873-367C-230
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 230, Application US/09873367C Publication No. US20030165839A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Publication No. US20030092903A1
                                                        APPLICANT: Carter, Kenneth
ITITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
TITLE OF INVENTION: Signature Gene Sets
FILE REFERENCE: 689290-64
CURRENT APPLICATION NUMBER: US/09/873,367C
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: U.S. 60/236,891
PRIOR APPLICATION NUMBER: U.S. 60/236,892
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: U.S. 60/236,842
PRIOR APPLICATION NUMBER: U.S. 60/244,867
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Young, Paul APPLICANT: Soppet, Day
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 09/125,619
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
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CURRENT APPLICATION NUMBER: US/10/143,024
CURRENT FILING DATE: 2002-05-10
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APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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les 100; Conserv
FILING DATE: 2000-11-01
APPLICATION NUMBER: U.S
FILING DATE: 2000-11-01
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                                                                                                                                                                                                                                                                                                              Soppet, Daniel
Endress, Gregory
Augustus, Meena
Ebner, Reinhard
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Pred. No. 4;
                     60/245,084
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US-10-045-674-593
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                                                                                              Matches
                                                                                                               Query Match
Best Local S
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SEQ ID NO 593
LENGTH: 1355
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HOUSENBOOM, HENDRICUS R. J. M.
APPLICANT: HOOSENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
TITLE OF INVENTION: LIBRARIES
CURRENT FILE REFERENCE: DYAX/002 CIP2
CURRENT FILING DATE: 2001-10-25
CURRENT FILING DATE: 2001-10-25
CURRENT FILING DATE: 2001-10-25
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 230
LENGTH: 14770
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                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
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                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: M13-III OTHER INFORMATION: nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equence 593, Aublication No.
                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
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                                          78 GGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCGGACTCAACGTTGAG 137
                                                                                                               Similarity 23.9%;
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COHEN, EDWARD H.
NASTRI, HORACIO G.
ROOKEY, KRISTIN L.
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                                                                                           Conservative
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48.7%; Pred. No. 5.7;
ative 0; Mismatches
                                                                                     7.3%; Score 33.2; DB 15;
23.9%; Pred. No. 1.8;
ive 91; Mismatches 174;
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                                                                                                                             Length 1355;
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                                                378 TAATTATGATCAGCTGGTTACCCGTGTTACCCATGAAATGGCACA 425
                                                                                                                                                    318 GAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCGCTGGT 377
                                                                                                                                                                                                    948 RYTWGAYWSYGTCGCYACWGAYTAYGGTGCTGCYATCGAYGGYTTYATYGGYGAYGTYWS 1007
                                                                                                                                                                                                                                                     258 TAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTG 317
                                                                                                                                                                                                                                                                                                                                                         198 TGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGA 257
                                                                                                                                                                                                                                                                                                                                                                                                    828 YGGYMSYGGRGYYGSYGGYMSYGGYGAYTTYGAYTAYGARAAATGGCWAAYGCYAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 САТТТАТСАGТАСĢĢТТССĢСТААСĢСТĢСGСŢТĢСТСТGСĀAĀGCGATĢСССGТАААТС
YCARGTYGGWGAYGGKGAYAAYWSWCCKYTWATGAAYAAYTTYMGWCA 1115
                                                                                                                                                                                                                                                                                                        YAARGGSGCYATGACYGARAAYGCYGAYGARAAYGCRCTRCARWSTGAYGCYAARGGYAA 947
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Search completed: March 17, 2004, 08:15:44
Job time: 407.736 secs

0 0 0 0

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Minimum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB seq
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length: 2000000000
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456
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em_gss_rod:*
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ВJ333958 ВJ333958	BJ333958	12	547	7.2	33	45
BJ367372 BJ367372	673	12	524		. 33	44
BJ331339 BJ331339	3133	12	456		33	43
912	791	10	1646		ω	42
321	932	9	788	•	ω	41
149	5	28	675	•	Ψ	40
AU295325 AU295325	5325	ø	629	7.3	ω	39
2975	G0729	29	592	•	Ψ	38
8900	9006	28	589	•	ü	37
378	245878	28	1026	•	ω	36
CD456845 Fg05 03nl	t m	14	856	7.3	33.4	35
BH578402 BOHNV61TF	840	28	853		·	ω 4
BH575194 BOHJO27TF	7519	28	835		ω ·	ω G
BH715216 BOMIM42TR	1521	28	830	7.3	Ü	32
BH438448 BOGVQ28TR	844	28	827		ω.	31
BH461716 BOHIV03TR	BH461716	28	815	7.3	ω.	30
BH578793 BOGLY20TR	879	28	785	•	ω.	29
BU444683 603765715	468	13	715	7.3	ω.	28
BH690914 BOHXR64TF	9091	28	709		ω.	27
BH651371 BOHXV71TF	5137	28	700	•	ω.	26
BI959328 HVSMEn001	5932	12	699		ω	25
BH663951 BOMBL85TR	6395	28	695	7.3	w ·	24
CC961526 BOIGS10TF	6152	29	679		ω.	23
BX506928 DKFZp7791	0692	13	664	•	u.	22
CB578319 AMGNNUC:N	CB578319	14	624	7.3	ω.	21
iticum	9250	σ	505	•	ω.	20
37982 EST67	798	14	712	٠	ω.	19
BJ336964 BJ336964	BJ336964	12	653		w	18
35653 BJ335	565	12	594		u.	17
6219 BY236219	621	13	374		·	16
196666 Tetraodo	ဂ္ဂ	29	1098		w ·	15
8280 PUJDF79T	828	29	941		w ·	14
637195 RPCI-11-	AQ637195	28	695	٠	w	13
65156 sas23f1	76515	13	559	٠	ü	12
7442	744	14	558	•	Ψ	11
4647	AA746477	9	365		w	10
058630	8630	9	296		ω	9
Z46900	46900	28	811	•	34	æ
1147	A7114	14	500	7.5	34	7
581	BB581987	10	234	7.5		σ
7 DRNBUBO	715	12	ū	7.5		5

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## ALIGNMENTS

TITLE JOURNAL COMMENT REFERENCE AUTHORS VERSION KEYWORDS RESULT 1 BJ618688/c LOCUS SOURCE ORGANISM ACCESSION DEFINITION Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available the Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 680)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Expressed genes in X. laevis embryo Unpublished (2001) EST BJ618688 MIBB Mochii normalized Xenopus early gastrula library Xenopus laevis cDNA clone XL186b22 5', mRNA sequence.
BJ618688 BJ618688.1 GI:37256713 Kohara,Y Xenopus laevis (African clawed frog) is available through the following EST 01-0CT-2003

Result No.

Score

Query Match

Length

B

SUMMARIES

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216.6 35.2 34.8 34.2

47.5 7.7 7.6 7.5

680 813 801 523

12 28 12

BJ618688 BZ204853 BI648266 BJ334624

BJ618688 BJ618688 BZ204853 CH230-390 BI648266 603278209 BJ334624 BJ334624

Description

FEATURES

Matches

306;

593

61

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Query Match
Best Local Similarity
                                              Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                        Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 Unpublished (1999)
Other_GSSs: CH330-390D21.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 GGCAÁCÓGTGCTGCAÓTTGÁCCAGACTGCATCTAACTCCTCCGTCAACGTGACTCÁGGTT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 ААТААСЯССЯСЯСТВЯТТААТТАТВАТСАВСТВЯТТАСССЯТЯТВЕТТАСССАТВААТВ
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                      BZ204853
BZ204853.1 GI:23862905
                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                  Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                            BZ204853
CH230-390D21.TV CHORI-230 Segment 2 Rattus
CH230-390D21, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTTŤĠGTÁAĊĀĀĊĠĊGĀĊCĠĊŤĊĀTĊĀĠŤĀĊŤĀĀ 138
                                                                                                                                                                                                          (bases 1 to 813)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTÁCTCTTGÁTCÁGTGGÁÁCGGCÁÁÁÁÁTTCTGÁAÁTGÁCGGTTAAACÁGTTCGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTGGTCÁGGGCTCAGÁTGACÁGCTCAÁTCGÁTCTGÁCCCÁACGTGGCTTCGGTÁÁCÁGC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTGÁÍTGCCGGTAACTCTGÁCTTGÁCTÁTTÁCCCAGGCATGGCGGGGGTAÁTGGTGCAGÁT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAPÁTTÓTGAGOTGÁACÁTTTÄCCAGTÁCGGTGGCGGTÁÁCTNTGCACTTGCTCTGCÁÁ 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTGTTGTTCCTCAGTACGGCGGCGGCGGTÁACCACGGTGGTGGCGGTÁATÁATAGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEOGTEGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://xenopus.nibb.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAAACTTTTAAAAGTAGCAGCAATTGCAGCAATCGTATTCTCCGGTAGCCCCTCTGGCA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="whole embryo"
/dev_stage="stage 10.5"
/clone_lib="NIBB Mochii normalized Xenopus early gastrula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus laevis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 216.6; DB
Pred. No. 8e-51;
0; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150; Indels
                                                                                                                                                                                                                                                                                                                                                        norvegicus genomic
                                                                                                                                                  Geer,K.,
Russell,D., Chen,D.,
                                                                                                                       MboI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                   GSS 11-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      680;
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                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                           KEYWORDS
SOURCE
                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
BI648266
                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                            DEFINITION
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deny
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information ca.
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          728
                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 GGТААТААСССС 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                668 AÅGATĆÁAGÁŤĆGÁĆĆÁAŤĠĠGÁTCTCÁTÁÁÁĆŤGĆAÁAGCŤTĆŤĠŤAĠĠĆAÁÁGGACAĆ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             608 TCTGGAACACÁTGGGCACTGGAÁAAAATTCCTGAÁCAAAACACCAÁTGGCTTATGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT
                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         548
                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                               BI648266.1 GI:15562502
                                                                                                                                                                                                                                                                                                                                        603278209F1 NCI_CGAP_Mam3 Mus
                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                          BI648266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTGGTTAGGAC 739
                                                                                                                                                                                                   (bases 1 to 801)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAÁGGACCTCCACATCÁAACCAGÁCACACTCAAÁCTAÁTÁGAAGAAÁAACTÁGGGAAGCA 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
Clones may be purchase contact Pieter de Jong (pdejong@mail.cho.org).
(http://www.chori.org/bacpac/or ering information.htm). BAC end
Plate: 390 row: D column: 21
Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medical Center Dr.,
301 838 0200
301 838 0208
                                                                                                                                                                                               Metazoa, Chordata, Craniata, Vertebrata, Eutheria, Rodentia, Sciurognathi, Muridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Brain"
/clone_ilb="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SsNHed/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.7%;
49.0%;
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Pred. No. 59;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ٥,
                                                                                                                                                                                                                                                                                                                            801 bp mRNA linear EST 12-SEP-2001
3 Mus musculus cDNA clone IMAGE:5318307 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98;
                information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                 Chu-Xia Deng
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                                                                                                                                                                                             Euteleostomi; 
; Murinae; Mus
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REFERENCE AUTHORS

TITLE JOURNAL

SOURCE ORGANISM VERSION KEYWORDS

SSD

ACCESSION DEFINITION RESULT 2 BZ204853

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293

413 181

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REFERENCE
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KEYWORDS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 AACTCCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGTTAATTATGAT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210 TACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTAT 269
                                                                                                                                                                                               Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                    Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

(bases 1 to 523)

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostelium discoideum at the aggregation
                                                                                                                                                                                                                                                                                                                                                                                                       Dictyostelium discoideum Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BJ334624 523 bp mRNA linear EST 05-MAR-24BJ334624 Dictyostelium discoideum cDNA library, AF Dictyostelium discoideum cDNA clone dda47o06 5', mRNA sequence.
                                                                                                                                                                                                                                                                             Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BJ334624.1 GI:19164754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: LLAM11807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACGCCACCTCGGACAATGGCAAAGACGGCCTGGCCTACTCCGCACTGCTGAAGAATGAG
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81-559-81-6855
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                                                                                                                    tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="tumor, gross tissue"
/dev stage="10 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam3"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Notl; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999)."
/db_xref="taxon:44689"
/clone="dda47o06"
                                      Btrain="AX4"
                                                                          organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:5318307"
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50.0%;
                                                         _type="mRNA"
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Pred. No. 76;
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BG671547
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MEDLINE
                Best Local
                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60;
Similarity 49.
90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech
Pudong New Area, P.R.China. Please contact with Zhang Xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031,
Tel: 86-21-64748700-121
Fax: 86-21-64713446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xiao,H.S., Huang,Q.H., Zhang,F.X., Bao,L., Lu,Y.J., Guo,C., Yang,L., Huang,W.J., Fu,G., Xu,S.H., Cheng,X.P., Yan,Q., Zhu,Z.D., Zhang,X., Chen,Z., Han,Z.G. and Zhang,X. Identification of gene expression profile of dorsal root ganglion in the rat peripheral axotomy model of neuropathic pain Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG671547 1036 bp mRNA linear EST 30-APR-2001 DRNBUB05 Rat DRG Library Rattus norvegicus cDNA clone DRNBUB05 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG671547.1 GI:13893646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BG671547
                                                                                                                                                                                                                                                                                                                                                            BACKWARD:
                                                                                                                                                                                                                                                                                                                                                                                   FORWARD: T3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus
                                                                                                                                                                                                                                                                                                                                                                                                    PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                           xu.zhang@ion.ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGAAGATGAATTGGAGAATAGATATATTGGAATCAATAGAAATGANGACAATAAT
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                                                                                                                                                                                                                                                                                                                                       primer: T3
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                                                                                            /tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat_DRG_Library"
                                                                                                                                                                                               /organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="Aggregation stage"
/clone_lib="Dictyostelium discoideum cDNA library,
                                                                                                                                                         sex="male"
                                                                                                                                                                            clone="DRNBUB05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="mat A"
                7.5%;
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57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                       .cn) or Han Zeguang (hanzg@chgc.sh.cn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
Score 34.2; DB 12;
Pred. No. 1.3e+02;
0; Mismatches 93;
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Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                     DB 12; Length 1036;
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BB581987/c
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                                                                                                                       source
                                                                                                                                                                                                 Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh.M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
trehalose and its application for the synthesis of full length
cDNA, Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Tomaru,Y., Carninci,P., Shibata,Y., Diabata,M., Kawai,J.,
Okazaki,Y. and Hayashizaki,Y., Ozawa,Y., Muramatsu,M.,
Automated filtration-based high-throughput plasmid preparation
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognathi, Writebrata; Euteleostomi; CE 1 (bases 1 to 234)

RS Aizawa,K., Akahira,S., Akimura,T., Arai,A., Arakawa,T., Carninci,P., Hanagaki,T., Hayatsu,N., Hiraoka,T., Hirozane,T., Hodoyama,Y., Tmotani,K., Ishii,Y., Itoh,M., Izawa,M., Kawai,J., Kojima,Y., Konno,H., Kusakabe,M., Matsuyama,T., Miyazaki,A., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Okazaki,Y., Okido,T., Owa,C., Sakai,C., Sakai,K., Sasaki,D., Sato,K., Shibata,Y., Shibata,Y., Shibata,Y., Shibata,Y., Shibata,Y., Takahashi,F., Tanaka,T., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A., Farka, Y., Shibata,Y., Takahashi,F., Tanaka,T., Toya,T., Watahiki,A., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshiki,A., RIEN Mouse ESTS (Aizawa,K. et al. 2000)

L Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
                                                                                                                                                                Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB581987 RIKEN full-length enriched, adult male cDNA clone 9030005005 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGTTGAGCATTTATCAGTACGGTTCCGGTAACGCTGCGCTTGCTCTGCAAAGCGATGCCC 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACAATGGGGCGGCGGCGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCGGACTCAA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTAGGAGTCCTCGCTGGTAACGATGCCGAGAGTGCACATCGATATCGGTGGGCGGTTA 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="9030005005"
                                                                       /organism≈"Mus musculus"
/mol_type="mRNA"
                                                                                                                                   Location/Qualifiers
                                                                  _type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yokohama, Kanagawa 230-0045, Japan
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AUTHORS
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CA711477/c
LOCUS
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140 CGAACGCCGGGTGCTTTATAGCCTTGTTCAAAATATGGTAGCGCATTTACCACCACCTTT
                                                                                                                                               E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 ATAACGGCGGCGAATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTT 154
                                                                                                                                                                                                                                                 Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                 Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,N. and Hanafey,M.K.
                                                                                                        Seq primer: M13.
                                                                                                                                                                                                                             Crop Genetics
                                                                                                                                                                                                                                                                         DuPont Wheat cDNA Sequence Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA711477.1 GI:25433270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               wdk2c.pk014.o3 wdk2c Triticum end, mRNA sequence. CA711477
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triticum aestivum (bread wheat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGCTAACGCTGCGCTTGCTCTGCAAAGCGATGC 188
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                                                                                                                Scott.V. Tingey@USA.dupont.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="RIKEN full-length enriched, adult male colon" note="Site 1: Sal1; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was GAGAGAGAGAGATCCAAGAGCTCTTTTTTTTTTTTTTVN 3'], CDNA Was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dev_stage="adult"
lab_host="DH10B"
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Pred. No. 73;
0; Mismatches
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aestivum cDNA clone wdk2c.pk014.o3 5'
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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                     Local Similarity
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                                                          236 CCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAA 295
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                                                                                                                                                        91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 811)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other GSSs: BOOAOS8TR
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic survey
BZ469000
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ATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACG 355
                             TGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGNTGNTGCAGTCGCAGCCNCCGGTCTCCCCGGCCGTNTCGAACCCCGCCGGAGCTCCCCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTAGGCAAGCATTGTAAAACTGTGTTTCCCCATTTCATCTACTGTTTATGACAAATGCT 551
                                                                                                                                                                                                                                                                                                                                                                                                            primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                          301-838-3523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Medical Center Drive, Rockville,
                                                                                                                                                        Conservative
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/tissue_type="kernel"
/clone_Tib="wdk2c"
/clone_Tib="wdk2c"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
XhoI; Wheat (Triticum aestivum L.) developing kernel, days after anthesis."
                                                                                                                                                                                                                                /clone="BOOAO58"
/clone_lib="BO_1.6_2_KB_tot"
/note="Vector: pHOS1; Site_1:
total_DNA_inserted_into_pHOS1
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/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
                                                                                                                                                                                                                                                                                                                                                                1. .811
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                                                                                                                                                                     7.5%;
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54.5%;
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Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tot
                                                                                                                                                                     Score 34; DB 28;
Pred. No. 1.3e+02;
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t Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                          provided
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       중
                                                                                                                                                        95; Indels
                                                                                                                                                                                                                                 BstXI; 1.6-2 kb sheared using BstXI linkers"
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                                                                                                                                                                                  Length 811;
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311 ACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCG 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430 AAGATA 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,H., Cowa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Tateno,M., Tomaru,Y., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., Tomino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV058630 AV058630 Mus musculus pancreas (clone 1810054H02, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermostabilization and thermoactivation of thermolabile enzymes trehalose and its application for the synthesis of full length clerco. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN Mouse ESTs
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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EST.
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                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-res@rtc.riken.go.jp
AGATGCCAAAATA 145
                                          CGCTGGTTAATTA 383
                                                                                               TCCAGTGAAGCACAAAAAATGAAGAAGAAAATGATTACCCAAAAGTTGGAATTAAGGTAG
                                                                                                                                                                                                    GTGGAGACCACAGTTTTTTCTAGGTCACCAAGGCTGGGTAAAGAAAAAAAGAAGCATCAACTG
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                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="pancreas"
/dev_stage="adult"
/clone_lib="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone="1810054H02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sex="male"
                                                                                                                                                                                                                                                                                                                           7.4%;
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                                                                                                                                                                                                                                                                                                   Score 33.8; Di
Pred. No. 93;
0; Mismatches
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CS7BL/6J
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                                                                                                                                                                                                                                                                                                                                                Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                               C57BL/6J adult'
                                                                                                                                                                                                                                                                                                      Indels
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RESULT 11
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AUTHORS
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VERSION
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AA746477/c
                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bonaldo, ph.D.

CDNA Library Arrayed by: Greg Lennon, ph.D.

DNA Sequencing by: Washington University Genome Sec

Clone distribution: NCI-CGAP clone distribution inf

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 661 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 292.

High quality sequence stop: 292.
                                                                                                                            119
                                           59 AGCGGCCTCGGAGGTACCCAGGCCGCACGGCCGACGCTACTGGCCGG
                                                                                        75
                                                                                                                                                               15
                                                                                                                                                                                                     62;
                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 365)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
AA746477
AA746477.1 GI:2786463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA746477 365 bp mRNA linear EST 27-JAN-1998 nw62e02.sl NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1251194 3' similar to TR:000555 000555 NEURONAL CALCIUM CHANNEL ALPHA 1A SUBUNIT ISOFORM A-1. ;contains element TAR1 repetitive element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                            ATGGGGCGGCGGTAATCATAACGGCGGCAATAGTTCCGGCCCG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                Unpublished (1997)
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                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                        | Double-stranded CDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1251194"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                   7.4%;
                                                                                                                                                                                                 0,
                                                                                                                                                                                           Score 33.8; DB 9;
Pred. No. 1e+02;
0; Mismatches 47;
                                                                                                                                                                                           47; Indels
                                                                                                                                                                                                                              Length 365;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       David Allman,
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RESULT 12
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AUTHORS
TITLE
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                          136 AGCATTTATC--AGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                              101 GACATTTANCCAAGANCGGTGGCGGNANCTCTGCNCTTGCTCTGNAA 55
                                                                                                                                                                                                                                                                                                                                                                                                           161 TGGCGCGGTGGCGGTAACCNCGGTGGTGGCGGTAATAATAAGCGGCCCAAATTCTANGCT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                            76
                                                                                                                                                          BU765156

BU765156

Seas23f11.y1 Gm-c1080 Glycine max cDNA clone SOYBEAN CLONE ID: Gm-c1080-4869 5' similar to SW.D100 ARATH Q00874

DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT100 PRECURSOR ;, mRNA
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                   Glycine max
                                                                    Glycine max (soybean)
                                                                                                             BU765156.1
                                                                                                                                   sequence.
BU765156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wuchereria bancrofti
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Wuchereria.

1 (bases 1 to 558)
Ndi, J. S., Ribeiro, J. M. and Nutman, T. B.
Toward the characterization of the Wuchereria bancrofti
microfilarial transcriptome with comparisons to those of Brugia
malayi and Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Building 4 Room 126, Bethesda,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2003)
Contact: Thomas B. Nutman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wuchereria bancrofti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD374421.1 GI:31229939
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGGGCGGCGGCAATAATCATAACGGCGGCGGAATAGTTCCGGCCCGGACTCAACGTTG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tnutman@niaid.nih.gov
mer: pBluescript T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from approximately 85,000 microfilariae isolated from the blood of an infected individual from Guyana, South America and converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by independent recombinants and the average insert size is lkb. The library was constructed by Sandra J. Laney. The library is available from Dr.S.A.Williams, email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome@smith.edu."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Wuchereria bancrofti microfilaria cDNA
(SAM95SjL-WbMf)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Wuchereria
/mol_type="mRNA"
/db_xref="taxon:6293"
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/lab_host="XL1-Blue MRF'"
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                                                                                                           GI:23733884
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60.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33.8; DB 14;
Pred. No. 1.2e+02;
0; Mismatches 40;
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Query Match 7.4%;
Best Local Similarity 55.6%;
Matches 65; Conservative
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This clone is available through: ResGen, Invitrogen Corp.
South Memorial Parkway Huntsville, AL 35801 For further ir
call: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Marrin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Public Soybean EST Project Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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                                                                                                                                                                        nitrogen. Stratagene's cDNA Synthesis Kit (cattalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nuclectide (V=A, C, or G) was added to the 3' end of the primer (GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTTCTCGAG(T)18V) to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the CDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The CDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first- strand synthesis primer was then restricted by digestion with XhoI from Promega (40U/u1); all XhoI sites in the CDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bb cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately lml. The column eluent was precipitated, redissolved, and ligated into Stratagene's pBluescript IX R Predigested vector (pBluescript II SK(+) vector that has been digested with BcoRI and XhoI, and phosphorylated by Stratagene). This library was constucted in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona University."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="Roots of 8 day old 'Bragg' supernodulating
mutant NTS382 seedlings"
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/lab_host="DH10B"
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       Score 33.8; DB 13; Length 559; Pred. No. 1.2e+02; O; Mismatches 52; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233
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                                                                                                                                                                                                                                                                 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            library availability, please contact Pieter de Jong (pieterdejong med.buffalo.edu). Clones may be purchased i (pieterdejong med.buffalo.edu). Clones may bufordering) BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301 838 0200
Fax: 301 838 0208
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The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
Other_GSSs: RPCI-11-481M9.TJ
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1 (bases 1 to 695)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao, William Nierman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
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CCATACATGTGGACACACATTAAAAGTCACATATAAGCATGGACACAAGTATACATTCAT
                                         TTACCCGTGTTGTTACCCATGAAATGGCACATGCAAACAACGCCACGGCTAACCAGTATT 454
                                                                                                                               ATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGTTAATTATGATCAGCTGG 394
                                                                                                                                                                                                                   TGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCG 334
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                                                                                                                                                                                                                                                                 Conservative
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BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/clone_tib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male_BAC_Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="GDB:7684616"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex="Male"
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sapiens genomic clone RPCI-11-481M9,
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Tetraodon nigroviridis
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genomic survey sequence.
CG178280
CG178280.1 GI:34069341
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Fax: 301-838-0208
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Other_GSSs: PUJDF79TB
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Whitelaw, C.A., Quackenbush, J.,
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/clone=1ib="ZM_0.6_1.0 KB"
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COT selected genomic DNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Zea mays"
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/strain="B73"
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Search completed: March 16, Job time: 2232.91 secs
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Heb: www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a larg scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizenes, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                   note="Genoscope sequence ID : COAG138AF12SP1~end
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result ი a 000 a a 229 227.2 227.2 227.2 227.2 227.2 220.6 220.6 2217.4 2117. 395. 395. 389. 287. 281. 34 . 35 4 306358 7 1711 7 10190 7 327773 2883 10370 292504 168267 172600 193168 301214 117541 Length 19201 DB 9 14 90 90 AX814798 AX655393 AXC55893 AK102629 AE001013 AF429315 AF7429315 AC116977 AC116977 AC116979 AE016786 AC101969 AE016786 AC146009 AE016786 AC146008 AC146008 AC146008 AC146008 AC146008 AX814811 ECOCSGAA AE016759 AF275733 AE005315 AE005315 AE015131 AE015131 AE016981 AP21726 ECO131756 AE016840 STAGFBA 144908 CSP515700 CFR515701 SEU53207 ECCSGABDG AE000205 D90741 SEU43280 STAJ2301 AE008749 AL627269 IJ **I44909** ALIGNMENTS AX814798 Sequence AX655933 Sequence AX658943 Oryza sat AK102629 Oryza sat AB0014339 Oryza sat AB001012 Archaeogl AF429315 Homo sapi AF429315 Homo sapi AF429345 Lactobaci AC116977 Dictyoste AC116979 Pan trogl AL359644 Human DNA AX814811 Sequence L04979 Escherichia AE016759 Escherich AF275733 Escherich AF002554 Escherich AP002554 Escherich AJ515702 Enterobac AE015131 Shigella AE016991 Shigella AF237726 Escherich AJ131756 Escherichia U53207 Salmonella X90754 E.coli cegG AE000205 Escherich D90741 Escherichia U43280 Salmonella AJ002301 Salmonell AE008749 Salmonell AL627269 Salmonell AC011969 AE016786 AC104285 AY247273 M59123 Ha AX416572 Sequence AC146008 Pan trogl I44908 Sequence 56 AJ515700 Citrobact AJ515701 Citrobact AE016840 Salmonell AJ000514 Salmonell Description 186 Pseudomon 285 Oryza sat 273 Medicago 3 Haloanaerob Sequence Salmonella

JOURNAL	TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	I44909	RESULT 1
Salmonella Patent: US 5635617-A 58 03-JUN-1997;	Methods and compositions comprising the agfA gene for detection of	Doran, J.L., Kay, W.W., Collinson, S. Karen. and Clouthier, S.C.	1 (bases 1 to 456)	Unclassified.	Unknown.	Unknown.	•	I44909.1 GI:2469622	I44909	Sequence 58 from patent US 5635617.	I44909 456 bp DNA linear PAT 07-OCT-1997		

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Salmonella enteritidis
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriacea; Salmonella.

1 (bases 1 to 2067)
Doran, J. L., Collinson, S.K., Burian, J., Sarlos, G., Todd, B.C.,
Munro, C.K., Kay, C.M., Banser, P.A., Peterkin, P.I. and Kay, W. W.
the structural gene for thin, aggregative fimbriae
J. Clin. Microbiol. 31 (9), 2263-2273 (1993)
                     J. Bacteriol. 178 (3), 96146512
                                           Salmonella enteritidis agfBAC operon encoding thin, aggregative
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Collinson, S.K., Clouthier, S.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="unknown"
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                              662-667 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 404.8; DB 6;
Pred. No. 8.9e-106;
0; Mismatches 32;
                                                                      Doran, J.L., Banser, P.A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA"
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                                                                                                                                                                                                                                                                                                 (agfA), and
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-10_signal
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Submitted (13-DEC-1995) S. Karen Collinson, Biochemistry and Microbiology, University of Victoria, P.O. Box 3055 Petch Blue Victoria, BC V8W 396, Canada
Victoria, BC V8W 396, Canada
                                                    /codon_start=1
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/db_xref="GI:1184715"
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SVRDGVGGQSHTQQKQTLSLPANQPIELSRLSVNISSEDSVKIIVTVSDGQSLHLSQQ
WPPSAQ"
                                                                                                                                                                                                 gene="agfC"
710. .2036
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loqmaaxsoltvgqyggnnaalvnqtasdssvmvrqvgfrnnatanqy"
                                                                                                                                                         function="unknown"
                                                                                                                                                                                gene="agfC"
                                                                                                                                                                                                                                                                                                                                  /gene="agfA"
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="AgfA fimbrin precursor"
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/db_xref="GI:1184714"
                                                                                                                                                                                                                                                                                                           product="AgfA fimbrin"
                                                                                                                                                                                                                                                                                        note="thin
                                                                                                                                                                                                                                                                                                                                                                       gene="agfA"
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'transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="putative signal sequence fimbrin-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="thin aggregative fimbrin subunit precursor; major
imbrial subunit of thin aggregative fimbriae precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="agfA"
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jaliggoygtdnsarvroegskllsvisoeggnnrakvdoagnynfayleotgnanda
jisosaygnsaaliokgsgnkanitoygtoktavvvokoshmalrvtor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="between putA and 571. .576
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note="fimbrin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="agfB"
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|mol_type="genomic_DNA"
|strain="27655-3b"
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1. .2067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roduct="AgfB"
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Best Local Similarity

88.8**%**;

Score 404.8; DB Pred. No. 1e-105;

1.

Length 2067;

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RESULT 3
STAJ2301
LOCUS
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AUTHORS
TITLE
JOURNAL
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AUTHORS
TITLE
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cegC genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AJ002301.1 GI:2739232
csgA gene; csgB gene; csgC gene; csgD
csgG gene.
Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STAJ2301 5103
Salmonella typhimurium csgG,
csgC genes.
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                                                                                                                                                                                                              Submitted (29-OCT-1997) Romling U.,
Karolinska Institute, MTC, Box 280,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       Romling, U., Bian, Z., Hammar, M., Sierralta, W.D. and Normark, S. Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhimurium
                                                                                                                                                                                                                                                                                       Romling,
                                                                                                                                                                                                                                                                                                                                                   J. Bacteriol. 180 (3), 98117058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                 9457880
                                                                                                                                                                                                                                                                                                                                                                                       regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 1612
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                                                                                                                                                                                                                                                                                                           (bases 1 to 5103)
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/codon_start=2
/transl_table=11
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                                                                                                             db_xref="taxon:602"
                                                                                                                                       mol_type="genomic
strain="SR-11"
                                                                               note="ORF179a"
                                                                                                                                                          organism="Salmonella typhimurium"
|mol_type="genomic DNA"
                                                                                                                                                                                                  . 5103
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csgG, csgF,
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CSGE,
                                                                                                                                                                                                                                  Department of Bacteriology, Stockholm, S-17177, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene; csgE gene; csgF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
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                                                                                                                                                                                                             Salmonella typhimurium LT2
Salmonella typhimurium LT2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Batterobacteriacea; Salmonella.

1 (bases 1 to 22411)
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Complete genome sequence of Salmonella enterica serovar Typhimurium
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The Salmonella typhimurium Genome Sequencing Project Direct Submission Submitted (29-MAR-2001) Genome Sequencing Center, Department of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.0%;
91.9%;
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Pred. No. 2.3e-103;
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n 53 of 220 of the complete
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gene

mat\_peptide sig\_peptide

gene CDS

BCT 23-APR-2003

mat\_peptide sig\_peptide

Sgo

gene

gene CDS		gene RBS CDS	PEATURES BOURCE	COMMENT
<pre>complement(14142303) /gene="STM1127" complement(14142295) /gene="STM1127" /gene="gene="STM1127" /gene="ge</pre>	/note="similar to E. coli PhoB-dependent, ATP-binding pho regulon component; may be helicase; induced by p starvation (AAC74105.1); Blastp hit to AAC74105.1 (354 aa), 92% identity in aa 71 - 354"  /codon_start=1 /cransI_table=11 /product="PhoB-dependent ATP-binding pho regulon component" /protein_id="AAL20057.1" /protein_id="AAL20057.1" /db_xref="GI:16419642" /transIlation="WCAHNRYQENAGDVYLOLKVLSWGRQKAVIKARREAKRYLRRDS RSHKQREEESVTSLVQMGGVEALGHARDSRDTSPVKARNEAQAHYLNAIDSKOLIFAT GEAGCGKTWISAAKAAEALIHKDVERIIVTRPVLQADEDLGFLPGDIAEKFAPVFRPV YDVLLKRLGASFMQXCLRPEIGKVEIAPFAYMRGRTEENAVVILDEAQNVTAAQMKMF LTRLGENVTVIVNGDITQCDLPRGVRSGLSDALERFEEDEMVGIVHFNKDDCVRSALC QRTLHAYS"	nonella Cypnimurium LTZ" mic DNA" SGSC 1412; ATCC 700720" 700720" 1:99287" STM1126" RBS for phoH; RegulonDB:ST		Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 AI43283  Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
gene	RBS gene CDS	gene	RB B B B B B B B B B B B B B B B B B B	RBS gene CDS

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/protein id="AAL20059.1"
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/db_xref="gi:16419644"
/db_xref="gi:16419644"
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DKFFPATQFHWSWTESTVPVLMIGFLFANIQQFTASQDVVQRYIVTDSIEETKKTLLT
NAKLVAVIPVFFAIGSALFVYYQQHPQLLFAQFNTGGILLFVVTTEMPVGIAGLIIA
AIFAAAQSSISSSLMSISSCRUSDIVGRISHKKTFBRRMKIAKUVILVAALISSAAS
VWLVWADESEIWDAFWSLIGLMGGPMTGLFMLGIFFKRANAGSAVLGIISVITVLGA
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/gene="STM1131"
6793. .6798
/gene="STM1131"
/note="putative RBS for STM1131; RegulonDB:STMS1H001402"
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Aldnngviyvglgtagtswykidlkkchkdnerikspegarrgvykytelndelyvfg
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Ehifdkyfidiaaaadeseknkviynyfnkdakdyffnkivstynaknglppspgeq
Pgagtagssvmgnnflmlingelkpglrtdviyrammdndkltwlknsqlppspgeq
Qqeglagafsgyshgvllvggganfpgakqnytngkfysheginkkyrdevyglingh
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/gene="SIM1129"
/note="similar to E. coli putative
/note="similar to AAC76255.1 (229 aa),
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complement(4413. .5099)
/gene="STM1129"
                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to E. coli orf, hypothetical protein (AAC77266.1); Blastp hit to AAC77266.1 (404 aa), 41% identity in aa 40 - 403" (codon_start=1) (trans1_table=1) (product=-putative inner membrane protein" (protein_id="AAL20061.1" (bx ref="GI-16419646")
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSLLARLEOSVHENGGLIVSCOPVPGSPMDKPEIVAAMAQAAAS
AGAVAKTIEGIENLRTVRPHLSVPIIGIIKEDLTGSPVRITPYLDVDALAQAGADII
AFDASFRSRRVDIOSLLTRIRHGLLAMADGSTVNEGISCHOKGIEFTGTTLGGYTGE
ITPVEPDLAMVTQLSHAGCRVIAEGRYNTPALAANAIEHGAMAVTVGSAITRIEHICO
                                                                                                                                                    WQYMGKMKQPLGYGVSVSYGDEVFLIGGENAKGKPVSSVTSFTMRDGNLLIK"
6793. .7497
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/gene="STM1128"
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/gene="STM1128"
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/gene="STM1128"
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/gene="STM1127"
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QARESKLRTMNALDMTK"
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5599. .6759
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protein_id="AAL20060.1"
db_xref="GI:16419645"
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/transl_table=11
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(AAC76702.1); Blastp hit to AAC76702.1 (571 aa),
identity in aa 7 - 478"
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                           AL627269
Salmonella enterica serovar Typhi (Salmonella typhi)
Complete chromosome; segment 5/20.
AL627269 AL513382
AL627269.1 GI:16502231
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTÁGGCCÁGGGTGCGGATÁÁCAGTÁCTÁTTGÁÁCTGÁCTCÁGÁÁTGGTTTTCÁGÁÁÁCAÁT
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/codon_start=1
/trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to E. coli putative transport protein (AAC77235.1); Blastp hit to AAC77235.1 (425 aa), 57% identity in aa 25 - 418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ctanelaelon="mkinkyllgmvsfiafssylgaatldyrheyadrtrinkdriai
IEKLPNGIGFYVDASVKSGGVODEQDKHLSDLVANAIELGVSYNYKVTDNEVLQPGFI
FESGPDTSIYKPYLRGQYNFDSGYYMAGRYRVDYARKTANYSDDEKTNRFDTYIGYVF
DELKLEYNFTWMDSDQIKFDNKKTNYEHNVALAWKLNKSFTPYVEVGNVAVRNNTDER
OTRYRVGLQYHF"
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7768. .7773
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780. .9060
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/protein_id="AAL20062.1"
/db_xref="GI:16419647"
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/transl_table=
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/note="similar to E. coli orf, hypothetical (AAC77267.1), Blastp hit to AAC77267.1 (241
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91.9%;
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Pred. No. 2.6e-103;
0; Mismatches 37;
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) strain CT18,
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l aa), 26%
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MEDLINE
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SOURCE
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TITLE
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Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK B-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Details of S. typhi sequencing on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentleys, D., Holden, M.T.G., Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Parry, C., Quail, M., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Complete genome sequence of a multiple drug resistant Salmonella Nature 413 (6858), 648-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella enterica subsp. enterica serovar Typhi salmonella enterica subsp. enterica serovar Typhi Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11677608
                                                                                                          /codon_Statt=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/S_typhi/)
Location/Qualifiers
/note="Pfam match to entry PF01433 Peptidase_M1, family M1, score 245.10, E-value 1.9e-84"
                                                                                   gene="STY1078"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Orthologue of E.
to AMPN_ECOLI (869 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="CT18"
/db_xref="taxon:90370"
181. .2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="STY1078"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: pepN"
181. .2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="STY1078"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Salmonella enterica subsp. enterica
Typhi"
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94% identity in 869 aa o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="STY1079"
/note="PS00911 Dihydroorotate dehydrogenase signature 1"
3874. 3936
/gene="STY1079"
/note="PS00912 Dihydroorotate dehydrogenase signature 2"
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                                             LLEGEVSPLKKSAMGDDGTILSCSCVPKTALRLEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (4716 . .5825)
/gene="STY1081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (4716. .5825)
/gene="STY1081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Orthologue of E. coli YCBW_ECOLI; Fasta hit to YCBW_ECOLI (192 aa), 90% identity in 180 aa overlap. I discrepency in position of translational start site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Pfam match to entry PF01180 DHOdehase, Dihydroorotate dehydrogenase, score 563.50, E-value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVDAEGLINRMGFNNLGVDNLVENVKKAHFDGILGINIGKNKDTPVENGKDDYLICME
KVYAYAGYIAINISSPNTPGLRTLQYGDALDDLLTAIKNKQNDLQVIHHKYVPVAVKI
APDLCEEELIQVADSLLRHNIDGVIATNTTLDRSLVQGMKNCQQTGGLSGRPLQLKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="PS00142 Neutral zinc metallopeptidases, zinc-binding region signature"
                                                                                                                                                                                                                                         /product="conserved hypothetical protein"
/protein id="CAD08186.1"
/db_xref="GC116502225"
/db_xref="GOA:082787"
                                                                                                                                                                                                                                                                                                                                                                                 /note="Orthologue of E. coli P75863; Fasta hit (369 aa), 86% identity in 367 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMNORLKPQVHCHSFSLEQAV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gemwtpgtgdaasvwlsdtaeqvnllvvepgenaalcllaqpgvv1agrtmqlgda1k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MMRIKPDDNWRWYYDEEHDRMMLDLANGMLFRSRFSRKMLTPDA
FCPTGFCVDDAALYFSFEEKCRDFELTKEQRAELVLNALVAIRYLKPQMPKSWHFVAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="conserved hypothetical protein"
/protein_id="CAD08185.1"
/db_xref="GI:16502234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="STY1080"
4174. .4719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="myypfvrkalfqldperaheftfqqlrritgtplealyrqkvpt
KPVTCMGLTfkNPLGLaAGLDKDGECIDALGAMGFGSLEIGTVTPRPQPGNDKPRLFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="dihydroorotate dehydrogenase"
|protein id="CAD08184.1"
|db_xref="GI:16502233"
|db_xref="GOA:082789"
|db_xref="SWISS-PROT:082789"
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                                                                                                                                                                                                                                                                                                                                            codon_start=1/
transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="SPTREMBL:Q8Z7S8"
                                                                                                                                                                                                                   xref="SPTREMBL:Q8Z7S7"
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Best Local Similarity
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                                                                                                                                                                                                                        CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                     GCCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACCGGCGGCGGCAATAGTTCCGGC 120
GTAGGCCAGGGTGCGGATAACAGTACTATTGAACTGACTCAGAATGGTTTCAGAAACAAT 89205
                                   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                                                                                                                                                                                                                                                                                      ATGAAACTTTTAAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 88965
                                                                                                                                                                                                                                                                                                                                                                                                                  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTCGGCAGTGCTCTGGCT
                                                                                                                                               AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
                                                                                                                                                                                            CCGGATTCCACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                                                                                                         GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Fasta hit to YBIT_ECOLI (530 aa), 32% identity in 526 aa overlap Fasta hit to YJJK_ECOLI (554 aa), 34% identity in 524 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6506.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                overlap
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/gene="STY1083"
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Uncharacterized protein family UPF0020, score 781.30,
E-value 3.7e-231"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="STY1082"
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protein id="CAD08187.1"

db_xref="GI:16502236"
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91.7%;
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DEFINITION
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Deng, W., Liou, S.-R., Plunkett, G. III, Mayhew, G.F., Rose, D.J.,
Burland, V., Kodoyianni, V., Schwartz, D.C. and Blattner, F.R.
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Deng, W., Liou, S.R., Plunkett III, G., Mayhew, G.F., Rose, D.J.,
Burland, V., Kodoyianni, V., Schwartz, D.C. and Blattner, F.R.
Comparative Genomics of Salmonella enterica Serovar Typhi Strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella enterica subsp. enterica serovar Typhi Ty2
Salmonella enterica subsp. enterica serovar Typhi Ty2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella enterica subsp. enterica serovar Typhi Ty2, section 7 of AE016840 AE014613
AE016840.1 GI:29137797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE016840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 185 (7), 2330-2337 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTTTTGGCAÁCAACGCCACGGCTÁACCAGTÁTTAA 89361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGTTACCCGTGTTACCCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (844. .1797)
                                                                                                               translation="MGDEKSLAHTRWNCKYHIVFAPKYRRQAFYGEKRRAVGSILRKL
CEWKOVRILEAECCADHHHMLLBIPPKMSVSSFMGYLKGKSSLMIYEQFGDLKFKYRN
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Complement (844. 1797)
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Salmonella typhi CT18"
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complement(164..622)
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                                                                                                                                                                                                                                                    /codon_start=]
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                  locus_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Salmonella enterica subsp. enterica serovar
Typhi Ty2="
/mol type="genomic rww"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           ement (164. .622)
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                                                                                                                                                                                                                  element
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                                                                                                                                                                                                                                                                                     gene
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complement(4488. .5591)
                                                                                                                                                                                                                                                                                                                                           codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="flgI"
/locus_tag="
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Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / TEARS LET IONE "MSSLINHAMSGLNAAQAALNITVSNNINNYNVAGYTRQTTILAQA
NSTLGAGGMIGNGVYVGGVQREYDA FITNQLRGAQNQSSGLITRYEQMSKIDNLLADK
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VSSNSNNADKTVSLTAKVUDSTRVQATDYKI VPOGTDMQVTRTADNTTFTATKDADGK
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SDNRNGGALLALQNBNVEYGGNKTFNDAYATLVSDVGNKTSTLKTSSTTQANVVKQLYK
SDNRNGQALLALQNBNVEYGGNKTFNDAYATLVSDVGNKTSTLKTSSTTQANVVKQLYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (3538. .4488)
/gene="flgJ"
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/gene="f1gJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            locus_tag="t1738"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="flagellar hook-associated protein 1"
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/transi_table=11
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complement(1812. .3473)
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CDS gene

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                         /translation="mdhaiytamgaasqtinqqavtasnlanastpgfraqinalrav pvDGLSLATRTLVTASTPGABMTQGQLDYTSRELDVALQODGMLVVQQADGAEGYTRN GNIQVGPTGQLTIQGHPVIGEGBTITVPEGSEITIAADGTISALNPGDPNTVAPVGR LKLVKAEGNEVQRSDDGFRLTAEAQAERGAVLAADPSIRIMSGVLEGSNVKPVEAMT DMIANARRFEMQMKVITSVDENEGRANQLLSMS"
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Salmonella typhi CT18"
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complement(7146. .7901)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (6350. .7132)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / tränelation="mokyalhaypvvalmövatltgcamipakplvogattaqpipgpy
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spgfptyverylgglegerradmeasggnsfnekgganasntfsgttltyvpdyvlangn
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complement (5597...6295)
                                                                                                                                                                                                                                      complement (7922. .9133)
                                                                                                                                                                                                                                                                                          complement (7922.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /locus_tag="t1741"
/note="distal rod protein; corresponds to STY1218
Accession AL513382: Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (6350. .7132)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGWLQRFFLNLSPM"
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salmonella typhi CT18"
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Salmonella typhi CT18"
                                                                                                                                      codon_start=1/
transl_table=
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 86.7%;
91.7%;
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Score 395.2; DB 1;
Pred. No. 9.8e-103;
                                                                                                                                                                                                                                                                                            . 9133)
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                                                                                                                    FlgE"
                Length 301983
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                                                                                                                                                                                                                                                        AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                          JOURNAL MEDLINE
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                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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                                                                                                                gene
                                                                                  CDS
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AJ000514.1 GI:2275119
agfA gene; agfB gene.
Salmonella typhimurium
Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (14-JUL-1997) Sukuppolvi S.S.,
University of Turku, Kiinanmyllynkatu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1048
Salmonella typhimurium agfB a
AJ000514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sukupolvi,S., Lorenz,R.G., Gordon,J.I., Bian,Z., Pfeifer,J.D., Normark,S.J. and Rhen,M. Expression of thin aggregative fimbriae promotes interaction of Salmonella typhimurium SR-11 with mouse small intestinal epithe.
                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 1048)
Sukupolvi, S.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Infect. Immun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTTTTGGCAACAACGCCACGCTAACCAGTATTAA 36855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
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                                                                                                                                 'gene="agfB"
.4. .553
                                                                                                                                                                                                 db_xref="taxon:602"
                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                             , Medical Biochemistry, 20520, FINLAND
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1 (bases 1 to 361)
Doran, J.L., Kay, W.W., Collinson, S. Karen. and Clout
Methods and compositions comprising the agfA gene
Salmonella
Patent: US 5635617-A 56 03-JUN-1997;
                                                                                                                                                                                                                                                                                                        ĠĠŦŦŦŦĠĠĊĀĀĊĀĀĊĠĊĀĊĊĠĠĊŦĀĀĊĊĀĠŦĀŦĀĀ 1047
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                                                                                                                                                                                                                                                                                                                                                                                        CTGGTTACCCGTGTTACCCATGAAATGCCACATGCAAGCGTAATGGTGCGTCAGGTT
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IDQWNAKNSDITVGQYGGNNAALVNQTASDSSVMVRQVGFGNNAPANQYN"
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SISQSAYGNSAAISAAIIQKGSGNKANITQYGTQKTAVVVQKQSHWAIQANITQYGTQ
                                                                                                                                                                                                           361 bp
US 5635617.
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Pred. No. 2.7e-101;
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Mismatches
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                                                and Clouthier, s.c. agfA gene for detec
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                                                                                                                                                                                                                PAT 07-OCT-1997
                                                  detection
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AUTHORS
TITLE
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ACCESSION
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Matches 289;
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Best Local Similarity
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Citrobacter sp. Fec2 csgB gene, csgA gene and csgD gen AJ515700

AJ515700

AJ515700

AJ515700.1 GI:31790491

csgA gene; csgB gene; csgD gene; curlin-csgA protein; csgA gene; csgB gene; csgB gene; curlin-csgA protein; Citrobacter sp. Fec2

Citrobacter sp. Fec2

Citrobacter sp. Fec2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304
                                                                                                                                                                                                                                                                                                                                                                               Zogaj,X., Bokranz,W., Nimtz,M. and Romling,U. Production of Cellulose and Curli Fimbriae by Members of the Enterobacteriaceae Isolated from the Human Gastrointestinal T Infect. Immun. 72 (7), 4151-4158 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                              Submitted (11-NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCCTGCAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammap
Enterobacteriaceae; Citrobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATG 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCGTTCCACAATGGGGCGGCGGGAATCATAACGGCGGGCAATAGTTCCGGCCCG
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                                                                operon"
                                                                                                                                                                                                                                                                                                             Karolinska Institute, Box 280, Location/Qualifiers
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                                                                                                                              complement (212.
/codon start=1
/trans1_table=11
/product="putative regulatory protein"
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                                                                                                                                                             /country="Germany"
complement(212. .8
                                                                                                                                              /gene≃"csgD"
                                                                                                                                                                                             db_xref="taxon:213763"
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                                                                                                                                                                                                           'isolation_source="faeces"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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99.0%;
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                                                                                                                              .862)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 287.2;
Pred. No. 8.
                                                                                                                                                              .862)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gammaproteobacteria;
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                                                                                                                                                                                                                                                                          ·ds
                                                                                       transcription
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80, S-17177 Stockholm,
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Ś В Ş 밁 á

773 181 Query Match Best Local

Similarity

85.4**%**; 91.0**%**;

/gene="agfA"

Conservative

593

ь

61

REFERENCE AUTHORS TITLE

JOURNAL

KEYWORDS SOURCE

ORGANISM

Unclassified, Unknown. RESULT 8
I44908
LOCUS
DEFINITION
ACCESSION
VERSION

**I44908** 

Sequence 56 from patent I44908

I44908.1

GI:2469621

Ś 밁 Ş 밁 Ş 밁 Ş В Ş . В

953 361 893 301 833 241

1013 421

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RESULT 10
CFR515701
LOCUS
                DEFINITION
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CFR515701 2920 bp
Citrobacter freundii csgB gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCGTCGTTCCACAATGGGGCGGCGGCGGCAATACCGGCGGCGGCAATAGTTCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                               CATAACGCCGCACTGGTGAACCAGACTGCGTCCGATTCCAGCGTTCTGGTGCATCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGGCCAGGGCTCAGATAACAGCACCATCGATCTGACTCAAAACGGCTTCAAAAACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGAAACTTTTACAAGTGGCAGCATTTGCAGCAATCGTGGTTTCTGGCAGTGCTCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                                                                                                                                                                                                                                  GGTTTTGGCAACAACGCCACCGCTAACCAGTACTAA 2571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCACCATCGATCAGTGGAACGGCAAAAATTCGGACATTACTGTGAGCCAGTATGGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGGAATCGACCCTGAGCATTTATCAGTCAGGAGTCAATAACGCCGCGCTTGCGCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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/transT_table=11
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/protein_id="CAD56672.1"
/db_xref="GI:31790494"
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/table=10GI:31790494"
/ta
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QaaiiGQvgtnnsakmrQegskllsvvsQeggsnrakvdQsgaynfayiaQsghsnda
SisQsnygnyamiiQkgsgnkanitQygtQktavvvQrQsQmairviQr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / translation="meneffshehthlitresloatallokkoslalsgklhnio
rslddissciuludmeadkklihymodnlsrknnnlktllluteddypyrdienwe
hingyfynddeervunglosilrgecyfsoklasyllithsgnyrsnssesallthre
keilnklrigasnieiarslfisentvkthlynlfkkiavknrtoavsmandnlrr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="csgA"
2119. .2571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="nucleation component of
/protein_id="CAD56671.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="csgA"
function="curli
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/function="nucleator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="csgB"
1623. .2078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        xref="GI:31790493"
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Pred. No. 4.3e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
        csgA gene and csgD gene
                                                     DNA
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Query Match
Best Local Similarity
Matches 322; Conserv
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밁 ક 밁 ક 뫄 ક 밁 S 당 र् 밁 S 밁 S

50.3%; ilarity 70.6%; Conservative

<u>,</u>

Score 229.2; DB 1; Pred. No. 5.9e-55; 0; Mismatches 128;

Length Indels

6

Gaps

1;

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JOURNAL
REFERENCE
AUTHORS
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ORGANISM
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                             CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zogaj, X., Bokranz, W., Nimtz, M. and Romling, U.
Production of Cellulose and Curli Fimbriae by Members of the Fami.
Enterobacteriacese Isolated from the Human Gastrointestinal Tract
Infect. Immun. 72 (7), 4151-4158 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               csgA gene; csgB gene; csgD gene; curlin-csgA protein; component of curlin monomers; regulatory protein. Citrobacter freundii
Citrobacter freundii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AJ515701
AJ515701.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 2920)
                                                                                                                                                                         /gene="csgA"
2123. .2572
/gene="csgA"
/function="curli subunit"
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1624. .2082
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                                                                                                                                                                                                                                                                                                NQAAIIGQVGTANSANTRQGGSKLLSVISQEGSGNRAKTDQTGSYNFAYIDQTGSSND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(211. .861)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              624. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /isolation_source="faeces"
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/db_xref="taxon:546"
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                                                                                                                                                                                                                                                                                                                                             translation="MKNKLLFMMFTMLGVPGIAAATTSYDLANSEYNFAVNELSKSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="genomic DNA" isolate="Fec4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function="nucleator"
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                                                                                                                                                                                                                                                                             Submitted (01-APR-1996) J.M. Cox, Food University of New South Wales, Sydney, Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                            Cox,J.M., Eglezos,S. and Woolcock,J.B. Virulence of Salmonella enteritidis in chickens correlates colony morphology and expression of SEF17 fimbriae unpublished
                                                                                                                                                                                                                                                                                                                                         Cox,J.M., Eglezos,S. and Woolcock,J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella enteritidis
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Salmonella enteritidis SEF17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                        strain="SE30"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     csgA gene; csgB gene; csgD gene; csgE gene; csg
oxfC gene.
Bscherichia coli
Bscherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                                                                                                                                                 SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (11-AUG-1995) M. Hammar, Karolinska Institutet,
Microbiology and Tumorbiology Center, Box 280, S-171 77 Stockholm,
                                                                                                                                                                                                                                                                                                                                                                                                                        Hammar, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hammar,M., Arnqvist,A., Bian,Z., Olsen,A. and Normark,S. Expression of two csg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
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                                                                                                                                                                                            æ
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1. .4680
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                                                                                                                                                                                         _xref="taxon:562"
                                                                                                                                                                                                                                                                                   xref="taxon:562"
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FEATURES

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misc_feature
                                                                                                                                                                                                                                                                        misc_feature
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HINGVEYSMEDOERVVNGLQGVLRGECYFTQKLASYLITHSGNYRYNSTESALLTHRE
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/db_xref="GI:1147562"
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/db_xref="SWISS-PROT:P52105"
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igadtoyoldoiavnlrvvnvstgeilssyntsktilsyevoagvfrfidyorllege
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GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 4184
                                                GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                     GGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT
                                                                                                                                                   CTGGTTACCCGTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                      GCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAAATGACGGTTAAACAGTTCGGTGGT
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        repeat_region
                                                                                                                                                                                                            AL Submitted (1)-OCT-1998) Labbratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (From the Human Genome determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using Genemark software, kindly supplied by 30332 [e-mall: mark@amber.gatech.edu]. Open reading frames that site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by ongoing task whose goal is to make the genome sequence more useful procrelated. Updated information will be available at the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by correlating it with other data. Comments to the authors are genome Project's World Wide Web site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and sequence changes. Annotation updates: updated gene identifications Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers RNA-encoding) are now designated as gene synonyms instead of names. This should allow them to be searched for in Entrez as gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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Plunkett,G. III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J.; Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
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Blattner, F.R.
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Escherichia coli K12
Bacteria, Proteobacteria, Gammap.
Enterobacteriaceae, Escherichia.
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Escherichia coli K12 MG1655 section
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complement(<1...48)
                                                                                                                                                                                   Location/Qualifiers
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                                                       _strain="MG1655"
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                                      /db_xref="GI:1787268"
/translation="MGGGTRCVQYTKKKPVLSYELFFKYGGEGGIDSLRSPCGQPAHC
VHGLSNWLSPVVDPRSGLL1PPVCAIHEKKARTFVRALL"
                                                                                                                       /codon start=1
/transT_table=11
/product="orf, hypothetical protein"
/protein_id="AAC74115.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MIDDYLTETREQDKRNLIYIYAIGLILIGFYWKNAGETEPSEDI
GVVSGILALVLYNFIEDLKAYWAYKCVTKNIDESWEKKKQNHKIELFLTQPLVAGELS
LIMLSAMSWGLYQLLPSLYALFLISLLGELVIFENERSGWITEKSIIALLILGVVLAIVAKKVKYK
SLTRYVLLSVCISTVVHLTISPLRNSDSFVTEGGWITEKSIIALLILGVGVVLAINLF
FLRESKRYAFLGRLFLQEIDLFFSSENALSTFFAKPLWIRLFILLVIEVMWITLVSVL
ATLUEWRIWFEAYFLLCYVPCLIYYFFYCRFLWHNDFWMACDMYFRWGHFNK"
                                                                                                                                                                                                                                     /function="orf; Unknown"
/note="083; This 83 aa ORF is 25 pct identical (7 gaps)
/note="083; This 83 aa ORF is 25 pct identical (7 gaps)
'gene="ycdV"
                                                                                                                                                                                                                                                                                                                                                                                                                                  note="factor Sigma70; predicted +1 start at 1096049"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="central position to predicted promoter: -104"
/bound_moiety="DeoR predicted site"
1253. .1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transI_table=11
/product="orf, hypothetical protein"
/protein_id="AAC74114.1"
/db_xref="GI:1787267"
                                                                                                                                                                                                                                                                                                                                         gene="b1030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="No predicted
/bound_moiety="DeoR
l337. .1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="ycdU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="ycd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to 191 residues of an approx.
SW: P47562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              function="orf; Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="ycdU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389. .1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/trans1_table=11
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LHLTHTVKWTESLDTFLNMPTPVAFLEISNKPYLGNMLNDFAGVDQQRVMHCRKAFSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="0328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="synonym: b1029"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="ycdU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="b1028"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="orf; Unknown"
/note="o107; This 107 aa ORF is 27 pct identical (0 gaps)
to 58 residues of an approx. 1888 aa protein FAS2_CANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="factor Sigma32; predicted +1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _note="factor Sigma70; predicted +1 start at 1094689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="IS3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This 328 aa ORF is 19 pct identical (4 gaps) les of an approx. 288 aa protein Y320_MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d promoter"
R predicted
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                                                                                                                                                                                                                                                        Local
                  181
                                                                                                                                            61
                                                                                                                                                                                                                                                        1 49.8%;
Similarity 68.6%;
AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGGTTATGGTAACGGCGCCGAT
                                                                    CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCCTCTGCAA 180
                                                CCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAA
                                                                                                                GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC
                                                                                                                                           GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC 120
                                                                                                                                                                                                            ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                   KSGDNDSADYALVWHPPVEMLAGRDLKAVFALGAGVDSILSKLQAHPEMLNĖSVPLFR
LEDTGNGEQMOEYAVSQVLHWFRFDDYRIQMSSHWOPLPEYHREDFTTGILGAGVL
GSKVAQSLQTWRFPLRCWSRTRKSWPDGVQSFAGREBLSAFLSQCRVLINLLPNTPETV
GIINQQLLEKLPDGAYLLNLARGVHVVEDDLLAALDSGKVKGAMLDVFNREPLFPESP
LWQHPRVTITHVAAITRPAEAVEYISRTIAQLEKGERVCGQVDRARGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative ribosomal protein"
/protein_id="AAC74116.1"
/db_xref="GI:1787269"
/ta_nalation="MCNIRKKSPYFRTSSSLNMAVRGGLTRFARFAGSPLTAFTVCPT
GCRQLSTPGRGFSSPRCVQYTKKKPVLSYELFFKYGGEGGIDSLRSPCGQPAHCVHGL
SNWLSPVVEPRGGLLIPPVCAIYEKKARTFVRALL"
                                                                                                                                                                                                                                                                                                          3383. 3410

/note="factor Sigma70; predicted +1

3396. 3423
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Sw: P45637"
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complement (2111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transT_table=11
/product="putative dehydrogenase"
/protein_id="AAC74117.1"
/db_xref="GI:1787270"
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/function="putative enzyme; Not classified"
/funct=0325; This 325 aa ORF is 32 pct identical (2 gaps)
/note="0325; This 325 aa ORF is 32 pct identical (2 gaps)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="tRNA-Ser"
/note="anticodon: GGA; CG
/function="RNA; tRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to47 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="ycdV"
/function="putative structure; Not classified"
/note="0137; This 137 aa ORF is 27 pot identical (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="serX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="serX"
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                      note="factor Sigma70; predicted +1 start at 1097992"
                                                                                                                                                                                                                                                                                                                                                                      'gene="ycdW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MRINFAQRFSGVSMDIIFYHPTFDTQWWIEALRKAIPQARVRAW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="synonym: b1033"
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Pred. No. 2.5e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kitakawa, M., Mada, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi; T., Kasai, H., Kashimoto, K., Isono, K., Isono, S., Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C.. Yamamoto, Y., and Yano, M.
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97061202
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Complete and shotgun sequencing;
csgA; ycdE; cls; nov; mdoG.
Escherichia coli K12
Escherichia coli K12
Bacteria; Proteobacteria; Gammapı
Members: (1995.4 - 1996.3)
Alba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A.,
Horiuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S.,
Horiuchi,T., Ikemoto,K., Kashimoto,K., Kim,S.,
Itoh,T., Kanai,K., Kasai,H., Kashimoto,K., Kim,S.,
Kitagawa,M., Kitakawa,M., Makino,K.,
Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K.,
Nakamura,Y., Nashimoto,H., Nishio,Y., Oshima,T., Saito,
                                                                                                                                                                                                                             Group:
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                                                                                                                                                                                                                                                                                                                 Fax:81-7437-2-5669)
Collaboration Information:
                                                                                                                                                                                                                                                                                                                                                                                                     and Technology, Res. & Edu. Center for Takayama, Ikoma, Nara 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-JUL-1996) Hirotada Mori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The systematic sequencing Unpublished (bases 1 to 15047)
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                                                                                                                                                                                                                                                                                                                                                                          (E-mail:hmori@gtc.aist-nara.ac
                                                                                                                                                                                                     The Japan E.coli genome DNA sequencing group
                                                                                                                                                                                                                                                              The Japan E.coli genome DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCAACGGTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAAATGACGGTTAAACAGTTCGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 15047)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      teria; Gammaproteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the Escherichia coli genome in Japan
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NA.
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1c.jp,
                                                                                                                                                                                                                                                           sequencing
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(23.7
                                                                                                                                                                                                                                                                                                                                                                                                                                      NARA Institute of Science
Genetic Info.; 8916-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   csgF; csgE;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.0
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     Saito, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cagD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCT 25-DEC-2002
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Seki, Y., Tagami, H., Takemoto, K., Wada, C.,

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Address: NARA Institute of Science Ikoma, 630-01, Japan E-mail: hmori@gtc.aist-nara.ac.jp URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Information operator:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Headed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Address: National Institute
E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sampei, G., Seki, Y., Tag
Yamamoto, Y. and Yano, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The Japan E. coli genome database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name: Hirotada Mori
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                                                      / translation="MNEFSILCRVLGSLYYRQPQDPLLVPLFTLIREGKLAANWPLEQ
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ADTPADHIGTLLLAASWLEDQSTEDESEALETLFSEYLLPWCGAPLGKVEAHATTPFW
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                                                                                                                                                                                                                                                                                                                                                             / tränslation="mypvdlimhtvasthaystlsdylaqakqkgiklfaitdhgpdm
Edaphhwhfinwriwprvdgygilrgibanikwrogidcesidcsgamposldli iagehe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2145. .2882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ORF_ID:o231#1
similar to SwissProt Accession
                                                                                                                                                                                                                              transl_table=11/
                                                                                                                                                                                                                                                                                                                       2906. .3460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="Diffssenalstffakplwirlfillvievmwitlvsvlative
WRIWFEAYFLLCYVPCLIYYFFYCRFLWHNDFWMACDMYFRWGHFNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="unnamed protein product; ORF_ID:o231#2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="Kohara clone #231"
/note="Nucleotide position 1097101-1112147 from initiation site of ThrA (O min.).~This clone is Kohara_lambda miniset library."
                                                                                                                                                                                                                                                  codon_start=1
                                                                                                                                                                                                                                                                                                                                              LNVSPRRLLNFLESRGMAPIAEFADL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ntergenic region
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product="Hypothetical 33.0 kd protein in proB-proA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAA35822.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="unnamed protein product; ORF_ID:o230#5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mol_type="genomic DNA"
strain="K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Escherichia coli K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       map="23.7-24.0 min"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .aist-nara.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xref="taxon:83333"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Technology
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gene
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KEILNKLRIGASNNEIARSLFISENTVKTHLYNLFKKIAVKNRTQAVSWANDNLRR"
                                                                                                                                                                                                                                                      similar to SwissProt Accession Number P52106"
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/note="ORF ID:0231#7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MRVKHAVVLLMLISPLSWAGTWTFQFRNPNFGGNPNNGAFLLNS
AQAQNSYKDPSYNDDFGIETPSALDNFTQAIQSQILGGLLSNINTGKPGRMVTNDYIV
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complement (5418...5807)
                                                                                                         /protein_id="BAA35830.1"
/db_xref="GI:4062613"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (5418.
/gene="csgE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Curli production
CsgF precursor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /\bar{n}ote="OR\bar{r}_ID:0231#6 similar to SwissProt Accession Number P52104"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon start=1
/transI_table=11
/product="curli production assembly/transport component
CsgG precursor:"
                                                                                                                                                                                                                transl
                                                                                                                                                                                                                                                                                            note="ORF
                                                                                                                                                                                                                                                                                                                  'gene="csgD'
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                                                                                                                                                                                  product="Probable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein_id="BAA35829.1"
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transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (4117. .4950)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MCSISFMAAFSAIMRGMNILLSIAITTGILSGIWGWVAVSLGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (4117. .4950)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="csgG"
/note="ORF_I
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RESULT 15
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                                                                                                                                                                                                                                                                                                                     Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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                                                                                                                                                                                                                                                          Peptides
Patent: WO 03064446-A 15 07-AUG-2003;
                                                                                                                                                                                                                                                                                                      Bjoerck, L., Olsen, A., Wikstroem, M. and
                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
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Similarity 68.6%;
13; Conservative
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/db_xref="GI:39104002"
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/mol_type="unassigned DNA"
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                         GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
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Search completed: March 15, 2004, 22:50:05 Job time : 1965.17 secs OLEGI HIN IQ TONG SHILL

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      Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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geneseqn2003bs:*
geneseqn2003cs:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                geneseqn2004s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
      GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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                                                               AAC64623
AAC74147
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AAC64628
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AAC64621
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7920.305 Million cell updates/sec
Aac64623 AgfA::PT3
Aaq87467 AgfA
Baqual
Aac74142 Salmonell
Aac64617 Salmonell
Aac64628 AgfA::PT3
Aac64628 AgfA::PT3
Aac64628 AgfA::PT3
Aac64629 AgfA::PT3
Aac64629 AgfA::PT3
Aac64629 AgfA::PT3
Aac64627 AgfA::PT3
Aac64621 AgfA::PT3
Aac64621 AgfA::PT3
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Aac64631 AgfA::PT3
Aac64631 Escherich
Aac64610 Fibronect
Aaq62646 FNB curli
Aac64610 AgfA (SEF
Aac64621 Leishmani
Aac64621 Leishmani
Aac64621 Leishmani
Aac64610 AgfA (SEF
Aac64621 Leishmani
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26-FEB-2001 AAC64623;

(first entry)

AAC64623 standard; DNA; 456

AgfA::PT3#2 DNA sequence SEQ ID NO:13.

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45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	28	27	26	25	24
33.4	34	34	34	34	34	34	34	34.2	34.4	34.8	35	35.4	35.4	35.4	37.4	37.6	40.6	40.8	41.6	43.2	44.8
7.3	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.5	7.6	7.7	7.8	7.8	7.8	8.2			8.9	9.1	9.5	9. 8
78	1344	1344	1344	1344	1344	1344	1344	2000	2751	1083	100	3412	3411	100	456	456	78	100	78	48	2000
9	σ	6	6	σ	w	w	N	7	δ	v	7	v	ഗ	7	w	w	w	7	w	ω	7
ACF36151	ABL51711	AAD27016	AAD29125	AAL41133	AAA14939	AAD00669	AAX09007	ADA71938	ABQ70750	AAS76745	ACD68808	AAS89144	AAS88526	ACD68807	AAC64620	AAC64618	AAC64606	ACD68809	AAC64605	AAC64616	ADA71938
Acf36151 E. coli C	Abl51711 Erwinia a	Aad27016 E. amylov	Aad29125 Erwinia a	Aal41133 Hypersens	Aaa14939 DNA encod	Aad00669 Erwinia a	Aax09007 Hypersens	Ada71938 Rice gene	Abq70750 Listeria	Aas76745 DNA encod	Acd68808 E. coli K	Aas89144 DNA encod	Aas88526 DNA encod	Acd68807 E. coli K	Aac64620 Escherich	Aac64618 Salmonell	Aac64606 SefA (SEF	Acd68809 E. coli K	Aac64605 SefA (SEF	Aac64616 S. enteri	Ada71938 Rice gene

## ALIGNMENTS

WPI; 2000-672631/65. P-PSDB; AAB36347. 05-APR-2000; 2000WO-CA000356 05-APR-1999; Salmonella enteritidis. Salmonella; agfh; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen; ds. White AP, 12-OCT-2000. WO200060102-A2. Synthetic. Escherichia (UYVI-) UNIV VICTORIA Doran JL, coli. 99US-0127888P Collison SK, Kay WW

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal. Disclosure; Page 136; 139pp; English.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the

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CC homologous species; (3) directing recombination of a recombinant gene CC back into the chromosome of the homologous species, replacing the native CC copy of that gene, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant aging protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonalla, E. coli or CC useful for the animal in conjunction with a carrier or diluent. (I) is CC system the heterologous antigens are presented in high numbers (up to copies/cell), the hybrid fimbrin protein possesses both the CC system the heterologous antigens are presented in high numbers (up to copies/cell), the hybrid fimbrin protein possesses both the CC vaccine, the carrier fimbrial submit proteins are usually strong companient, the inserted epitope, and hybrid fimbriae are usually strong conspensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                           25-MAR-2003
26-JUN-1995
Salmonella
                     Salmonella; AgfA;
                                                AgfA sequence.
                                                                                                                    AAQ87467;
                                                                                                                                    AAQ87467 standard; DNA; 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Simi
Matches 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 456 BP; 118 A; 109 C; 121 G; 108 T; 0 U; 0 Other;
                                                                                                                                                                                                             421
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                                                                                                                                                                                                                                                                                                                                               GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
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                                                                     (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Silarity 100.0%; Silarity 100.0%; Silarity 0;
          vaccine; genetic immunization;
                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 456; DB 3; I
Pred. No. 2.2e-138;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The DNA encodes the Salmonella AgfA protein. The DNA and isolated proteins are used in genetic immunization and vaccine compositions, respectively, to elicit an immune response to Salmonella in animals food producing animals) and humans. (Updated on 25-MAR-2003 to corre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 7B; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-358275/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR74625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kay WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP. (KING/) KING J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-APR-1993;
    421
                             421
                                                       361
                                                                                 361
                                                                                                          301
                                                                                                                                   301
                                                                                                                                                    241 GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
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                                                                                                                                       241 ĠŦĀĠĠĊĊĀĠĠĠŦĠĊĠĠĀŦĀĀŦĀĠŦĀĊŦĀŦŦĠĀĀĊŦĠĀĊŦĊĀĠĀĀŦĠĠŦŦŦĊĀĠĀĀĀŦĀĀŦ
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     GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                              AATAACGĆĆGCGCŤGĠŤŤÁATĆÁGACCGCATĆTGÁŤTĆCÁĠĆĠŤÁÁŤĠĠŤĠĆĠŤĊÁĠĠŤŤ
                                                                                                                                                                                                                                                                                                                                                                  1 ATGAAACTTTTAAAAGTGGCAGCAGTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                                CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT 420
                                                                                   ĠĊĊĀĊĊĀŤĊĠĀĊĊĀĠŤĠĠĀĀĊĠĊŤĀĀĀĀĀĊŤĊĊĠĀŤĀŤŤĀĊŤĠŤĊĠĠĊĊĀĀŤĀCĠGCGGT
                                                                                                    GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
                                                                                                                                                                                                       AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGAT 240
                                                                                                                                                                                         AGCGATGCCCGTAAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGCGAT
                                                                                                                                                                                                                                          CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                                                                                                               GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
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/note= "AgfA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                   88.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clouthier SC,
                                                                                                                                                                                                                                                                                                                                                                                                              Score 404.8; Defended No. 1.2e-0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                              8; DB 2;
1.2e-121;
hes 32;
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Gaps

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RESULT 3 AAT74142

RESULT 2 AAQ87467

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Best Local S
Matches 424
                                                                                                                                                                                                                                                                                                                                    The present sequence represents an isolated agfA gene derived from Salmonella enteritidis 27655-3b. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                              Sequence 456 BP; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-309886/28.
P-PSDB; AAW23570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Col 19-112; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collinson SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enteropathogenic bacteria; enterobacteria; S.enteritidia; antibody; da.
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29-SEP-1997
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GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAAATGGTTTCAGAAATAAT 300
                                           AGCGATGCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCGAT
                                                                                              CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCCGGC
                                                                             CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
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(first entry)
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/label= agfA_gene_fragment
/transl_except= (pos:367. .369,aa:Pro)
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                                                                                                                                                                                                                                                      93.0%;
                                                                                                                                                                                                                                                                                              A; 112
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                                                                                                                                                                                                                                                                                              C; 122 G; 105
                                                                                                                                                                                                                                        Score 404.8; DB 2;
Pred. No. 1.2e-121;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                              T; 0 U;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                  Length 456;
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                     CC The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign ppitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) CC directing recombination of a recombination of a recombination of the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native CC comprising separating an amino and (4) eliciting an immune response in an animal, CC comprising separating an amino and containing a replacement segment or segments of foreign amino CC Enterobacteriaceae host cell, from the host cell and introducing the colymer into the animal in conjunction with a carrier or diluent. (I) is colymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for cell, the hybrid fimbrial presentation constituent has a constituent of the containing an amino conjunction with a carrier of the tell to conjunction an animal. In a fimbrial presentation conjunction protein which is useful for the expression of recombinant and in high numbers (up to compare the heterologous antigens are presented in high numbers (up to terms).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
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adhesion properties relevant
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Best Local Simi
Matches 424;
   White AP,
                                                     05-APR-2000; 2000WO-CA000356
                                       05-APR-1999;
                                                                          12-OCT-2000
                                                                                                             Synthetic.
                                                                                                                             Salmonella enteritidis
                                                                                                                                         Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen; ds
                    (UYVI-) UNIV VICTORIA
                                                                                           WO200060102-A2
                                                                                                                    Escherichia coli.
                                                                                                                                                                     AgfA::PT3#7 DNA sequence SEQ ID NO:23.
                                                                                                                                                                                           26-FEB-2001
                                                                                                                                                                                                             AAC64628;
                                                                                                                                                                                                                           AAC64628 standard; DNA; 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
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  Doran JL,
                                                                                                                                                                                        (first entry)
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                                    99US-0127888P
  Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.8%;
93.0%;
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Pred. No. 1.2e-121;
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DR P-PSDB, AAB36352.

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PT

Recombinant agfA gene having a segment replaced by a foreign DNA sequence pr

which encodes foreign epitope or antigen, expresses recombinant AgfA

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PS

Disclosure; Page 137; 139pp; English.

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CC

The present invention describes a recombinant agfA gene (I) where a compensation of the gene has been replaced by a segment of a foreign DNA component of the gene has been replaced by a segment of a foreign DNA component of the gene has been replaced by a segment of a foreign DNA component of thin aggregative fimbriae (SEF1)/TAP1 nucleation depended are: component of strains of Salmonella, Escherichia coli and component of strains of Salmonella, Escherichia coli and component of strains of salmonella, Escherichia coli and component of strains of salmonella, Escherichia coli and component of sequence of the component of a recombinant gene into the chromosome of the composus species; (3) directing recombination of a recombinant gene comprising recombination of a recombinant gene comprising separating an amino acid polymer comprising a recombinant agene comprising a replacement segment of a recombinant AgfA component in an animal, component of the component of sequence or sequences grown on a Salmonella, E. coli or component on the animal in conjunction with a carrier or diluent. (I) is conjunction with a carrier or diluent. (I) is conjunction with a carrier or diluent. (I) is conjunction with a carrier or diluent. (I) is conjunction with a carrier or diluent in conjunction with a carrier or diluent. (I) is conjunction, the hybrid fimbrin protein poseesses both the conjunction with a carrier or diluent in the useful for immunogenicity and adhesion properties relevant for an efficient live value of the component of the present of dimunogens, which may be important for directing an immune response in an expensive to purify in large amount. The present sequence is given in
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Matches Query Match Best Local 9 Sequence 456 BP; 119 A; 110 C; 120 G; 107 T; 0 U; 0 Other; 361 301 301 241 241 181 121 181 121 410; 61 61 <u>ب</u> ш Similarity CATGAAATGGCACATGCAAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT 420 GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG 360 GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT GCCACCATCGACCAGTGGAACGCTAAAAACTATGATCAGCTGGTTACCCGTGTTGTTACC 360 GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180 GGCGTCGTTCCACAAIGGGGCGGCGGCGGCGGTAATCATAACGGCCGGCGGCAATAGTTCCGGC 120 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT ccesa crea a certica de la respecta de la composição de l GGCGTCGTTCCACAATGGGGCGGCGGCGGCGAATAGTTCCGGC atgaaacttitiaaaagigecagcaticecagcaatcetagtiteticecagiecicicec ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT Conservative 83.9%; Score 382.4; DB 3; 89.9%; Pred. No. 2.4e-114; tive 0; Mismatches 46; 0; Length Indels 0 Gaps 300 300 240 180 120 60

421

GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456

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421

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CC The present invention describes a recombinant agfA gene (1) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SER17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the CC useful for the expression of recombinant AgfA protein which is useful for CC useful for the expression of recombinant. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to CC useful containity and adhesion properties relevant for an efficient live translation, the hybrid fimbrin protein seems both the commongenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong CC immunogens, which may be important for directing an immune response CC against the inserted epitope, and hybrid fimbriae are easy and CC inexpensive to purity in large amount. The present sequence is given in tx
                   Query Match
Best Local Similarity
     Matches 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                           Sequence 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
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 Score 376; DB 3;
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Escherichia coli.
                                                        Disclosure; Page 137; 139pp; English
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                                                                                                                                                                                                                                                                                                           Doran JL,
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                                                                                                                                                                                                                                                                                                                 SK,
                                                                                                                                                                                                                                                                                                              Kay WW
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The present invention describes a recombinant agfA gene (I) where

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agra, Caga and Agra, homologue fimbrin subunits, respectively; (2)
CC directing recombination of a recombinant gene into the chromosome of the chromosome of the chromosome of the chromosome of the copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant Agra acid sequence or sequences grown on a Salmonella, E. coli or copymer into the expression of recombinant agrant in the expression of recombinant agrant in the expression of recombinant agrant in the expression of recombinant agrant and introducing the useful for the expression of recombinant agrant agrant in the heterologous antigens are presented in high numbers (up to copies/cell), the hybrid finbrin protein possesses both the communogenicity and adhesion properties relevant for an efficient live communogens, which may be important for directing an immune response community in large amount. The presentation in assist the inserted epitope, and hybrid fimbriae are easy and the exemplification of the present invention.
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Best Local (
                                                    AAC64625;
                                                                              AAC64625 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 456 BP; 116 A; 111 C; 120 G; 109 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SERIT/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunnits, respectively; (2)
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                                                                                                                                                            GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
                                                                                                                                                                                       GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                            CTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                       AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAĞCGTAATGGTĞCGTCAĞGTT
                                                                                                                                                                                                                                                                                                                                                                                       GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                                                                                                                                                                                             GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.3%; Score 361.6; DB 3; Length 456; Conservative 0; Mismatches 59; Indels 0
                                                                                DNA;
                                                                              456
                                                                          ВP
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В Ś д Ś В Ś 밁 Ś 밁 Ś

26-FEB-2001

(first entry)

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                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 136; 139pp; English.
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Escherichia coli
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121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA::PT3#4 DNA sequence SEQ ID NO:17.
                                                                                                                                                                                               393;
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                                                                                                                                 1 ATGAAACTITTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                                                                                                                                                                                            Similarity
                                                 ĠĠĊĠŦĊĠŦŦĊĊĀĊĀĀŦĠĠĠĠĠĠĠĠĠĠĠĠĠŦĀĀŦĊĀŦĀĀĊĠĠĊĠĠĊĠĠĊĠĠĊĀĀŦĀĠŦŦĊĊĠĠĊ
                                                                       GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCGAATAGTTCCGGC 120
                                                                                                              456 BP; 120 A; 110 C; 122 G; 104 T; 0 U; 0 Other;
                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                       77.9%;
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                                                                                                                                                                                   Score 355.2; |
Pred. No. 1.8e
0; Mismatches
                                                                                                                                                                                        0;
                                                                                                                                                                               2; DB 3;
1.8e-105;
hes 63;
                                                                                                                                                                               Indels
                                                                                                                                                                                                              Length
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                                                                                                                                                                             0
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAR) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA. CegA and AgfA-homologue fimbria nubunite, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, agfA
                                                                                                                                                                                                                                                       Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
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                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                    p-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                    White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                      (UYVI-) UNIV VICTORIA.
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DB; AAB36353.
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The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF1/T/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CSGA and AgfA, homologue fimbrin subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene cc copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC eliciting an immune response in the host cell and introducing the polymer into the animal in conjunction, with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for segment of the expression of recombinant for an efficient live conjunction, the hybrid fimbrin protein sare usually strong the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier imbrial subunit proteins are usually strong to immunogenic the carrier imbrial subunit proteins are usually strong to immunogenic the carrier imbrial subunit proteins are usually strong to immunogenic the carrier imbrial subunit proteins are usually strong to immunogenic the carrier imbrial subunit proteins are usually strong to immunogenic the carrier in the interior and immune response in the immune response of immunogenic transport to the carrier in the carrier in the content of the carrier in the carrier in the carrier in the carrier in the carrier in the carrier in the carrier in the carrier in the carrier in the carrier in the carrier in the carrier in the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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P-PSDB; AAB36354.
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                                    Doran JL,
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                                                                                                                99US-0127888P
                                                                                                                                                                                                                                                                                                                                              response;
                                                                                                                                                                                                                                                                                                                                                chromosomal gene replacement; fimbrin; epitope; esponse; immunogen; ds.
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85.5%;
                                      Collison SK,
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Pred. No. 6.8e-104;
0; Mismatches 66;
                                    Kay WW;
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P-PSDB; AAB36351.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 137; 139pp; English.

The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF1/T/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent (I) is CC useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to CC 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live constitute the inserted epitope, and hybrid fimbriae are usually strong CC immunogens to the inserted epitope, and hybrid fimbriae are easy and consequence is given in the exemplification of the present invention

Sequence 456 BP; 112 A; 113 C; 125 G; 106 T; 0 U; 0 Other;

Matches Query Match Best Local 301 421 361 361 301 241 241 181 181 121 121 390; 61 61 1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAGTCGTAGTTTCTGGCAGTGCTCTGGCT Similarity GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT GCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCCGGC GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC 120 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456 CTGGTTACCCGTGTTACCCATGAAATGGCACATGCAAGGCGTAATGGTGCGTCAGGTT GCACATGCAGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT GTAGGCCAGGGTGCGGATAATTATGATCAGCTGGTTACCCCGTGTTGTTACCCCATGAAATG AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180 Conservative 76.8%; 85.5%; 0, Score 350.4; DB 3; Pred. No. 6.8e-104; Mismatches DB 3; 66; Length 456; Indels 0, Gaps 420 240 420 240 180 120 60

421

456

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                                        Query Match
Best Local :
                                                                                                                                     Sequence 456 BP; 113 A; 110 C; 124 G; 109 T; 0 U; 0 Other;
                                                                                                                                                                                                                                     immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                                                                                       exemplification of the present invention
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B; DB 3;
2.3e-103;
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37. .60
                                                                                                                                                                                                                                                                 /note= "TAF6 primer (pair with TAF5)"
complement (292. .402)
                                                                                                                                                                                                                                                                                                                                    /note= "TAF3 primer (pair
complement (103. .129)
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/note= "TAF5 primer (pair with TAF6)"
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primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KING/)
                                                                            primer_bind
                                                                                                                                                                                Enteropathogenic bacteria;
                                                                                                                                                                                                       Salmonella enteritidis 27655-3b TnphoA mutant agfA gene fragment.
                                                                                                                                                                                                                                  25-MAR-2003
30-SEP-1997
                                                                                                                                                                                                                                                                        AAT74141;
                                                                                                                                                                                                                                                                                               AAT74141 standard; DNA; 361 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 361 BP; 94 A; 93 C; 94 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eliciting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  an immune response to Salmonella - using attenuated Salmonella vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                       enteritidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                (revised)
(first entry)
                                /label= Primer_TAF5
52. .69
  /*tag= c
/label= Primer_TAF3
complement(103. .128)
                                                                            /label= agfA_gene_fragment
16. .60
                                                                                                                            Location/Qualifiers
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99.0%;
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                                                                                                                                                                                S.enteritidis; antibody;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an isolated agfA gene fragment derived from Salmonella enteritidis 2765-3b TnphoA mutant strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                        Sequence 361 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Col 107-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enteropathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collinson SK,
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enteropathogenic bacteria of the Enterobacteria family.
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                                                                           GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC 303
                                                                                                                                  GATGCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCCGATGTA
                                                                                                                                                                                             GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC
                             ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATG
                                                                                                                   GATGCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCGATGTA
                                                                                                                                                                            GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC
                                                                                                                                                                                                                                      GTCGTACCACAGTGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCG
ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACG
                                                          GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC
                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay WW,
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/label= Primer_TAF6
complement(294..312)
/*tag= e
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Primer_TAF4
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Pred. No. 2.7e-83;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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            222222211111111110
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26543210987654321098
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                                                                                                                                                                                                                                                                                                                                                                                                                                              404.8
287.2
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         Query
Match
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Gapop 10.0 , Gapext 1.0
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                       Copyright
                       Length
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   US-08-233-788A-58
US-08-233-788A-56
US-09-233-788A-56
US-09-431-614-5
US-09-431-614-5
US-09-431-614-5
US-09-125-619-3
US-08-363-475-18
US-08-363-475-21
US-08-417-103-15
US-09-08-417-103-15
US-09-016-434-1303
US-09-016-434-1303
US-09-103-840A-2
3 US-09-103-840A-2
3 US-09-103-840A-1
US-09-643-597-153
US-09-643-597-153
US-09-66-421B-153
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Sequence 58, Appl Sequence 1, Appli Sequence 1, Appli Sequence 5, Appli Sequence 3, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 15, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 152, Appli Sequence 152, Appli Sequence 152, Appli Sequence 153, Appli Sequence 2, Appli Sequence 1, Appli Sequence 153, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 113, Appli Sequence 153, Appli Sequence 153, Appli Sequence 153, Appli Sequence 153, Appli Sequence 153, Appli Sequence 153, Appli Sequence 153, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Ap
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Query Match Best Local Simi Matches 424;	US-08-233-788A-58  US-08-233-788A-58  Sequence 58, Application US/08233788A  Patent No. 5635617  GENERAL INFORMATION: APPLICANT: Doran, James L. APPLICANT: Collinson, Karen S. APPLICANT: Collinson, Karen S. APPLICANT: Clouthier, Sharon C. IIILE OF INVENTION: METHODS AND COMPTITLE OF INVENTION: OF SALMONELLA NUMBER OF SEQUENCES: 61 CCRRESPONDENCE ADDRESS: ADDRESSEE: Seed and Berry STREET: 6300 Columbia Center, 701 CITY: Seattle STATE: Washington COUNTRY: U.S.A. ZIP: 98104-7092 COMPUTER ENANABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER FRANABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: 1BM C Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, v CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/233,788A FILING DATE: 26-APR-194 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: King, Joshua REGISTRATION STATE: 920043.40 TELEFAN: (206) 682-6031 TELEX: 3723836 SEEDAMBERRY INFORMATION FOR SEQ ID NO: 58: SEQUENCE CHARACTERISTICS: LENGTH: 456 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear FEATURE: NAME/KEY: CDS US-08-233-788A-58		5 29. 29.	C 42 29.4 43 29.4	29.	37 29. 38 29.	35 29. 36 29.	33 29.	1 29.	9 30.
88. milarity 93. Conservative	788A-58 788A-58 788A-58 788A-58 788A-58 788A-58 788A-58 788A-58 788A-58 788A-58 788A-58 788A-58 788A-58 788A-58 788A-58 788A-58 788A-58 788A-58 788A-58		.4 366 .4 920	6.4 1252 6.4 1939	.4 91 .4 125	.4 42 .4 75	.5 403 .5 97	.5 361	.5 107	.6 214 .6 214
8%; Score 404.8; 0%; Pred. No. 1.5 0; Mismatches	ion US/08233788A  James L. Son, Karen S. son, Karen S. ier, Sharon C. ier, Sharon C. ier, Sharon C. ier, Sharon C. ier, Sharon C. ier, Sharon C. ier, 701 Fi. on Sharon C. on SalMONELLA  RES: and Berry lumbia Center, 701 Fi. on on  PC-DOS/MS-DOS tin Release #1.0, Ver. N DATA: IN BAR18 194 435 VIN Release #1.0, Ver. N DATA: BER: US/08/233,788A -APR-194 435 VINFORMATION: hua 1571CS: 1871CS:	ALI GNMENTS	56	4 US-09-954 4 US-08-961	288	ឌូឌូ	5 5	ផ្លួន	g g g	3,2,2
104.8; DB 1; No. 1.5e-131; natches 32;	OSITIONS FOR Fifth Avenue Fifth Avenue	ENTS	-991A-12269 -506-1	-697-29	-659A-22 -756-29	-991A-7641 -659A-18	-434-1369 -352-2055	-506-2 -434-1234	-991A-10818	3-09-606-421B-154 3-09-221-107-154 3-09-252-991A-10904
Length 45 Indels	DETECTION		sequ sequ	Seques Seques	Sequ Sequ	Sequ Sequ	sequ sequ	Sequ Sequ	rbes Sequence Seq Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Seq	request Sequest
0; Gaps			lence 1226 lence 1, A	Sequence 29, Sequence 310,	lence 22,	mence 7641 tence 18,	ence 1369	ience 2, Aj	mence 1081	Sequence 154, App Sequence 154, App
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Query Match Best Local Similarity Matches 424; Conserv

Score 404.8; DB 1; Pred. No. 1.5e-131; 0; Mismatches 32;

0;

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RESULT 2
US-08-233-788A-56
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 bass
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                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
CONCUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kay, William ...
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                              STREET: USCATTLE Seattle
                                                                                                                                                                                                                                                                                                                          ZIP: 98104-7092

MPUTER READABLE FORM:

MEDIUM TYPE: Floppy
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ร 6356)
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                                                                                                                                                                                                                                                                                                                                                                                                                           6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seed and Berry
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PILING DAID:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/055,108
APPLICATION NUMBER: US 60/055,108
FILING DATE: 06-AUG-1977
ATTORNEY/AGENT INFORMATION:
NAME: GOLDMAN, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1581
TELECOMMUNICATION INFORMATION:
TELEPAN: (716) 263-1304
TELEPAN: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TRNGTH: 1344 base pairs
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Patent No. 6262018
GENERAL INFORMATION:
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Best Local Similarity
Matches 289; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120 0000
FILING DATE:
CLASSIFFT:
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kim, Jihyun Francis
APPLICANT: Beer, Steven V.
TITLE OF INVENTION: HYPERSENSII
TITLE OF INVENTION: ERWINIA AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTTGCTCTGCAAAGC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 GTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rochester
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Nixon, Hargrave, Devans & Doyle LLP P.O. Box 1051, Clinton Square
                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
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Pred. No. 1.8
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US-09-120-927-1
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US-09-431-614-5/c
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                                                                                                                     Sequence 3, Application US/09125619 Patent No. 6437116
                                                                                                       GENERAL INFORMATION:
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Matches
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LENGTH: 1
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                                                   APPLICANT:
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APPLICANT:
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Patent No. 6624139
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APPLICANT: Schading, Richard L.
APPLICANT: Schading, Richard L.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
TITLE OF INVENTION: RESISTANCE
FILE REFERENCE: 21829/41 (EBC-003)
CURRENT APPLICATION NUMBER: US/09/431,614
CURRENT APPLICATION NUMBER: US/09/431,614
CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 60/107,243
EARLIER FILING DATE: 1998-11-05
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ORGANISM: Erwinia amylovora
-09-431-614-5
                     APPLICANT:
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       APPLICANT:
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l Similarity 54.9%;
67; Conservative
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JING-REN, STEVEN J.
JING-REN, ZHANG
HARDHAM, JOHN M.
HOWELL, JERRILYN K.
BARBOUR, ALAN G.
WEINSTOCK, GEORGE M.
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Pred. No. 0.13;
0; Mismatches
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Pred. No. 0.13;
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FILE REFERENCE: UTSH:234
CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 7766
TYPE: DNA
ORGANISM: Borrelia burgdorferi
FEATURE:
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5/486473-3/c
15/486473
2 PATECENT NO. 5486473
2 APPLICANT: FUKITA, HIROYUKI; YOSHIDA, IWAO; TAKAGI, MITSUO;
2 MANABE, SADAO; FUKAI, KONOSUKE
3 TITLE OF INVENTION: A DIA CODING FOR A FLAVIVIRUS ANTIGEN
3 NUMBER OF SEQUENCES: 16
3 CURRENT APPLICATION DATA;
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FILING DATE: 05-DEC-1988
APPLICATION NUMBER: 932,419
FILING DATE: 19-NOV-1986
SEQ ID NO:3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: R = A OR
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FILING DATE: 09-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 809,255
FILING DATE: 18-DEC-1991
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                                                                       298
                                                                                                                                                                                                            238 GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT 297
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84
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                                                                                                                                                                                                                                                                                       CAAGTCACTGACCGAAGCTAGGTAACAGTAACTGCGCACATCTGCGAGGTTGGCTGCTTC
                                                                                                                                                                                                                                                                                                                                                           CAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCC 237
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   ATCGCCTTCCAGTACCAGATCAACCCATGTAGCTCC
                                                                AATGCCACCATCGACCAGTGGAACGCTAAAAACTCC 333
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.6
Matches 60; Conservative
                                                                                            SENERAL INFORMATION:
                                                                                                            equence 21, Application US/08363475
              APPLICANT: Chiang, Shu-Jen
APPLICANT: Burnett Jr., Willian V.
APPLICANT: TONZI, Sean M.
TITLE OF INVENTION: PUNICILLIN V AMIDO:
TITLE OF INVENTION: FUSARIUM OXYSPORUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (609) 252 45:
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: ON TELECOMMUNICATION INFORMATION: TELEPHONE: (609) 252 4956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              atent No. 5516679
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/00
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chiang, Shu-Jen
APPLICANT: Burnett Jr., Wi
APPLICANT: TONZi, Sean M.
                                                                                                                                                                                           1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Savitsky, Thom
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLE OF INVENTION: PENICILLIN V AMIDOHYDROLASE GENE FROM TLE OF INVENTION: FUSARIUM OXYSPORUM
                                                                                                                                                                                                                                                   278 CTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCCGATA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDRESSEE:
                                                                                                                                                                          TTAGTATCTGCCGTCTTGCCGCCCATGTTTCCGGCGTTGTTTCCAATG 1284
                                                                                                                                                                                                    TTACTGTCGGCCAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATG 385
                                                                                                                                                                                                                          CCCCAATCGITTCTGGGGGCAACGCCTTCCTCGACCATTTCACAATAGGCAGAAGCACA 1332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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: New Jersey
RY: U.S.A.
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1..1521
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ADDRESS
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                          PENICILLIN V AMIDOHYDROLASE GENE
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Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                            Length 1767;
                                                                                                                                                                                                                                                                                   Indels
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US-08-415-823-1
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                                                                                                                                                                                                                                                                                                               Sequence 1,
Patent No. !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                        ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               APPLICANT:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Saviteky, Thomas R.
REGISTRATION NUMBER: 31,66
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                 ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     TITLE OF INVENTION:
      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA;
ADDITONNATION ANDRED. 116 / 106 / 176
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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STREET: P.O. Box 4C
CITY: Princeton
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2284 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                           338 TTACTGTCGGCCAATATGATCAGCTGGTTACCCGTGTTGTTACCCATG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 СТСАСААТССТТТСАСАААТААТСССАССАТССАССАСТССВАДСССТАВААДСТССССАТА 337
                                                                                                                                                                                                                                                                                                  INFORMATION:
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                                                                                                                                                                                                                                                                                                                    Application US/08415823
                                                                                                                                                1601 Market Street, 36th floor
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            PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                        Panitch Schwarze Jacobs & Nadel, P.C.
                                                                                                                                                                                                                                                                              Donovan, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                      A.S. Nadel
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241..1836
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                                                                                                                                                                                                         BĀCILLUS THURINGIENSIS ADP AND DPP
PROTEASE GENES AND ALKALINE PROTEASE DEFICIENT AND NEUTRAL
PROTEASE DEFICIENT B.T. STRAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.68;
US/08/415,823
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Pred. No. 1.6;
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RESULT 10
US-09-086-662-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09086662
Patent No. 5962264
GENERAL INFORMATION:
 Query Match
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Best Local Similarity 48.1%;
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TYPE: nucleic acid
STRANBEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (geno
                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1750 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/086,662
                                                                                                                                                                                                                                                                                                                                                           ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                      MOLECULE TYPE:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
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                                                                         TOPOLOGY: ci
                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1601 Market Street, CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Panitch Schwarze Jacobs & Nadel, P.C.
                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                509 TGTGGAATATGCAGAACCGAATTATTACGTTCACGCCTTTTGGACTCCAAACGACCCATA 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88;
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                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                           circular
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                                                      DNA (genomic)
                                                                                        double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purduy
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PROTEASE GENES AND ALKALINE PROTEASE DEFICIENT AND NEUTRAL
PROTEASE DEFICIENT B.T. STRAINS
 6.8%;
                                                                                                                                                                                                  08/415,823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,,</u>
 Score 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36th floor
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Length 1750;
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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-417-103-15
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                                     Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/08417103 Patent No. 5723299
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                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,283
APPLICATION NUMBER: US 07/816,283
APPLICATION NOMBER: US 07/816,283
APPLICATION NUMBER: US 07/816,283
APPLICATION NUMBER: 37,259
REGISTRATION NUMBER: 37,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,103
FILING DATE: 05-APR-1995
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1147 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: AR TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                             STRANDEDNESS:
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P.O. Box 4433
                                                                                                                                                                                                                         1147 base pairs
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                                               Score 30.6; DB Pred. No. 1.8; 0; Mismatches
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US-07-816-283-5/c
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Best Local Similarity 48.1%;
Matches 87; Conservative
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ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, C. Steven
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
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NUCLEIC A
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
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APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
TITLE OF INVENTION: SOMATOSTATIN RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                       394 C 394
                                                 250 AATGATGCAGACCACAAAATAGATGAATGTGAGGACTGCATTGCTTGTCAGGTCATAGTA 191
                                                                                                334 GATATTACTGTCGGCCAATATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCA 393
                                                                                                                                                  310 GGTCTTCATCTTGGCATAGCGGAGGATGACATAAATGACAAGTGTGTTGGCACACAACCC
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; NAME/KEY:
; LOCATION:
US-08-417-103-5
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RESULT 14
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US-08-417-103-5/c
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (512) 474-757
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 01-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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APPLICANT: Yamada, Yuichiro
APPLICANT: Seino, Susumu
APPLICANT: Seino, Susumu
APPLICANT: SOMATOSTATIN RECEPTORS
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Palan-
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REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: Un
ZIP: 77210
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5. 5723299
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US-09-016-434-1303/c

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RESULT 15
US-09-134-000C-1552/c
; Sequence 1552, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
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US-09-016-434-1303
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Best Local Similarity 48.1%;
Matches 87; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 845-4166 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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IMMEDIATE SOURCE:
LIBRARY: GENBANK
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3174 PORTER DRIVE
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Pred. No. 2;
0; Mismatches 94; Indels
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PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1552
LENGTH: 1797
TYPE: DNA
ORGANISM: Enterococcus faecalis
US-09-134-000C-1552
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Search completed: March 16, 2004, 04:37:25
Job time: 53.6647 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032 CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                            Local Similarity
                                                                               661
                                                                                                                                                                                   361 CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT 420
                                                                                                                     421 GGTTTTGGC 429
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                                                                                                                                                        CTGGTTTTTCTTCTGCTTCTTCATGAAATTGCACATATAAGCGCAATAATTCATTAATTG 662
                                                                               GTTGTTGGC 653
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65.2%;
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Result
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Listing first 45 summaries
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456
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.Seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Ggn2_6/ptodata/2/pubpna/US09E PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09E PUBCOMB.seq:*
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(cgn2_6/ptodata/2/pubpna/pcTUS_PUBCOMB.seq:*
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_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                                       4 9 US-09-879-248-5

4 14 US-10-010-390-6

4 15 US-10-441-736-5

15 US-10-369-493-26980

2 14 US-10-156-761-3483

8 14 US-10-156-761-1

6 12 US-10-222-566-3

14 US-10-222-162-3

6 14 US-10-223-162-3

6 14 US-10-143-024-3
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US-09-880-371-6
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US-10-424-599-88945
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Sequence 3563, Ap
Sequence 6, Appli
Sequence 6, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 26980, A
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Sequence 1, Appli
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Sequence 3, Appli
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6.7	7	6.7	6.7	6.7	6.7	6.7	6.8	6.8	6.9	6.9	6.9	6.9	6.9	6.9		7.0	7.0	7.0	7.0	7.0	7.0		7.0		7.1	7.1	7.1	7.1	7.1
1608	1510	1351	1164	1110	1110	421	2886	487	2074	2007	1287	269	269	6003	4830	52101	24081	4590	4589	978	750	750	983	972	708	568	596	596	596
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US-09-815-242-3923	115-10-292-798-677	US-10-305-720-1303	US-10-282-122A-13500	US-10-225-567A-313	US-09-826-509-570	US-09-918-995-33997	US-09-801-368-131	US-10-060-036-4434	US-10-425-114-27886	US-10-425-114-31950	US-10-369-493-46950	US-09-923-876-5903	US-09-923-876-5903	US-10-010-901-9	US-10-282-122A-27869	US-10-132-134-1	US-10-132-134-13	US-09-764-891-8846	US-09-764-891-8845	US-10-369-493-24265	US-10-184-634-104	US-10-184-644-104	US-09-764-864-465	US-10-333-631-4	US-10-282-122A-27953	US-10-333-631-1	US-10-063-685-100	US-10-184-634-310	US-10-184-644-310
Sequence 3923, Ap		Sequence 1303, Ap	Sequence 13500, A	Sequence 313, App	Sequence 570, App	Sequence 33997, A	131, Ag	Sequence 4434, Ap		Sequence 31950, A	46950,	Sequence 5903, Ap	590			Sequence 1, Appli		Sequence 8846, Ap		24265		e 104,	465					•	Sequence 310, App

## ALIGNMENTS

S 밁 8 US-10-398-221-3563 US-10-398-221-3563 TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION UMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION UMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
ORIGHNAPPLICATION UMBER: FR 00/12 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: Patentin version 3.0
SEQ ID NO 3563
LENGTH: 2751
TYPE: NAT Query Match 7.5%; Best Local Similarity 52.0%; Matches 77; Conservative GENERAL INFORMATION: Sequence 3563, Application US/10398221 Publication No. US20040018514A1 APPLICANT: KUNST, Frederik APPLICANT: GLASER, Philippe FEATURE:
NAME/KEY: misc\_feature
LOCATION: (1)...(end)
OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u TYPE: DNA
ORGANISM: Listeria monocytogenes 321 381 AÄAGAAGCAÄTGGATCGTTTTGGCAGTGÄTÄAACCAGATATTCGTTTTGGTTTTAGÄATTA 440 298 238 GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT 297 GATGTAGTGAAAGAAGCGAAAAATATTACTATCGACAAACCGTTTCCTCGTATGACATAT 380 AATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGAT 357 Score 34.4; DB 15; Length 2751; Pred. No. 1.1; O; Mismatches 71; Indels O; <u>,</u> Gaps

US-10-282-122A-24385

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PRIOR APPLICATION NUMBER: 60/198,359
NUMBER OF SEQ ID MOS: 12
SOFTWARE: Patentin Ver. 2.1
LENGTH: 1344
TYPE: DNA
ORGANISM: Erwinia amylovora
US-09-835-684-6
                                                                                                                                                                                                                                                                                                                                               US-09-835-684-6/c
                                                                                                                                                  APPLICANT: Qiu, Dewen
APPLICANT: Renick, Dean
TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE
TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR
CURRENT ENVENTION: DESICCATION
CURRENT APPLICATION NUMBER: US/09/835,684
PRICE ADDITION: 2001-04-16
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09835684 Patent No. US20020019337A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_51326C.1
US-10-424-599-88945
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LENGTH: 616

TYPE: DNA
FEATURE: Glycine max
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US-10-424-599-88945/c
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Can Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER: US/10/424,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 88945, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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OTHER INFORMATION: unsure at all n locations
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Pred. No. 0.56;
0; Mismatches 78;
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US-09-879-248-5/c
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                                                                                                                                                        Sequence 5, Application US/09879248 Patent No. US20020062500A1
                                                APPLICANT: Fan, Hao
APPLICANT: Wei, Zhong-Min
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITING DOMAINS
FILE REFERENCE: 21829/81
                                                                                                                                                       GENERAL
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; TYPE: DNA
; ORGANISM: Erwinia amylovora
US-09-880-371-6
CURRENT APPLICATION NUMBER: US/09/879,248
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/212,211
PRIOR FILING DATE: 2000-06-16
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US-09-880-371-6/c
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SEQ ID NO 6
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APPLICANT: Derocher, Jay
TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC
FILE REFERENCE: 21829/91
CURRENT APPLICATION NUMBER: US/09/880,371
PRIOR APPLICATION NUMBER: 60/211,585
PRIOR APPLICATION NUMBER: 60/211,585
NUMBER OF SEQ ID NOS: 16
NUMBER OF SEQ ID NOS: 16
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Patent No. US20020059658A1
GENERAL INFORMATION:
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Best Local S
Matches 67
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                                                                                                                                                INFORMATION:
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67; Conservative
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54.9%;
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Pred. No. 1;
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Pred. No. 1;
0; Mismatches 55
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RESULT 6
US-10-010-390-6/c
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US-10-441-736-5/c
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; TYPE: DNA
; ORGANISM: Erwinia amylovora
US-10-010-390-6
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TYPE: DNA
; ORGANIZM: Erwinia amylovora
US-09-879-248-5
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Sequence 5, Application US/10441736
Publication No. US20040016029A1
GEMERAL INFORMATION:
APPLICANT: We1, Zhong-Min
APPLICANT: Schading, Richard L.
APPLICANT: Schading, Richard L.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
TITLE OF INVENTION: RESISTANCE
TITLE OF INVENTION: RESISTANCE
TITLE OF INVENTION: RESISTANCE
TITLE OF INVENTION: RESISTANCE
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Best Local
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APPLICANT: Leon, Ernesto
APPLICANT: Leon, Ernesto
APPLICANT: Oviedo, Agustin
TITLE OF INVENTION: METHODS OF INHIBITING DESICCATION OF CUTTINGS REMOVED
TITLE OF INVENTION: PROM ORNAMENTAL PLANTS
FILE REFERENCE: 21829/111
CURRENT APPLICATION NUMBER: US/10/010,390
CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: 60/248,169
PRIOR PILING DATE: 2000-11-13
NUMBER OF SEQ ID NOS: 14
SOFTMARE: Patentin Ver: 2.1
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l Similarity 54.9%;
67; Conservative
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54.9%;
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Pred. No. 1;
0; Mismatches
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Pred. No. 1;
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/60/369,493
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
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RESULT 9
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US-10-369-493-26980/c
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US-10-369-493-26980
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US-10-441-736-5
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 26980
LENGTH: 1625
TYPE: DNA
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CURRENT FILING DATE: 2003-05-20
PRIOR APPLICATION NUMBER: 60/107,243
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 09/431,614
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                                                                                   Local Similarity 61.1%;
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Local Similarity 54.9%;
les 67; Conservative
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                                                         ATTCTGATGGGGTGGATGCCCTTGTCAATA 306
                                                                                            AATATGATCAGCTGGTTACCCGTGTTGTTA 379
                                                                                                                                       TCGGAAATTCTGTCAAGCTCGGCCACAGCAATGTCGCAAGCTTGGTCATAACCGTCGGCG
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                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                      7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 34; DB 1; Pred. No. 1; 0; Mismatches
                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                 Score 34; DB 15;
Pred. No. 1.1;
                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                      Length 1625;
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US-10-156-761-3483/c

Sequence 3483, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:

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APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2002-05-29
PRIOR FILING DATE: 3001-05-30
PRIOR FILING DATE: 3001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 3001-08-02
PRIOR FILING DATE: 300
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APPLICANT: IKEDA
APPLICANT: ISHIK
APPLICANT: HORIK
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; NAME/KEY: CDS

; LOCATION: (1).. (1662)

US-10-156-761-3483
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                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29 PRIOR APPLICATION NUMBER: JP 2001-204089 PRIOR FILING DATE: 2001-05-30
                                                                                                   TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
EQ ID NO 1
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                 FEATURE:
NAME/KEY: misc feature
LOCATION: (4187715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ISHIKAWA, JÜN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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ORGANISM: Streptomyces avermitilis
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HORIKAWA, HIROSHI
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g, other or unknown
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RESULT 12
US-10-222-162-3
; Sequence 3, Application US/10222162
; Publication No. US20030060618A1
; GENERAL INFORMATION:
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APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HARDHAM, JOHN M.
APPLICANT: BARBOUR, ALLAN G.
APPLICANT: BARBOUR, ALLAN G.
ITITLE OF INVENTIONS: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
CURRENT APPLICATION NUMBER: US/10/222,566
PRIOR FILING DATE: 2002-08-16
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
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SEQ ID NO 3

LENGTH: 7766

TYPE: DNA
ORGANISM: Borrelia burgdorferi
FEATURE:
NAME/KEY: modified_base
LOCATION: (127)
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US-10-222-566-3
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Best Local Similarity
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Similarity 47.8%;
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Pred. No. 5.8;
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Pred. No. 1.8e+02;
0; Mismatches 68;
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APPLICANT: NORRIS, STEVEN J.

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; FEATURE:
NAME/KEY: modified_base
LOCATION: (127)
OTHER INFORMATION: R = A OR
US-10-143-024-3
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SEQ ID NO 3
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SEQ ID NO 3
LENGTH: 7766
TYPE: DNA
ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH: 234USD1
CURRENT APPLICATION NUMBER: US/10/143,024
CURRENT FILING DATE: 2002-05-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYM K.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH: 234USD4
CURRENT APPLICATION NUMBER: US/10/222,162
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR PILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 09/125,619
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 48
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NORRIS, STEVEN J. APPLICANT: JING-REN, ZHANG
                                                                                                                                                                             SOFTWARE: Patentin Ver.
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                                                                                                  TYPE: DNA
ORGANISM: Borrelia burgdorferi
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NAME/KEY: modified_base
LOCATION: (127)
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HARDHAM, JOHN M.
HOWELL, JERRILYN K.
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RESULT 15
US-10-282-122A-24385
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US-09-949-654-3
Sequence 24385, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
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APPLICANT: YAN, Chunhua et al.
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000817
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Best Local Similarity
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/949,654
CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: 60/231,572
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature LOCATION: (1)...(368004) OTHER INFORMATION: n = A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Human FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                                  165240 AAGTCTTCA 165248
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                                                                                                                                                                     448 CAGTATTAA
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Pred. No. 48;
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APPLICANT: Wang, Liangsu APPLICANT: Zamudio, Carlo APPLICANT: Malone, Cheryl

Carlos

APPLICANT:

Haselbeck, Robert

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APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITPRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-010-23
PRIOR APPLICATION NUMBER: 60/253,625
Search completed: March 17, 2004, 08:15:58 Job time: 415.736 secs
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; ORGANISM: Listeria monocytogenes
US-10-282-122A-24385
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24385
LENGTH: 1776
                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 7.2%; Score 32.8; DB 12; Length 1776; Best Local Similarity 51.4%; Pred. No. 3; Matches 76; Conservative 0; Mismatches 72; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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                                                                                                                                                                                                835 AAAGAAGCAATGGATCGTTTTGGCAGTGATAAACCGGATATTCGTTTTGGTTTAGAATTA 894
                                                                                                                                                                                                                                             298 AATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGAT 357
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                                                                                                CAAAATGTATCCGATGTCGTAAAAGATG 922
                                                                                                                                                   CAGCTGGTTACCCGTGTTGTTACCCATG 385
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Zyskind, Judith
Wall, Daniel
Trawick, John
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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                            Query
Match
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456
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                                            Length
    523
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   BJ618688
BJ334624
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BZ295150
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                                                                    SUMMARIES
BJ618688 BJ618688
BJ334624 BJ334624
CF446143 EST682488
BZ295150 CG1320.rl
                                            Description
                                                                                                    REFERENCE
AUTHORS
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KEYWORDS
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BJ618688/c
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                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                          Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Jap
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available
URL.
                                                                                                                                                                                                                                                                         Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Barrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus
1 (bases 1 to 680)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
                                                                           Expressed genes in X. laevis embryo Unpublished (2001)
                                                                                                                                                              BJ618688.1 GI:37256713
EST.
                                                                                                                                                                                      BJ618688 NIBB Mochii normalized Xenopus early gastrula library Xenopus laevis cDNA clone XL186b22 5', mRNA sequence.
                                                                                                                                                                               BJ618688
                                                                                                                                                     Xenopus laevis (African clawed frog)
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F19524
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BJ333958
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                                           411-8540, Japan
           available through the following
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A1809250 Triticum
BU776718 SJEBCA03
BU780674 SJEFZH02
B1959328 HVSMEn001
BU944683 603765715
BZ300068 KD0510.p1
AU295325 AU295325
AU139321 AU139321
                                                                                                                                                                                                                                                                                                                                                         F19524 HSPD04128 H
AA746477 nw62e02.8
CD374421 TNWbmfC2H
BU755156 sas23f11.
CG178280 PUJDF79TD
AL196666 Tetraodon
CF437982 EST674327
BZ469000 BOOAO58TF
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BZ204853 CH230-290
CB210843 OML01123
AV976624 AV976624
BQ0141266 NF017G03P
AW686303 NF036D06N
AW573882 EST316473
BJ331339 BJ3367372
BJ331339 BJ3367372
BJ333958 BJ333598
BJ335968 BJ3336903
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BJ33697 BJ33637
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BB581987 BB581987
CA711477 wdk2c.pb6
BB757100 BB757100
BB757100 BB757100
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                     Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-6856
Fax: 81-559-81-6855
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                                                                                                                             Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 523)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the
                                                                                                           Unpublished (2002)
                                                                                                                                                                                                                                                    BJ334624 Dictyostelium discoideum cDNA libear EST 05-MAR-20 discoideum cDNA clone dda47006 5', mRNA sequence.
                                                                                                                                                                                             Dictyostelium discoideum Dictyostelium discoideum
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BJ334624.1 GI:19164754
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                                                                                                                                                                                                                                                                                                                                                                                      GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                              ĠĠĊŦŦŦĠĠŦĀĀĊĀĀĊĠĊĠĀĊĊĠĊŦĊĀŦĊĀĠŦĀĊŦĀĀ 138
                                                                                                                                                                                                                                                                                                                                                                                                               GGCAACGGTGCTGCAGTTGAĆĊÁGACTGCATĊTAACTČCTCČGŤCÁACĠŤĠACŤĊÁĠĠŤŤ
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Location/Qualifiers
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tshini@genes.nig.ac.jp
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/mol type="mRNA"

/db_Xref="taxon:8355"

/clone="XL186b22"

/tissue_type="whole embryo"

/dev_stage="stage 10.5"

/clone_lib="NIBB Mochii normalized Xenopus early gastrula
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Pred. No. 3.5e-53;
0; Mismatches 144;
                                          411-8540, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                         Contact: Havey MJ
Department of Horticulture
USDA-ARS and University of Wi
1575 Linden Drive, Madison, W
Tel: 608-262-1830
Fax: 608-262-4743
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 744)
Havey, M.J., Cheung, F., Va
Expressed Sequence Tags f
tissues (Allium cepa)
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 GATGTAGGCCAGGGTGCGGATAATAGTACTTATTGAACTGACTCAGAATGGTTTCAGAAAT 297
                                                                                                                                                                                                                                                                       http://haveylab.hort.wisc.edu
Seq primer: CAG GAA ACA GCT ATG
                                                                                                                                                                                                                                                                                                   Email: mjhavey@facstaff.wisc.edu
TIGR sequence name ACAHU74TR. For more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allium cepa
Allium cepa
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CF446143
CF446143.1 GI:34468845
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EST682488 normalized cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
/tissue_type="Callus, roots, and young bulbs"
/clone_Tib="normalized cDNA library of onion"
/note="Vector: pcMvSport6.1-ccdb (Invitrogen); Site_1:
ROORV (5'); Site_2: NotI (3'); Equal molar amounts of mRNA
from callus, roots, and young bulbs were combined to
synthesize the library. Normalization to enrich for
low-copy transcripts was performed by proprietary
techniques of Invitrogen."
                                                                                                                                                                    /mol_type="mRNA"
/cultivar="Red Creole(bulbs), unknown(callus),
Texas Legend(roots)"
                                                                                                                                           /db_xref="taxon:4679"
/clone="ACAHU74"
                                                                                                                                                                                                                      organism="Allium cepa"
                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Dictyostelium
/mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dev_stage="Aggregation stage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:44689"
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Pred. No. 30;
0; Mismatches
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A library
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30;
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Query Match Best Local Similarity

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Score Pred.

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BZ295150/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wong S
Department of Genetics, S
Trinity College Dublin
Dublin 2, Ireland
Tel: 353 1 6082319
Fax: 353 1 6798558
Email: swongercd.ie
Class: plasmid ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 TGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 549)
Wong, S., Fares, M.A., Zimmermann, W., Butler, G. and Wolfe, K.H.
Evidence from comparative genomics for a complete sexual cycle
the 'asexual' pathogenic yeast Candida glabrata
Genome Biol. 4 (2), R10 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BZ295150
549 bp DNA linear GSS 31-OCT-200 CG1320.r1 Candida glabrata Random Genomic Library Candida glabrata genomic clone CG1320, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic clone
BZ295150
                                                                                                                                                                                                                                                  h 7.6%;
Similarity 52.0%;
78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida glabrata
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Candida glabrata
                                                                                                              GAAAATTGACAGTGTGTGTATCAGCAAACACATCTAGATCGCAACCAGCTCCTATATCAG
                                                                                                                                                                              TTATAGTTTTTGCTCCTACAAAGGCCAAATTTTCAGTGAAAAAAGCTGAAAATTTTTGCA
                                                                                                                                           GAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTAC
                                                                         TGTCGGCCAATATGATCAGCTGGTTACCCG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAGGTTGGTTTTGGCAACAACGCCACGGCTAACCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGCGGAGAGAAAGCAACTCTTTTTATGATGAATCTGTTCATAATGTTGGCAAGGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATA
                                        TGTCTGCCAAGAATATCCTTTTGATAACCG 142
                                                                                                                                                                                                                 TTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGATTTAACAACTTCAACAACAAATCGGCCTCGAAGT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATAACAATAGTAACAGCAAATGGATCTCTAAAAAGGTGTGTTGATACTATCAATAATGA
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                                                                                                                                                                                                                                                                                                                                                                                         organism="Candida glabrata"
/mol_type="genomic DNA"
/strain="CBS 138"
                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:5478"
/clone="CG1320"
/clone_lib="Candida glabrata
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                  Score 34.8; D:
Pred. No. 68;
O; Mismatches
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                                                                                                                                                                                                                                                                                     28;
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AUTHORS
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VERSION
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BZ204853
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AUTHORS
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ORGANISM
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BJ335653
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Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Ge Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Ruggs,F., de Jong,P. and Fraser,C.M.
Riggs,F., de Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 Mb Unpublished (1999)
Other_GSSs: CH230-390D21.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, U
Tel: 301 838 0200
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                       SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66;
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1 (bases 1 to 594)

Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostelium discoideum at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            594 bp mRNA linear EST 05-MAR-20
BJ335653 Dictyostelium discoideum cDNA library, AF Dictyostelium
discoideum cDNA clone dda51h06 5', mRNA sequence.
BJ335653
                                                                                                                                                                                                                                                                                     Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                       CH230-390D21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum
Dictyostelium discoideum
                                                                                                                                                                                                                 Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1111 Yata, Mishima,
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Tadasu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BJ335653.1 GI:19165783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGA 356
                                                                                                                                                                                              (bases 1 to 813)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Dictyostelium
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Aggregation stage"
/clone_lib="Dictyostelium discoideum cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="dda51h06"
/sex="mat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:44689"
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                       USA
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FEATURES

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Best Local
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                                                                                           Plant Molecular Genetics
Graduate School of Biotechnology, University of Korea
136-701 Anam-dong 5/1 Seoul, Korea
Tel: 00 82 2 3290 3430
Fax: 00 82 2 927 9028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178
                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 540)
                                                                                                                                                                              Contact: Jeong Sheop Shin
                                                                                                                                                                                            Oryza minuta HybriZAP-2.1 XR library Unpublished (2003)
                                                                                                                                                                                                                                                                                                  Oryza minuta
Oryza minuta
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OML01123 Oryza
                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                CB210843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: szhac@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
Plate: 390 row: D column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n 7.6%;
Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGATĆĀAGĀTČGĀĆCĀĀTĞGGĀTCTCĀTĀĀĀČTGĆĀĀAGCTTĆTĞTAĞĞCAĀĀ 721
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Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   СААА ССВАТ ССССТАЛА ТСТВАЛАССВАССАТТАСССАВА ССВСТТАТСВТЛАССВСССС 237
                                                                             jsshin@kuccnx.korea.ac.kr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 838 0208
/organism="Oryza minuta"
/mol_type="mRNA"
/db_xref="taxon:63629"
/dev_stage="4-weeks after germination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell_type="Brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                      540 bp mRNA linear EST 05-FEB-2003 minuta HybriZAP-2.1 XR library Oryza minuta cDNA 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34.8; DR
Pred. No. 80;
0; Mismatches
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Best Local Sim
Matches 106;
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KEYWORDS
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AV976624
LOCUS
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TITLE
JOURNAL
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FEATURES

REFERENCE AUTHORS

VERSION KEYWORDS

ORGANISM

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RESULT 7 CB210843 LOCUS

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402 CGTAATGGTGCGTCAGGTTGGTTTTGGCAACAACGCCACGGCTAA
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les 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 GGAGGCTCTCCAAAGACAGCATACTACTGATGCCTCCCAGCTAGTGGCA 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      285 ТОСТТТСАБАЛАТАЛТСССАССАТССАССАСТОВЛАСССТАЛАЛАСТСССВАТАТТАСТСТ 344
                                                                                                                                                                                                                                                                                  Similarity
                                             TGATGTCACACCTGÁTAÁTGTCACTACTAATGATGTCÁCACCTGÁTGATGTCACTAACTAA
                                                                           тетсеессалтателтелестветтасссететтеттасссателалтерсасатеслае 401
                                                                                                               TGÁTGTCACCÁCTAÁTGATGTCÁCCÁCTAÁTGÁTGTCÁÁAGCTGÁTGÁTGTCACTÁCTÁA
                                                                                                                                              GAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAAACTCCGATATTAC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: satch@ascidian.zcol.kyoto-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Nori Satch
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T. Expressed genes in Ciona intestinalis Unpublished (2000)
                                                                                                                                                                                TGATGTCAAAGCTCATGATGTCACACCTGATGATGTCACCACTAATGATGTCACCACTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kyoto University
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Ciona intestinalis
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Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV976624 Mori Satoh unpublished cDNA library, egg Ciona intestinalis cDNA clone cieg42j24 5', mRNA sequence.
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                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
                                                                                                                                                                                                                                                                                                                                    clone_lib="wori Satoh unpublished cDNA library,
                                                                                                                                                                                                                                                                                                                                                             dev_stage="egg"
                                                                                                                                                                                                                                                                                                                                                                          /clone="cieg42j24"
/tissue_type="whole animal"
                                                                                                                                                                                                                                                                              7.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Oryza minuta HybriZAP-2.1 XR library"
/note="Organ: immature leaf"
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                                                                                                                                                                                                                                                      Score 34.6; DB 9;
Pred. No. 78;
0; Mismatches 119;
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Pred. No. 77;
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KEYWORDS
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bource
                                                                                                                                                               129 AACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGCGATGC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247
                                                                                                                                                                                                             116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
OK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        539 bp
NF017G03PH1F1024 Phoma-infected
NF017G03PH 5', mRNA sequence.
BQ141266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert Length: 539 Std Error: 0.0 Plate: 017 row: G column: 03 Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gonzales,R.A., Bell,C.J., Inman,J.T., Waugh,M.E., Sullivan,J.P., May,G.D. and Paiva,N.L. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula Phoma-infected library Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Watson, B.S., Shin, H.-S.,
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BQ141266.1 GI:20277392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicago truncatula (barrel medic)
GGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCAT 308
                                                                              CCGTAAATCTGAAACGACCATTACCCAGGAGCGGTTATGGTAACGGCGCCGATGTAGGCCA 248
                                       ACGTGATCCACCTGAGATTCCTCCACAATTGCAAAACACCTTGGTCGGCTATCCTGCTAA 352
                                                                                                                          TGATGTCAAAGCTGATGATGTCACTACTAATGATGTCACACCTAA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 221 7317
580 221 7380
                                                                                                                                                                                                             Conservative
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Length: 539 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                  humid dishes. Pools of leaves were harvested at 0, 15, ar 30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96, hours, and used to prepare total RNA. CDNA was prepared from polyA+ enriched, pooled samples of equivalent amounts of total RNA from each sample. The cDNA was directionally ligated into the Uni-Zap XR vector (Stratagene) and packaged using the Gigapack III Golden extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using ExAssist helper phage and the E. coli strain XII-Blue MRF'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="leaf"
/dev_stage="Pathogen-induced, young trifoliate"
/clone_lib="Phoma-infected"
/note="Vector: pBluescript SK(-); Young trifoliate leaves
of Medicago truncatula were excised and dip-inoculated in
a spore suspension of Phoma medicaginis, and incubated in
                                                                                                                                                                                                                                                                                                                       (Stratagene). Excised plasmids were plated using SOLR
cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="NF017G03PH"
                                                                                                                                                                                                                              7.5%;
                                                                                                                                                                                                                            Score 34.4;
Pred. No. 88;
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lopez-Meyer, M., Scott, A.D., Inman, J.T., Waugh, M.E., Su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                  DB 13;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert Length: 665 Std Error: 0.0 Plate: 036 row: D column: 06 Seg primer: TCACACAGGAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2510 Sam Noble Parkway, Ardmore,
Tel: 580 221 7317
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
On Apr 14, 2000 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R. Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Paiva,N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: nlpaiva@noble.org
Email: nlpaiva@noble.org
Email: nlpaiva@noble.org
Email: nlpaiva@noble.org
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The Samuel Roberts Noble Foundation
OK 73402,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Paiva NL
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TGTCGATAGTTTTAGTTCTCCATTGCCTCAGAACGCAATTCTAAATCATCTTTATAT 409
                                                                                                                                    CCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCA 248
                                         GGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCAT 308
                                                                                        ACGTGATCCACCTGAGATTCCTCCACAATTGCAAAACACCTTGGTCGGCTATCCTGCTAA 349
                                                                                                                                                                                     AACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGCGATGC 188
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                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="root"
/dev_stage="Pooled developmental"
/clone_lib="Nodulated root"
/note="Vector: Lambda Zap; Four-week old Rhizobium
meliloti-inoculated Medicago truncatula roots, cont
a mixture of young and old roots and nodules."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="NF036D06NR"
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Pred. No. 89;
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COMMENT
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Best Local Similarity
Matches 116; Conserv
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AW573882
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR sequence name:MTCAJ64TK
More information is available at.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 Borlaug Hall, 1991 Upper Buford Circle, Tel: 612 625 5715 Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l (bases 1 to 627)

1 (bases 1 to 627)

1 (bases 1 to 627)

Fedorova, M., Pierson, B.L., Samac, D.A., Vance, C.P., Gantt, J.S., Fedorova, M., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.

ESTs from one month old nitrogen-fixing root nodules of Medicago
                                            AACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGCGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: vance004@maroon.tc.umn.edu
Minnesota EST name:M252780e
               'http://chrysie.tamu.edu/medicago'
Seq primer: SKmod (CTA gAA CTA gtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                   /tissue type="N2-fixing root nodules"
/tissue type="N2-fixing root nodules harvested one month
/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab host=""a. coli|strain XIOLR"
/clone_lib="GVN"
/note="Vector: pBlueecript SK-; Site_1: EcoRI; Site_2:
XhoI; CDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
inoculation with Sinorhizobium meliloti. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="mRNA"
cultivar="genotype A17"
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                                                                                                                                                                                                                                                                                                                                                                                            one="pGVN-49K8"
                                                                                                     7.5%;
                                                                                   Score 34.4; DI
Pred. No. 93;
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BJ367372
BJ367372 Dictyostelium discoideum cdiscoideum cdiscoideum cDNA clone ddc42p08 5',
BJ367372
BJ367372.1 GI:19276674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
                                                                                                                                                                                                                                                                                               Similarity
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81-559-81-6855
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                                                                                                                                                                                                                                                                                              7.5%;
55.5%;
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298 ААТӨССАССАТСӨАССАӨТӨӨААСӨСТАААААСТССӨАТАТТАСТӨТСӨӨССААТАТӨА 356
                                                                                                                                                                                                                                  264 GATGAAGATGAATTGGAGAATAGATATATTGGAATCAATAGAAATGAGGACAATAAT 323
                                                                                                                                                                                                                                                                238 GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota, Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 456)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BJ331339 Dictyostelium discoideum cDNA linear EST 05-MAR-20
discoideum cDNA library, AF Dictyostelium
discoideum cDNA clone dda34m22 5', mRNA sequence.
                                                                                                                                              CGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAGCTGGTTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Dictyostelium
/mol_type="mRNA"
/strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                            dev_stage="Aggregation stage"
clone_lib="Dictyostelium discoideum cDNA library,
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                                                                                                                                                                                                                                                                                                                                                 Score 34.2;
Pred. No. 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum Dictyostelium discoideum
                                                                                                                                                                                                                                           Contact: Tadasu
                                                                                                                                                                                                                                                       Unpublished (2002)
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Urushihara, H., Tana
                                                                                                                                                                                                                                                                                                                                Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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nilarity 55.5%;
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                                                                                                                          tshini@genes.nig.ac.jp.
Location/Qualifiers
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Location/Qualifiers
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/mol_type="mRNA"
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1 (bases 1 to 553)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the
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BJ336903 Dictyostelium discoideum cDNA library, J
discoideum cDNA clone dda55g13 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Tadasu Shin-i
Center For Genetic Resource Information
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Pred. No. is the number of results predicted by chance to have a

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Patent: US 5635617-A 58 03-JUN-1997;

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## REFERENCE AUTHORS KEYWORDS SOURCE ORGANISM RESULT 1 I44909 LOCUS DEFINITION ACCESSION VERSION Result No. a Ω 0 0 0 ററ ი TITLE 44403354331116 44403376 44103376 44103376 44103376 44103376 44103376 403.2 403.2 395.2 395.2 395.2 395.3 395.2 397.8 397.8 397.8 397.8 397.8 397.8 397.8 397.8 397.8 397.8 397.8 2084.2 2094.2 Sequence I44909 Unknown. Unknown. 1 (bases 1 to 456) Doran, J.L., Kay, W.W., Collinson, S.Karen. and Clouthier, S.C. Methods and compositions comprising the agfA gene for detection Salmonella Unclassified. I44909.1 [44909 88.4 2067 86.7 5103 86.7 52411 86.3 254050 86.3 254050 86.3 1048 86.3 254050 86.3 254050 1048 62.3 1048 62.3 2920 49.4 10190 49.4 10190 49.4 10190 49.4 10190 49.4 10190 49.4 10190 49.4 10190 49.4 10190 49.4 10190 49.4 10190 49.4 10190 49.4 10190 49.4 10190 49.4 10190 49.4 10190 49.4 10190 49.4 10190 48.8 48.8 44.6 44.6 44.6 9.1 10.6 10.6 58 from 8 196539 8 168267 7 163619 1425 302156 313430 108366 110000 2883 230 10370 292504 3 437 4 19201 5 1212 GI:2469622 Length patent 멂 D90742 ECC011756 EXC011756 EXC011756 EXC011759 AX814798 AF343445 AF1000409 ECCUW677 AE000409 ECCUW672 AC1458070 AC145912 AC145912 AC119493 AC119493 AE009405 AF173043 AF173043 AF173043 AC119683 AC119683 144908 CSP515700 CFF515701 AF275733 AB0025315 AP002554 CCCSGABDG AB000205 D90741 AB016759 AX814811 ECCCSGAB ESA515702 SEU53207 AB0169131 AB0169131 AB0169131 I44909 SEU43280 STAJ2301 AE008749 AL627269 AE016840 STAGFBA รูบ 456 bp I US 5635617. SUMMARIES ALIGNMENTS DNA linear AF343445 Lactobaci AC116977 Dictyoste AE000409 Bscherich AC020660 Homo sapi Continuation (3 of AC145917 Gallurana AC145912 Gallus ga AC145919 Pan trogl AC119493 Rattus no AE008209 Agrobacte AE429315 Homo sapi I44908 Sequence 56 AJ515700 Citrobact AJ515701 Citrobact AJ515701 Citrobact AF275733 Escherich AE002514 Escherich AP002554 Escherichia AB000205 Escherichia AB000205 Escherichia AB016759 Escherichia AX814811 Sequence L04979 Escherichia AJ515702 Enterobac U04979 Escherichia AJ515702 Enterobac L04979 Escherichia AJ515702 Enterobac L04979 Escherichia AB016581 Shigella AB016581 Shigella AB016581 Shigella AB016591 Scherichia AJ131756 Escherichia U43280 Salmonella AJ002301 Salmonell AE008749 Salmonell AL627269 Salmonell AE016840 Salmonell AJ000514 Salmonell Description PAT 07-OCT-1997 Sequence 58 Salmonella 3 Orientia 3 Rattus no 7 Rattus no 3 Rattus no 3 Oryza sat of.

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Collinson, S.K., Clouthier, S.C.,
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1 (bases 1 to 2067)
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92.8%;
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                                                                       encoding thin, aggregative
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les 33;
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-10_signal
88.4%;
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Submitted (13-DEC-1995) S. Karen Collinson, Microbiology, University of Victoria, P.O. B Victoria, BC V8W 3P6, Canada
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1352..1645
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                                                                                                                                                                                                                                                                                 subunit
                                                                                                                                                                                                                                                       /note="thin aggregative fimbrin subunit; major fimbrial subunit of thin aggregative fimbriae"
                                                                                                                                                       function="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fimbrial subunit
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/gene="agfA"
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SISQSAYGNSAAIIQKGSGNKANITQYGTQKTAVVVVQKQSHMAIRVTQR"
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696. .1151
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|strain="27655-3b"
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Score 403.2; DB 1; Pred. No. 3.1e-111;

Length 2067;

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                                                                                                                                                                                                       Submitted (29-OCT-1997) Romling
Karolinska Institute, MTC, Box :
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            Romling, U., Bian, Z., Hammar, M., Sierralta, W.D. and Normark, S. Curli fibers are highly conserved between Salmonella typhimur and Escherichia coli with respect to operon structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella typhimurium Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             csgA gene; csgB gene; csgC csgG gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhimurium csgG, csgF, csgC genes.
AJ002301.1 GI:2739232
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                                                                                                                                                                                                                                                                                                                                              98117058
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Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
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                                                                                                                                                                                                                          mling U.,
Box 280,
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                                                                                                                                                                                                                                                                                                                                                            (1998)
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                                                                                                                                                                                                                            Department Stockholm,
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S-17177, SWEDEN
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                                                                                              .2896)
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Page 4
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                            JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
CONSRTM
TITLE
JOURNAL
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SOURCE
ORGANISM
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AE008749
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4386 GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 4421
                                                                                                                                                 Salmonella typhimurium LT2
Salmonella typhimurium LT2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Locales in Calain
McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W.,
McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W.,
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Complete genome sequence of Salmonella enterica serovar Typhimurium
Complete genome sequence of Salmonella enterica serovar Typhimurium
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Submitted (29-MAR-2001) Genome Sequencing Center, Department of
                        The Salmonella typhimurium Genome Sequencing Project
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420
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21534948
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AE008749 AE006468
AE008749.1 GI:16419641
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Salmonella typhimurium LT2, sect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTTTTGGCAACGACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATAACGCCGCGCGCTGGTTAATCAGACCGCATCTGATTCCAGGCGTAATGGTGCGTCAGGTT 4385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTÁGGCCÁGGGTGCGGATAÁCAGTÁCTATTGAÁCTGACTCÁGAÁTGGTTTTCÁGAAÁCAÁT 4265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 4205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccddarrccacdridadcarriarcagraccgriccdcraacgcrecdcriccdcriccaca 4145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.7%;
91.7%;
                                                                                                                                   852-856 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 395.2; DB 1;
Pred. No. 9.1e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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n 53 of 220 of the complete
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gene

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.4533

CDS gene

mat\_peptide sig\_peptide

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.4809

CDS

gene

mat\_peptide 819\_peptide

4085

4025

0,

gene CDS		gene RBS CDS	PEATURES SOURCE	СОМИЕНТ
Complement (14142303)  /gene="STM1127"  Complement (14142295)  /gene="STM1127"  /gene="STM1127"  /gene="STM1127"  /gene="STM1127"  /gene="STM1127"  /gene="STM1127"  /note="paintlar to E. coli orf, hypothetical protein (AAC75480.1); Blastp hit to AAC75480.1 (285 aa), 29%  identity in aa 15 - 264"  /codon start=1  /codon start=1  /product="putative transcriptional regulator"  /protein_id="AAL20058.1"  /protein_id="AAL20058.1"  /db xref="gi:1641943"  /translation="MEBOPPRIKEGKILDTIGAMQKSLTRASQRIAQYILAFPRQVTQ  SSIADLSRETQAGEATVIRFCRTLGYKGFQDFKMDLALELATTESDDSSPLLDAEWSE  SDDAHAIGLKLQNTISNYLSETLMLDMQQVLGVVDALRHCHSVYIFGVGSSGITALD  MKHKLMRIGLRGDAVSNNHFMYMQATLLKAGDVAMGVSHSGTSPETVHSLRLARQAGA	/gene="phoH" /gene="phoH" /note="ginilar to E. coli PhoB-dependent, ATP-binding pho regulon component; may be helicase; induced by P starvation (AAC74105.1); Blastp hit to AAC74105.1 (354 aa), 92% identity in aa 71 - 354" /codon start=1 /transl table=11 /product="PhoB-dependent ATP-binding pho regulon component" /product="PhoB-dependent ATP-binding pho regulon /protein id="AAL20057.1" /protein id="AAL20057.1" /db_xref="Gi:16419642" /translation="MCAHNRVQENAGDVYLQLKVLSMGRQKAVIKAREAKRVLRRDS RSHKQREESSYTSLVQMGGYBAIGWARDSADTDFVYGARNEAQAHYLNAIDSKQLIFAT GEACCGKTWISAAKABALIHKDVERITYTRPU-QADEDLGFLPGDIAEKRAPYERPV YDVLLKRLGASFMQYCLRPEIGKVEIAPFAYMRGRTFENAVVILDEAQNVTAAQMKNF LTRIGENVTVIVNGDITQCDLPRGVRSGLSDALERFEEDEMVGIVHFNKDDCVRSALC ORTILAYS"	ym: STM1126" ive RBS for	The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and ReguonDB; http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone. Location/Qualifiers 12411 /organism="Salmonella typhimurium LT2" /mcl_type="genomic DNA" /mcl_type="genomic DNA" /mcl_type="genomic DNA" /mcl_type="genomic DNA" /mcl_type="genomic DNA" /mcl_type="taxon:9287"	Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 AI43283 Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://www.tigr.org/softlab/glimmer.glimmer.html and GeneMark; http://www.genome.ad.jp/kegg/, and Pedro Romero and Genemes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at Ecocyc;
gene	RBS gene CDS		RBS gene	RBS gene CDS

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Blastp hit to AAC76255.1 (229 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="putative RBS for STM1129; RegulonDB:STMS1H001401"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="putative RBS for STM1128; RegulonDB:STMS1H001400"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (4083. .4088)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (2580. .4076)
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                                                                                                                                                                                                                                                                                                                                                                           membrane protein"
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70% identity in aa 1 -
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'gene="STM1131"

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RESULT 5
AL627269
                                  VERSION
                                                   ACCESSION
                                                                                        DEFINITION
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Best Local Similarity
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                                                                                                                                                                                                                                                  421
                                                                                                                                                                                                                                                                                                                               361
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          AL627269
Salmonella enterica serovar Typhi
complete chromosome; segment 5/20.
AL627269 AL513382
AL627269.1 GI:16502231
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                                                                                                                                                                                                               GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                        AATAACGCCGCGCGCTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 18188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGGATTCCACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCGTCTATGATCAGCTGGTTACCCCGTGTTGTTACCCCATGAAATGGCACATGCATCCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="putative sugar transport protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative outer membrane protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to E. coli putative transport protein
(AAC77235.1); Blastp hit to AAC77235.1 (425 aa), 57%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="putative RBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to E. coli orf, hypothetical (AAC77267.1); Blastp hit to AAC77267.1 (241 identity in aa 4 - 239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.7%; Score 395.2; DB
91.7%; Pred. No. 1e-108;
tive 0; Mismatches 3
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                                                            (Salmonella typhi)
                                                                                        DNA
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                                                      BCT 04-JUL-2003
) strain CT18,
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.

ICE 1 (bases 1 to 254050)
RS Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Commerton, P., Cronin, A., Davis, P., Davies, R. M., Dowd.L., White, N., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parray, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G.
Complete genome sequence of a multiple drug resistant Salmonella Nature 413 (6858) 848-882 (2001)
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Submitted (25-QCT-2001) Submitted on behalf of sequencing team, Sanger Centre, Wellcome Trust Hinxton, Cambridge CB10 1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Details of S. typhi sequencing on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill, J.
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ADDGSGYQFLVEMLTUNSRNPQNASRLIERPLIRLKRYDDKRAFAADAFH

LSGDT.YFKITKALA"
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Location/Qualifiers
/note="Pfam match
family M1, score
1060. .1089
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Orthologue of E.
to AMPN_ECOLI (869 aa),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="synonym:
81. .2793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mo1_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:90370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Salmonella enterica subsp. enterica
Typhi"
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the Sal Salmonalla ome Campus,

available

coli pepN (AMPN ECOLI); 94% identity in 869 aa c

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match to entry PF01433 Peptidase\_M1, score 245.10, E-value 1.9e-84" Peptidase

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
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APDLCEBELIQVADSLLRHNIGGVIAINTTLDRSLVQGMKNCQOTGGLSGRPLQLKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="STY1079"
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/tranalation="MATLSRL HIPVKSMRGIGLTHALADISGLAFDRIFMVTESDGT
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PTAINQWLSGFFSRDVQLCWVGPQLTRRVKRHNAVPLGFADGYPYLLTNEASLRDLQQ
RCPAGYQMEQFRPNLVVSGVAAWEEDSWKVLRIGDUTIEDVKPCSRCIFTTVSPEKGQ
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LDDSVTPEKHPDGSVTIDWGGQTFCGNNQQVLLEQLENQGIRIPYSCRAGICGCCRIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="STY1079"
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Dihydroorotate dehydrogenase, score 563.50, E
                                         LLEGEVSPLKKSAMGDDGTILSCSCVPKTALRLEN"
                                                                                                                                                                                                                                                                                                                                                                                                complement (4716. .5825)
/gene="STY1081"
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/gene="STY1081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEMWTPGTGDAASVWLSDTAEQVNLLVVEPGENAALCLLAQPGVVIAGRTMQLGDAIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MMRIKPDDNWRWYYDEEHDRMMLDLANGMLFRSRFSRKMLTPDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMNDRLKPQVHCHSFSLEQAV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIIRRLSLELKGQLPIIGVGGIDSVIAAREKIAAGATLVQIYSGFIFKGPPLIKEIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to PYRD ECOLI
                                                                                                                                                                                                                                                                                                                                                    /note="Orthologue of E. coli P75863; Fasta (369 aa), 86% identity in 367 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="STY1080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="PS00912 Dihydroorotate dehydrogenase signature 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=
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                         .4955)
                                                                                                                                                                                                                                                                                    protein"
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) aa overlap. N
l start site."
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GTAGGCCAGGGTGCGGATAACAGTACTATTGAACTGACTCAGAATGGTTTCAGAAACAAT 89205
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/note="Similar to Haemophilus influenzae hypothetical protein hi0116 H0016 SW:YCEY HAEIN (P44524; P43945) fast: grotein hi0116 H0016 SW:YCEY HAEIN (P44524; P43945) fast: scores: E(): 0, 60.3% id in 710 aa Orthologue of E. coli YCBY_ECOLI; Fasta hit to YCBY_ECOLI (702 aa), 92% identity in 702 aa overlap"
                                                                                                 VDMSRTYLEWAERNLRLNGLSGRAHRLIQADCLGWLREANEQFDLIFIDPPTFSNSKR
MEESFDVQRDHVALMKDLKRLLRKGGTIMFSNNKRGFRMDLEGLAELGLTAQEITQKT
                                                                                                                                                                     NQFGGWNLSLFSASPDLLGSLQLRADKQFKAKNGPLDCVQKNYHIAETTADSKPATVA
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RAGIGELITFEVKDVAQLSNPLPKGPYGTVISNPPYGERLDSDPALIALHSLLGRTMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5924. .8032
                                                                   LSPDFARNRQIHNCWLIRAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="conserved hypothetical protein"
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table=
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re 55.90,
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/note="Pfam match to entry PF01170 UPF0020,
Uncharacterized protein family UPF0020, score 781.30,
E-value 3.7e-231" overlap 526 aa overlap Pasta hit to YJJK\_ECOLI (554 aa), 34% identity in 524 aa 3045. .9952 /gene="STY1083" gene="STY1083" note="PS01261 Uncharacterized protein family UPF0020 gene="STY1082" note="Fasta hit to YBIT\_ECOLI (530 aa), ignature" 32% identity 'n

88906 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 88965 Similarity ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCATCCGGC 120 GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240 CCGGATTCCACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGG 89025 Conservative 86.3%; 91.4%; <u>.</u> Score 393.6; DB 1; Pred. No. 3.9e-108; Mismatches Indels Length 254050; 0 Gaps 89145 89085 60

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AUTHORS
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AUTHORS
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DEFINITION
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                                                                              Sgo
                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                        SdC
                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella enterica subsp. enterica serovar Typhi Ty2
Salmonella enterica subsp. enterica serovar Typhi Ty2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Interobacteriacea; Salmonella.

1 (bases 1 to 301983)
Deng,W., Liou,S.R., Plunkett III,G., Mayhew,G.F., Rose,D.J.,
Burland,V., Kodoyianni,V., Schwartz,D.C. and Blattner,F.R.
Comparative Genomics of Salmonella enterica Serovar Typhi Strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-SEP-2002) Laboratory of Genetics, University of Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deng, W., Liou,
Burland, V., Ko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 185 (7), 2330-2337 (2003)
22531367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salmonella enterica subsp. enterica serovar Typhi Ty2, section 7 of AE016840 AE014613
AE016840 AE014613
AE016840 1 GI:29137797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 301983)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATAACGCCGGGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submission
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                                                                                                             complement (844. .1797)
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IS200"
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Typhi Ty2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="Ty2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ou,S.-R., Plunkett,G. III, Mayhew,G.F., Rose,D., Kodoyianni,V., Schwartz,D.C. and Blattner,F.R.
                                                                                                                                                                                                                                                                                                                                                          ement (164. .622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _type="genomic DNA"
                                   _tag="t1736"
                                                                                                                                                                                                                                                                                                                                                                                                        ement (164. .622)
                                                                                                                                                                                                                                                                                                                            _tag="t1735"
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                                                                                                                                                                                                                                                         table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,D.J.,
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gene

gene CDS

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complement (4488. .5591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement (4488. .5591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ITTTEYENGEAKKYKAKFRVYSSYLEALSDYVALLTRNPRYAAVTTAATAEQGAVALQ
NAGYATDPNYARKLASMIQQLKAMSEKVSKTYSANLDNLF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="t1738"
note="corresponds to !
Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Lears lation="MSLINHAMSGLNAAQAALNTVSNNINNYNVAGYTROTTILAQA
NSTLGAGGMIGNGVYVSGVQREYDAFITNQLKGAQQNQSSGLTTRYEQMSKLDNLLADK
SSLLSGSLQSFFTSLQTLVSNAEDPAARQALIGKAEGLVNQFKTDQYLRDQDKQVNI
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VQDGGTYNLITMANGYTLVQGSTARQLAAVPSSADPTRTTVAYVDEAAGNLEIPEKLN
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SDNRNGQALLDLQNSNVVGGNKTFNDAYATLVSDVGNKTTSTLKTSSTTQANVVKQLYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="flgJ"
/locus_tag="t1738"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (3538. .4488)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QQQSVSGVNLDEEYGNLQRYQQYYLANAQVLQTANALFDALLNIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus_tag="t1737"
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Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="GI:29137800"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="flagellar hook-associated protein 1"
protein_id="AAO69361.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
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TQQVDSARTMYIGHTGAQIFMSITSNAVPBEDGSDSKNLFYMLDTAIAALKTPVEGN
DVEKEKAAAAIDKTNNGLKNSLNNVLTVRAEDFGDLSELSTLDSLGSDRALGQKLQMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /locus_tag="t1737"
complement(1812. .3473)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLVDVDWNSVISSYVNQQAALQASYKTFTDMQGMSLFQLNR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1/transI_table=11/product="flagellar hook-associated protein/protein_d="Alagellar hook-associated protein_d="Alagellar hook-assoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="fl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tag="t1739"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STY1221 from Accession AL513382:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from Accession AL513382:
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
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Salmonella typhi CT18"
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Salmonella typhi CT18"
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QGQAAPVQVGQLNLTTFMNDTGLESIGENLYIETQSSGAPNESTPGLNGAGLLYQGY
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Complement (7146. 7901)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LHVVGEKQIAINQGTEFIRFSGVVNPRTISGSNSVPSTQVADARIEYVGNGYINEAQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="flagellar L-ring protein
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Accession AL513382: Salmonella typhi CT18"
                                                                                                                                   codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             locus_tag="t1741"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         locus_tag="t1740"
 86.3%;
91.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                  table=11
                                                                                                                                       table=11
 Score 393.6; DB 1;
Pred. No. 4e-108;
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Direct Submission
Submitted (14-JUL-1997) Sukupolvi S.S.,
University of Turku, Kiinanmyllynkatu, 2
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 1048)
Sukupolvi, S.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sukupolvi,S., Lorenz,R.G., Gordon,J.I., Bian,Z., Pfeifer,J.D., Normark,S.J. and Rhen,M. Expression of thin aggregative fimbriae promotes interaction of Salmonella typhimurium SR-11 with mouse small intestinal epithel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agfA gene; agfB gene.
Salmonella typhimurium
Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria;
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                                                                                                                                                                                                 /db_xref="taxon:602"
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/mol_type="genomic DNA"
                                                                                                         gene="agfB"
                                                                                                                              /gene="agf8"
.4. .553
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Query Match Best Local : Matches

Similarity

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Doran, J.L., Kay, W.W., Collinson, S.Karen. and Clouthier, S.C. Methods and compositions comprising the agfA gene for detection Salmonella
Patent: US 5635617-A 56 03-JUN-1997;
                                                                                                                                                                                                                                                                                                            GGTTTTGGCAACAACGCACCGGCTAACCAGTATAA 1047
                                                                                                                                                                                                                                                                                                                                     GGTTTTGGCAACAACGCCACGGCTAACCAGTATTA
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593. .>1048
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/db_xref="SPTREMBL:033801"
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                                                                                                                                                                                                                                                                                                                                  Submitted (11-NOV-2002) Romling U., Microbiology and Tumorbiology Center, Karolinska Institute, Box 280, S-17177 Stockholm, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Citrobacter sp. Fec2
Citrobacter sp. Fec2
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Citrobacter.
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CSP515700

CRITODACTER Sp. Fec2 csgB gene, csgA gene and csgD gen AJ515700

AJ515700

AJ5157001

GI:31790491

csgA gene; csgB gene; csgD gene; curlin-csgA protein; component of curlin monomers; regulatory protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                Zogaj,X., Bokranz,W., Nimtz,M. and Romling,U. Production of Cellulose and Curli Fimbriae by Members of the Family Enterobacteriaceae Isolated from the Human Gastrointestinal Tract Infect. Immun. 72 (7), 4151-4158 (2003)
                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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286; Conserv
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                                                                                                                                                                                                                                                                                                                         Karolinska Institute,
Location/Qualifiers
/codon_start=1
/trans1_table=11
/product="putative regulatory protein"
/protein_id="CAD56670.1"
/db_xref="GI:31790492"
                                                                                                                                                                        complement (212.
                                                                                                     /gene="csgD"
/function="necessary
                                                                                                                                       complement (212. .862)
                                                                                                                                                                                                                                                           /organism="Citrobacter
/mol type="genomic DNA"
/isolate="Fec2"
                                                                                                                                                                                                     /isolation_source="faeces"
/specific_host="Homo sapiens"
/db_xref="taxon:213763"
                                                                                                                                                         gene="csgD"
                                                                                                                                                                                        country="Germany"
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/mol_type="unassigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.3%;
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Pred. No. 4.3e-75;
                                                                                                                                                                        .862)
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REFERENCE AUTHORS

TITLE JOURNAL

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Unknown. Unclassified.

Sequence 144908

I44908.1

RESULT I44908 LOCUS

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953 361 893 301

833 241 773 181 713 121 653

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CFR515701 2920 bp DNA linear BCT Citrobacter freundii csgB gene, csgA gene and csgD gene.
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                                                                                                                                                                                                                                                                                                                                                                                  CATAACGCCGCACTGGTGAACCAGACTGCGTCCCGATTCCAGCGTTCTGGTGCATCAGGTT
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DQWNGKNSDITVSQYGGHNAALVNQTASDSSVLVHQVGFGNNATANQY"
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SISQSNYGNTAMIIQKGSGNKANITQYGTQKTAVVVQRQSQMAIRVIQR"
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hingveyvaddeervvnglogilkeecyfsoklasyllthsgnyrynssesallthe
klilnklrigasnieiarslfisentvkthlynlfkkiavknrtoavsmandnlrr"
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/db_xref="GI:31790494"
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/transT_table=11
/product="nucleation component of
/protein_id="CAD56671.1"
/db_xref="GI:31790493"
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function="curli
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function="nucleator"
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L623. .2078
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Pred. No. 3e-
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Production of Cellulose and Curli Fimbriae by Members of the Fami
Enterobacteriacese Isolated from the Human Gastrointestinal Tract
Infect. Immun. 72 (7), 4151-4158 (2003)
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Citrobacter freundii
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component of curlin monomers; regulatory protein.
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QWNAKNADISVTQFGGRNGALVNQTASDSNVLIQQVGFGNNATANQH"
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function
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/function="curli subunit"
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/db_xref="taxon:546"
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/isolate="Fec4"
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AF275733
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Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
1 (bases 1 to 1711)
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Escherichia coli :
CsgA protein (csg/
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Direct Submission
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                                                                                                                          /gene="csgB"
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Enterobacteriaceae, Escherichia.

1 (bases 1 to 10190)

Perna, N. T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1433
                                                                                                                                                                                                                                                                                                                                                                                      418
                                                                                                                                                                                                                                                                                                                                                                                                                                                  358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1253
                                                                                                                                  Escherichia coli 0157:H7 |
Escherichia coli 0157:H7 |
Bacteria; Proteobacteria;
                                                                                                                                                                                                        AE005315
                                                                                                                                                                                                                        AE005315
                                                                                                                                                                                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118
                                                                                                                                                                                                                                                                       AE005315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGAAACTTTTAAAAGTGGCAGCAATCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                                                                                                                                                                                                                                                                                                                      GTTGGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 1711
                                                                                                                                                                                                                                                                                                                                                              GTTGGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                            GEOGGCÁÁCEGTECAGOEGTTGÁCCAGACTECÁTCTAÁTTCCÁCCETCÁACETAACTCÁG 1672
                                                                                                                                                                                                                                           155
                                                                                                                                                                                                                                                                                                                                                                                                                  GGTAATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCCAGCGTAATGGTGCGTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCGCCACTCTTGATCAGTGGAACGGTAAAGACTCTCATATGACAGTTAAACAATTCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTTGGTAAC 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chágc trád rác trád hac trát rác trád trád rác chág car do rac rác rác rác rác rac 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAAGCGATGGCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GĠĊĊĊĠAĀŦŦĊĀGĀĠĊŤĠĀĀŦĀŦŤŦĀŦĊĀĠŦĀĊĠĠŤĠĠŦĠĠŦŶĀĊŦĊŤĠĊĀĊŦŦĠĊŦĊŦĠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GETGTTGTTCCTCAGTACGGCGGCGGTGGCGGTAACCACGGTGGTGGCGGTAATAACAGC 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCA---TGAAATGGCACATGCATCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAAACTTTTAAAAGTAGCAGCAATTGCAGCAATCGTATCTCCCGGTAGCGCTCTGGCA 1312
                                                                                                                                                                                                 AE005174
.1 GI:12514572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/codon_start=1
/codon_start=1
/transI_table=11
/product="CsgA protein"
/product="CsgA protein"
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/translation="MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNS
ELNIYQYGGGNSALALGADARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSA
FILDQMNGKDSHMTVKQFGGGNGAAVDQTASNSTVNVTQVGFGNNATAHQY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GI:14039400"
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QAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGSSNRAKIDQTGDYNLAYIIQAGSANDA
SISQGAYGNTAMIIQKGSGNKANITQYGTQKTAIVVQRQSQMAIRVTQR"
1253. .1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.48;
                                                                                                                                                                                                                                              10190 bp
0157:H7 EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 225.4; DB 1;
Pred. No. 3.8e-57;
0; Mismatches 136;
                                                                                                                          EDL933
EDL933
Gammaproteobacteria;
                                                                                                                                                                                                                                           genome,
                                                                                                                                                                                                                               linear BCT 21-MAR-2001 contig 1 of 3, section 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                      Enterobacteriales;
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FEATURES

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JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                               Sac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perna, N.T., Plunkett, G. III, Burland, V., Mau, B., Glasner, J.D., Rose, D.J., Mayhew, G.F., Evans, P.S., Gregor, J., Kirkpatrick, H.A., Posfai, G., Hackett, J., Klink, S., Boutin, A., Shao, Y., Miller, L., Grotbeck, E.J., Davis, N.W., Lim, A., Dimalanta, E., Potamousis, K., Apodaca, J., Anantharaman, T.S., Lin, J., Yen, G., Schwartz, D.C., Apodaca, J., and Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-OCT-2000) Laboratory of Genetics, UWisconsin, 445 Henry Mall, Madison, WI 53706, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome
Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21074935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 10190)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence of enterohaemorrhagic Escherichia coli 0157:H7 409 (6819), 529-533 (2001)
                                                                                       /gene="csgC"
/function="putative structure; Not classified"
/function="putative structure; Not classified"
/note="Residues 1 to 110 of 110 from Escherichia coli K-12
MG1655: B1043"
                                                                                                                                                                                                                                                                                                    /translation="MKLLKVAAIAAIVFSGSALAGVVPQYGGGGGNHGGGGNNSGPNS
ELNIYQYGGGNSALALQADARNSDLTITQHGGGNGADVGQGSDDSSIDLTQRGFGNSA
TLDQWNGKDSHMTVKQFGGGNGAAVDQTASNSTVNVTQVGFGNNATAHQY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 residues 1 to 151 MG1655: B1042"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="regulator; Cell exterior constituents: Surface
structures"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QAAIIGQAGTNNSAQLRQGGSKLLAVVAQEGSSNRAKIDQTGDYNLAYIDQAGSANDA
SISQGAYGNTAMIIQKGSGNKANITQYGTQKTAIVVQRQSQMAIRVTQR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Residues 1 to 151 of 151 are 100.00 pct identical to residues 1 to 151 of 151 from Escherichia coli K-12
                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/transl_table=11
/product="curlin major subunit,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strain MG1655: B1041"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="structural component; Cell exterior
constituents: Surface structures"
                                                                                                                                                                                                                                                        /gene="csgC"
/product="putative curli production
/protein_id="AAG55789.1"
                                                /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAG55788.1"
/db_xref="GI:12514574"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="Residues 1 to 152 of 152 are 96.71 pct identical to residues 1 to 151 of 151 from Escherichia coli K-12 Strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="synonym:
1113. .1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="minor curlin subunit precursor, similar ro CsgA"
/protein_id="AAG55787.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="synonym:
517. .1072
                                                                                                                                                                                                                                  note="synonym:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="csgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="csgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="csgB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Escherichia
/mol_type="genomic DNA"
/strain="EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MKNKLLFMMLTILGAPGIAAAAGYDLANSEYNFAVNELSKSSFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="GI:12514573"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="csg8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="enterohemorrhagic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serotype="0157:H7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .10190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          xref="taxon:155864"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .1072
                                                _table=11
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                                                                                                                                                                                                                                     Z1677"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z1676"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coli 0157:H7 EDL933"
                                                                                                                                                                                                                                                                                                                                                                                                                                               coiled surface structures;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of
                                                                                                                identical to
i K-12 Strain
                                                                                                                                                                                                            SGS
                                                                                                                                                                                                                                                                              gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gg
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/function="orf; Unknown function"
/note="Residues 1 to 385 of 385 are 99.22 pct i
                                                                                                                                                                                                                                                                                                                                                                    SLAANDVAVVHAĞYARWRKKLLRYGVELYELKPTREQSSTLHDRGITGNSGASLHAKT
FSIDGKTVFIGSFNFDPRSTLLNTEMGFVIESETLAQLIDKRFIQSQYDAAWQLRLDR
WGRINWVDRHAKKEIVLKKEPATSFWKRVMVRLASILPVEWLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                EKSLDAFAARYRLAEMSEHTLDVQYYIWQDDMSGRLLFSALLAAAKRGVRVRLLLDDN NTPGLDDILKILDSHPRIEVRLFNPFSFRLLRPLGYITDFSRLARRMKNKSFTVDGVVTLVGGRNIGDAYFGAGEEFLFSDLDVMAIGPVVEDVADDFARYWYCKSVSFLQQVDV PEGEWADRIELPASWHNDAWTHRYLKRMESSPFINHLVDGTLFLIWAKRTLLSDDPAK GEGKAKRHSLLPASWHNDAWTHRYLKRMESSPFINHLVDGTLFLIWAKRTLLSDDPAK GEGKAKRHSLLPQRLFDIMGSPSERIDIISSYFVPTRAGVAQLLRWVRKXVKLAILTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mnallllaalssqitpnttqqqdmytiipevtltqsclcrvqil
slregssgqsqtxqektlslpanqpialtklslnispddrvkivvtvsbgqslhlsqq
wppsseks"
                                                                                                                                                                                                                                              /note="synonym: Z1681"
complement(4453. .5610)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="orf; Unknown function"
/note="Residues 1 to 177 of 177 are 100.00 pct identical
to residues 1 to 177 of 177 from Escherichia coli K-12
Strain MG1655: B1045"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /runction="orf; Unknown function"
/note="Residues 1 to 103 of 103 are 98.05 pct identical to
residues 1 to 103 of 103 from Escherichia coli K-12 Strain
MG1655: B1044"
/transl_table=11
/product="orf, hypothetical protein"
/protein_id="AAG55793.1"
                                                                                                                                                                                                                                                                                                                                         complement (4453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EENAHLYERLLTQQGDE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mktrihvvQgdItklavdvIvnaanpslmggggvdgaihraagp
alldaClkvrQQQgdCptghavItlagdlpakavvhtvggvwrggeqnedqllqdayl
nslrlvaansytsvafpaistgvygypraaaaeIavktvsefitrhalpeqvyfvCyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2489. .3022
/gene="Z1679"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2489. .3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /producī="putative synthase"
/protein id="AAG55792.1"
/db_xref="Gi.12514578"
/translation="MMKKTPTSTKDŠLPNKEMNDLPRLASAVLPLCSQHPGQCGLFPL
                                                                                  codon_start=1
                                                                                                                                                                                                                         'gene="ymdD"
                                                                                                                                                                                                                                                                                                               'gene="ymdD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon start=1
transI table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /G1655: B1046"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Residues 1
residues 1 to 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAG55790.1"
/brotein_id="AAG55790.1"
/db_xref="GI:12514576"
/translation="Mfrepfunslwildsleppfialagstaqggvihpygqivepacdv
STQSSPVEMNCPQNGSVPGKTYSSKALMSGNVKNAQIASVKVQYLDKQKKLAVMNIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="ymdC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="synonym: Z1680"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="putative polyprotein"
protein_id="AAG55791.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="Z1679"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                function="putative enzyme; Not classified"
note="Residues 1 to 493 of 493 are 99.59 pct i
ssidues 1 to 493 of 493 from Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene="ymdC"
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K-12 Strain
                                                                                                                                             K-12
                                                                                                                                          Strain
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CDS

gene

linear section BCT

T 21-DEC-2002 5/20.

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Query Match
Best Local S
Matches 320
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           GTTGGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ATGAAACTTTTAAAAGTGGCAGCAGTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
                                                                    ĠĠccgcaáċċġgrĠċagcġġrfgácċáġáċrġċáfċŕaáfrċċácċġrcáacġraacġraacrċáġ
                                                                                                       GGTAATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAG
                                                                                                                                                    AGCĠĊĊĀĊŦĊŤŦĠĀŦĊĀĠŤĠĠĀĀĊĠĠŤĀĀĀGĀĊŤĊŦĊĀŤĀŤĠĀĊĀĠŤŦĀĀĀĊĀĀŤŦĊĠĠŦ 1472
                                                                                                                                                                                     AATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGC 357
                                                                                                                                                                                                                                         GATGTTGGTCÁGGGCTCAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTTGGTAAC 1412
                                                                                                                                                                                                                                                                        GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT 297
                                                                                                                                                                                                                                                                                                                            CAAGCTGATGCTCGTAACTCTGATCTTACTATTACCCAGCATGGTGGTGAACGGTGCA 1352
                                                                                                                                                                                                                                                                                                                                                          CAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCC 237
                                                                                                                                                                                                                                                                                                                                                                                                                ĠĠĊĊĠaĀŢŢĊĀGĀĠĊŢĠĀĀŢĀŢŢĀŢĊĀĠŢĀĊĠĠŢGGŢĠĠŢĀĀĊŢĊŢĠĊĀĊŢŢĠĊŢĊŢĠ 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCCTCTG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCCA---TGAAATGGCACATGCATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="periplasmic glucans biosynthesis protein"
/protein_id="AAG55794.1"
/db_xref="periplasmic glucans biosynthesis protein"
/db_xref="periplasmic glucans biosynthesis protein"
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KFVVMPGRDTVVDVQSKLYLARDKOGLGFAGFKVLYPINSLDKRLTIYALLDSPRATGAY
KFVVMPGRDTVVDQSKLYLARDKVGKLGVAPLTSMFLFGRAQPSPANNYRBELHDSNG
KFVMPGRDTVVDQSKLYLARDKVGKLGVAPLTSMFLLGRGNPSFREDLDDRYDLRFS
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KLHAPDNAWVQOTRRSTGDVKOSNLIRQPDGTIAFVDFTGAEMKKLPEDTPVTAQTS
KLHAPDNAWVQOTRRSTGDVKOSNLIRQPDGTIAFVDFTGAEMKKLPEDTPVTAQTS
KLHAPDNAWVQOTRSTGVKGWRLVMRVKVKDAKKTTEMRAALLVNADQTLSETWSYQLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="synonym: Z1684"
7531. 10074
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/function="enzyme; Osmotic adaptation"
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FKINENSDKTNKKESMVKLSVIFLCLGIGYAVIRRTIFIYVPPILSNGTENEIVMQTL
VTTMVLGLMAVLOVFSFGHRLLNFQSAEVTYFVNASLFTAYLNQRYCSGDAMYETES
TSNWLGFLCGLIFVVGIAIILYEIHLRIPLKFLFGGKPVVKRENDKAPAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /function="enzyme;
/note="Residues 1 t
residues 1 to 511 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="synonym: Z1683"
5003. .7538
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Pred: No. 4.5e~57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Osmotic adaptation"
to 511 of 511 are 99.80 pct identical to
of 511 from Escherichia coli K-12 Strain
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                                                                                                            Japan (B-mail:ken@gen-info.osaka-u.ac.jp,
URL:http://www.gen-info.osaka-u.ac.jp/, Tel:81-6-6879-8365
Fax:81-6-6879-2047)
                                                                                                                                                                                   Submitted (26-JUN-2000) Ken Kurokawa, Information Research Center; 3-1, Yame
                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                          5 (bases 1 to 327773)
Ohnishi,M., Kurokawa,K.,
Hayashi,T.
                                                                                                                                                                                                                                                                                                                              Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12 DNA Res. 8 (1), 11-22 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashi,T., Makino,K., Ohnishi,M., Kurokawa,K., Ishii,K., Yokoyama,K., Han,C.-G., Ohtsubo,E., Nakayama,K., Murata,T., Tanaka,M., Tobe,T., Iida,T., Takami,H., Honda,T., Sasakawa,C., Ogasawara,N., Yasunaga,T., Kuhara,S., Shiba,T., Hattori,M. and Shinagawa,H.
                                                                                                                                                                                                                                                                     Hayashi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete nucleotide sequence of the prophage VTI-Sakai carrying the Shiga toxin 1 genes of the enterohemorrhagic Escherichia coli 0157:H7 strain derived from the Sakai outbreak gene 258 (1-2), 127-139 (2000)
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Comparative analysis of the whole set of rRNA operons between enterohemorrhagic Escherichia coli 0157:H7 Sakai strain and an Escherichia coli K-12 strain MG1655

Syst. Appl. Microbiol. 23 (3), 315-324 (2000)
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Kurokawa,K., Yasunaga,T., Yokoyama,K., Makino,K., Shinagawa,H.
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Kurokawa,K., Ishii,K., Hattori,M., Tatsuno,I., Abe,H., Iida,T.,
Yamamoto,K., Ohnishi,M., Hayashi,T., Yasunaga,T., Honda,T.,
Sasakawa,C. and Shinagawa,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli 0157:H7
Escherichia coli 0157:H7
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Escherichia coli 0157:H7 DNA,
AP002554 BA000007
AP002554.1 GI:13360491
/organism="Escherichia
/mol_type="genomic DNA"
/strain="0157:H7"
                                                                      Location/Qualifiers
1. .327773
                                                                                                                                                                                                                                                          Makino,K., Yasunaga,T., Shinagawa,H. and
                                   coli 0157:H7'
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Yamadaoka, Suita, Osaka
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RRTRNEGRVRALKAMERERGERREVMCTAKMOVEEASRSGKI VEEMEDVCYQVDGKQL
VKDFSAQVLEDKI ALI GENGCGKTTLLKLMCDGLQADSGRIHVGTKLAYFDQHALA
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LARLFLKPSNLLLILDEFTNDLDVETLELLEELI DSYQGTVLLVSHDRQFVDNTVTECW
IFEGGGKIGRYVGGYHDARGQQEQYVALKQPAVKKNEEPAAFKAETVKRSSSKLSYKL
                                                                                                      QGLRSCSCCTAILPADEPVCPRCGTKGYVRRRNSLQWTLALLVTSIMLYLPANILPIM
VTDLLGSKMPSTILAGVILLMSEGSYPVAAVIFLASIMVPTLKMIAIAMLCWDAKGHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to PQIA_ECOLI gi|1787183 percent identity 99 in 417 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tranblation="MSLISMHGAWLSFSDAPLLDNAELHIEDNERVCLVGRNGAGKST
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DISKLVMNDPSEKNLNELAKVQEQLDHNLWQLENRINEVLAQLGLDPNVALSSLSGG
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                                                                    TMFSAMTFDPRLSWDRQPESEHEES"
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2270. .4177
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HRGRWGFSGWAQHDEAIWQEVKAEAQTRARKGLAEYSSHFYGSDSDARVIQRARTNAR
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RNSQYGAMKVKDAIVDAFTRKNLPRPNVDRDAPDIRVNVWLHKETASIALDLSGDGLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="ECs1034"
4307. .5560
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99 in 702 aa (Conserved in E.coli K-12)"
gene="EC81035"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="putative ATP-binding component of a transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to UUP_ECOLI gi|1787182 percent identity 99
n 635 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative oxidoreductase"
/protein_id="BAB34455.1"
/db_xref="GI:13360492"
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150. .2258
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150. .2258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="ECs1034"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein_id="BAB34456.1"
db_xref="GI:13360493"
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transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MNSLFASTARGLEELLKTELENLGAVECQVVQGGVHFKGDTRLV"
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성 용 성 용

118 GGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTG 177

GGTGTTGTTCCTCAGTACGGCGGCGGTGGCGGTAACCACGGTGGTGGCGGTAATAACAGC 326540

GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCA---TGAAATGGCACATGCATCC 117

ATGAAACTTTTAAAAGTAGCAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCTCTGGCA 326480

326481

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                                                                                       Query Match
Best Local
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ATGAAACTTTTAAAAGTGGCAGCAGTTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
                                                                  Conservative
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ipvlirieperlkmylfsenapvyehlgelkeglkglktgnlytgalyvgldfypnt
paitgirefncyqiifyvsgglaqiqorlmealdkinklplapmiedatsytstlsesort
paitgirefncyqiifyvsgglaqiqorlmealdkinklplapmiedatsytstlsesort
kknlgttldsmnkliasqsmodlfpdmostlrelinesmogfpdpgsaaynkmvaddmorl
                                                                                                                                                                                                                                                                                                                                  /gene="ECs1038"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="identical to RMF_ECOLI gi|1787186 (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mtiaalwlagcssgeinknyyqlpvvQsgtqstasQgnrllwve
QVAVPDYLAGNGVVYQTSDVKYYIANNNLwaspldQQlrntlvanlstqlpgwvvasQ
pLGSAQDTLNVTVTEFNGRYDGKVIVSGEwllnhQGQlikRpfrlegvQTQDGYDEMV
                                                                                                                                                                                                                                                                                    complement (8258 .8776)
/gene="ECs1038"
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                                                                                                                                                            /evidence=not_experimental
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
/protein_id="BAB34459.1"
/db_xref="GI:13360496"
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7217. .7765
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transl_table=11
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evidence=not_experimental
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                                                                                                                                                                                                                                   note="similar to FABA ECOLI gi|1787187 percent identity 00 in 172 aa (Conserved in E.coli K-12)"
                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="BAB34460.1"
db_xref="GI:13360497"
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evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                               translation="MKRQKRDRLERAHQRGYQAGIAGRSKEMCPYQTLNQRSQWLGGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="similar to YMBA_ECOLI gi|1787185 percent identity 8 in 182 aa (Conserved in E.coli K-12)"
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                                                             Score 225.4;
Pred. No. 6e-5
0; Mismatches
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6e-57;
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ECCSGABDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (11-AUG-1995) M. Hammar, Ka. Microbiology and Tumorbiology Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                   SWEDEN
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Expression of two csg of
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Enterobacteriaceae; Escherichia.
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Escherichia coli
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orfC gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microbiol. 18 (4), 661-670 (1995)
                                                               /insertion_seq="IS2 (partial)"
complement(133. .966)
/gene="csgG"
                                                        complement (133.
                                                                                                                                  db_xref="taxon:562"
                                                                                                                                                       organism="Escherichia"
mol_type="genomic_DNA"
/strain="W3110"
                                                                                                                                                                                                                        db_xref="taxon:562"
                                                                                                                                                                                                                                                                    organism="Escherichia coli"
                                                                                                                                                                                                                                            strain="MC4100"
                                                                                                                                                                                                                                                                                                                                                                         organism="Escherichia"
                                                                                                                                                                                                                                                                                                          map="23.15 minutes"
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strain="K12"
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er, Box 280, S-171 77 Stockholm,
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                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1/transl_table=11/
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                                                                      GGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT
                                                                                                         AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420
                                                                                                                                                                                                                                                           GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
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                               GGTTTTGGCAACAACGCCACGCTAACCAGTATTAA 456
                                                                                                                                                                                 GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
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GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 4184
                                                                                                                                                                                                                        GTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTCGGTAACAGC
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68.2%;
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RESULT 15

/strain="K12

organism="Escherichia"

coli

'genomic DNA"

.10346 rganism=" ol\_type="

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AL Submitted (13.0CT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director).

Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli KI2 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 3032 [e-mail: markamber:gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World wide wab site (http://www.genetics.wisc.edu). *** The E. coli KI2 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein- or RNA-encoding) are now designated as gene synonyms instead of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blattner,F.R.
Direct Submission
Submitted (07-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoll@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
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Blattner, F. R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
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Direct Submission
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3 (bases 1
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repeat\_region

complement (<1. .48)

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                                                                                                                /codon_start=1
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/producE=orf, hypothetical protein"
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/db_xref="GI:1787268"
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                                                                                                                                                                                                                                                                                                                                                                                                                /gene="b1030"
/function="orf; Unknown"
/functe="083; This 83 aa ORF is 25
to81 residues of an approx. 616 a
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/product="orf, hypothetical protein"
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/note="No predicted
/bound_moiety="DeoR
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/transl_table=11
/product="orf, hy
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/bound_moiety="DeoR predicted site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ycdU"
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/function="orf; Unknown"
/note="0318; This 328 aa ORF is 19 pct identical (4 gaps)
to 191 residues of an approx. 288 aa protein Y320_MYCGE
SW: P47562"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="synonym:
389. .1375
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LHLTHTVKWTESLDTFLNMPTPVAFLEISNKPYLGNMLNDFAGVDQQRVMHCRKAFSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="factor Sigma32; predicted +1
389. .1375
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/function="orf, Unknown"
/note="0107; This 107 aa ORF is 27 pct identical (0 gaps)
to 58 residues of an approx. 1888 aa protein FAS2_CANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="b1028"
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predicted
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AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
                                                                   CCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAA
                                                                                                                    CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGGTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                          GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC
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KSGDNUSADYALVWHPPVEMLAGRDLKAVFALGAGVBSILSKLQAHPEMLNESVPLFR
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GSKVAQSLQTWRFPLRCWSRTRKSWPGYQSFAGREELSAFLSQCRVLINLLENTPETV
GIINQOLLEKLPDGAYLLNLARGVHVVEDDLLAALDSGKVKGAMLDVENREPLPPESP
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3383 .3410
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/product="putative dehydrogenase"
/protein_id="AAC74117.1"
/db_xref="GI:1787270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /function="putative enzyme; Not classified"
/note="0325; This 325 aa ORF is 32 pct identical (2 gaps)
to 177 residues of an approx. 312 aa protein YPRA_CORGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="factor Sigma70; predicted +1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="factor Sigma70; predicted +1 start
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'function="RNA; tRNA"
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/gene="serX"
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/protein_id="AAC74116.1"
/db_xref="GI:1787269"
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/note="0137; This 137 aa ORF is 27 pct identical (1 gap)
to47 residues of an approx. 80 aa protein RS37_YEAST Sw:
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9412	9353 GGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT 9412	9353	망
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9232	9173 ACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGCGGGGGGGTAATGGTGCAGAT 9232	9173	8

Search completed: March 15, 2004, 22:50:09 Job time: 1965.17 secs

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Result
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## ALIGNMENTS

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RESULT 1
AAC64624
Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen; ds.
                                                                                               P-PSDB; AAB36348.
                                                                                                      WPI; 2000-672631/65.
                                                                                                                   White AP,
                                                                                                                                            05-APR-1999;
                                                                                                                                                          05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                   WO200060102-A2
                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                       Escherichia
                                                                                                                                                                                                              Salmonella enteritidis.
                                                                                                                                                                                                                                             AgfA::PT3#3 DNA sequence SEQ ID NO:15.
                                                                                                                                                                                                                                                           26-FEB-2001
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                                                                                                                  Doran JL,
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                                                                                                                                             99US-0127888P
                                                                                                                   Collison
                                                                                                                                                                                                                                                                                     456
                                                                                                                   SK,
                                                                                                                  Kay WW;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 136; 139pp; English.

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RESULT 2
AAQ87467
ID AAQ8
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AC AAQ8
XC AAQ8
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DT 26-J
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DE Agfa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 456
                             Salmonella
                                                                                                     25-MAR-2003
26-JUN-1995
                                                  Salmonella; AgfA;
                                                                            AgfA sequence
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                                                                                                                                                                  standard; DNA; 456
                                                                                                                                                                                                                                              GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
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                                                                                                                                                                                                                                                                            AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
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                                                                                                                                                                                                                                                                                                                                                GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
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(first entry)
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                                                  vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 456; DB 3; Length 456; 100.0%; Pred. No. 8.5e-141;
                                                  genetic
                                                                                                                                                                  BP.
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Sequence 456 BP; 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 7B; 95pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
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P-PSDB; AAR74625.
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                                                                                                                                                             GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
                                                                 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                                                                                      gécacearedaceadredaaceeraaaaacreegararracredeceacearaceegeege
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/note= "AgfA"
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Pred. No. 2.9e-123;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Col 19-112; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella enteritidis 27655-3b agfA gene
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29-SEP-1997
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DB; AAW23570.
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GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                      AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
                                                                                                                                                                                                                       GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGAATAGTTCCGGC
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                                                                                                                                CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                                                                                                                                                                         ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
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                                          AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
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92.8%;
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Pred. No. 2.9
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          The present invention describes a recombinant agfA gene (1) where a cegment of the gene has been replaced by a segment of a foreign DNA ceguence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended cegasembly system of strains of Salmonella, Escherichia coli and centerobacteriaceae for the production of fimbriae comprising recombinant AgfA. CogA and AgfA-homologue fimbrin subunits, respectively; (2) centerobactering recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene centeroback into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino cardiaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation conjunction with a carrier or diluent. (I) is system the heterologous antigens are presented in high numbers (up to immunocenticity and adhesion recombinant for an afficient live immunocenticity and adhesion recombinant for an afficient live
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant agfA gene having a segment replaced by a foreign DNF which encodes foreign epitope or antigen, expresses recombinant protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-1999;
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                                                                                                                                        Salmonella; agfA; vaccine; immune re
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                                                                                                                                                                                                               AAC64626 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given the exemplification of the present invention
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                                                                                                                                    response; immunogen;
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92.8%;
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                                                                                                                                gene replacement; fimbrin; epitope;
unogen; ds.
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Pred. No. 2.9e-123;
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CC Sequence which encodes a foreign epitope or a segment of the gene has been replaced by a segment of a foreign DNA CC (1) use of thin aggregative fimbriae (SER17/TAP) nucleation described are: assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA-homologue fimbria (SER17/TAP) nucleation depended CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively, (2) CC homologous species, (3) directing recombinant gene into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant QC comprising separating an amino acid polymer comprising a recombinant AgfA (2) protein containing a replacement segment or segments of foreign amino CC polymer into the animal in conjunction with a carrier or diluent. (1) is CC useful for the expression of recombinant AgfA protein gene into the heterologous antigens are presented in high numbers (up to vaccine, the heterologous antigens are presented in high numbers (up to vaccine, the carrier fimbrial subunit proteins are usually strong companied. The interest of finbrial subunit proteins are usually strong companied. The interest of purify in large amount. The present sequence is given in CC inexpensive to purify in large amount. The present sequence is given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 137;
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301 GCCACCATCGACCAGTGGAACGCTAAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA AATAACGCCGCGCTTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT AATAACGCCGGGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420 ĠĊĀĠĠĊĊĀĠĠĠŤĠĊĠĠĀŤĀĀŤĀĠŤĀĊŦĀŤŤĠĀĀĊŤĠĀĊŤĊĀĠĀĀŤĠĠŤŤŤĊĀĠĀĀĀŤĀĀŤ GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT AGCGÁTGCCCGTAÁÁÁTATGÁTCAGCTGGTTÁCCCGTGTTGTTACCCATGÁAATGGCACÁT AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGAT c cega crea a contra de contra de contra con Similarity CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTCTGCTACAA GÉCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCATCCGGC 120 Conservative 78.9%; 0, Score 360; DB 3; I Pred. No. 6.4e-109; 0; Mismatches 60; Length 456; Indels <u>°</u> Gaps 420 360 360 300 300 240 180 180 60 60 0,

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Query Match
Best Local Similarity
Matches 392; Conser
                                                                                                                                                                                                                                                      AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SER17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                        system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                           Sequence 456
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   Conservative
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                                                                         120 A; 110 C; 122 G; 104 T; 0
                   77.5%;
86.0%;
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                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                        Disclosure; Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                            Salmonella enteritidis.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                      AgfA::PT3#7 DNA sequence SEQ ID NO:23.
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                                                                                                                 WPI; 2000-672631/65.
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                                                                                                                                                                                                                                                                                                                                                vaccine; immune response;
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                                                                                                                                                                                                                                                                                                                                                 immunogen;
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The present invention describes a recombinant agfA gene (I) where

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                                                     AAC64622;
                                                                                  AAC64622 standard;
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                (first
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ilarity 85.7%;
Conservative
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              entry)
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Pred. No. 2.9e-106;
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Best Local :
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Escherichia coli.
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                                                      GECGTCGTTCCACAATGEGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SERIT/TAR) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, agfA
                                                                                                                                                                                                                                   Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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Escherichia coli.
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immune response; immunogen; ds.
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0; Mismatches 65;
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CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA grotein containing a replacement segment or segments of foreign amino cci sequence or sequences grown on a Salmonella, E. coli or an expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to containing an immune response in an animal. In a fimbrial presentation cc system the heterologous antigens are presented in high numbers (up to immunogens, which may be important for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong contained the inserted epitope, and hybrid fimbriae are easy and the exemplification of the present invention
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rife present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA. (SGA and AgfA-homologue fimbriae comprising recombinant
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      The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAP) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC anterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CSGA and AgfA-homologue fimbria subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene CC back into the chromosome of the homologous species, replacing the native CC comprising separating an amino acid polymer comprising a recombinant AgfA CC comprising separating an amino acid polymer comprising a recombinant AgfA CC comprising separating an amino acid polymer comprising the containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the CC useful for the axpression of recombinant AgfA protein which is useful for CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to CC unmunogenicity and adhesion properties relevant for an efficient live communicans. Which may be immorrant for for Airecting are usually strong communicans.
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Best Local Similarity
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Escherichia coli.
 WPI; 2000-672631/65
                                   White AP,
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                                                                                                       05-APR-1999;
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                                                                                                                                                                                                                                                                                                                      vaccine; immune
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                                                                                                                                                                                                                                                                                                                    response;
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                                   Kay WW;
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P-PSDB; AAB36351

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 137; 139pp; English.

CC requence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC assembly system of strains of Salmonella, Escherichia coli and CC atterobacteriaceae for the production of fimbriae comprising recombinant CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant gene into the chromosome of the homologous species; (3) directing an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant or comprising a replacement segment or segments of foreign amino CC comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC comprising separating an amino acid polymer comprising a recombinant AgfA colidates and the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to South of the colidates and adhesion properties relevant for an efficient live converse, which may be important for directing an immune response CC imexpensive to purify in large amount. The present sequence is given in the exemplification of the present invention

Sequence 456 BP; 112 A; 113 C; 125 G; 106 T; 0 U; 0 Other;

1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAGTCGTAGTTTCTGGCAGTGCTCTGGCT Similarity GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456 AATAACGCCGCGTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT GCCACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATACGGCGGT GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180 GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC 120 **AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT** GCACATGCAGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT GTAGGCCAGGGTGCGGATAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT Conservative 76.5**%**; <u>,</u> Score 348.8; DB 3; Pred. No. 3.3e-105; Mismatches 67; 456 Indels Length 456; o ; Gaps 420 360 300 180 120 420 240 60

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Copy of that gene; and (4) eliciting an immune response in an animal, Comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement generating a recombinant AgfA comprising a replacement generation of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the CC golymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for CC eliciting an immune response in an animal. In a fimbrial presentation CC system the heterologous antigens are presented in high numbers (up to System the heterologous antigens are presented in high numbers (up to comples/cell), the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties relevant for an efficient live immunogens, which may be important for directing an immune response concepts, which may be important for directing an immune response the inserted epitope, and hybrid fimbriae are easy and concepts the inserted epitope, and hybrid fimbriae are sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence is given in the present sequence in the present sequence is given in the present sequence in the present 
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AAC64631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(1) use of thin aggregative fimbriae (SERI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and nucrobacteriaceae for the production of imbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of a recombination of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-672631/65:
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vaccine; immune response; immunogen; ds.
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                                                          exemplification of the present invention
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RESULT 14
AAQ73066
ID AAQ73

AAQ73066 standard; DNA; 361

27-AUG-2003 25-MAR-2003 26-JUN-1995

(revised) (first entry)

AAQ73066;

AgfA sequence

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421

421 361

GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456

GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456

AATAACGCCGCGCTGGTTÄÄTCAGÄCCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT GCCACCTATGATCAGCTGGTTACCCCGTGTTGTTACCCCATGAAATGGCACATGCAGGCGGT GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT

420 420 360 360 GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT

GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT

300 300 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCGTTGCTCTGCAA

240

240

180

AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT

CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA

180

120 60

GGCGTCTATGATCAGCTGGTTACCCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC 

GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120

361 301 301 241 241 181 181 121 121 61 61

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                       26-APR-1993;
                                                                                                   26-APR-1994;
                                                                                                                                                                      10-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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                           93US-00054452
                                                                                                   94WO-IB000207
                                                                                                                                                                                                                                                                                                                                                                                                 complement (292. .402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(103. .129)
/*tag= e
                                                                                                                                                                                                                                                                                                                                                                                                                         note= "TAF6 primer (pair with TAF5)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= d
/note= "TAF5 primer (pair with TAF6)"
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                                                                                                                                                                                                                                                                                                                 "TAF4 primer (pair with TAF3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (pair with TAF4)"
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ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT

Matches Query Match Best Local !

387;

Similarity

75.8**%**; A; 110

0;

Score 345.6; DB 3; Pred. No. 3.8e-104; 0; Mismatches 69;

Indels Length 456;

0,

Gaps

60

Sequence 456 BP; 113

C; 124

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109 T; 0 U; 0 Other

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RESULT 15
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      primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The DNA encodes the Salmonella enteritis27655-3b TnphoA mutant strain agfA gene cloned into pUC19. The DNA and isolated proteins are used in genetic immunization and vaccine compositions, respectively, to elicit immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-MAR-2003) to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kay
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                                     primer_bind
                                                                           primer_bind
                                                                                                                                                                          Enteropathogenic bacteria;
                                                                                                                                                                                               Salmonella enteritidis 27655-3b TnphoA mutant agfA gene fragment
                                                                                                                                                                                                                          25-MAR-2003
30-SEP-1997
                                                                                                                                                                                                                                                             AAT74141;
                                                                                                                                                                                                                                                                                    AAT74141 standard; DNA; 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 361
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                                                                                                                                                                                                                                                                                                                                                               AATACGGCGGTAATAACGCCGCGCGCTGGTTAATCAGACCGCATCTGATTC 398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          an immune response to Salmonella - using attenuated Salmonella vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                    enteritidis
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(first en
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/*tag= c
/label= Primer_TAF3
complement(103. .128)
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/label= Primer_TAF5
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                                                                            /label= agfA_gene_fragment
l6. .60
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99.0%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                 Sequence 361 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated Salmonella gene agfA - used for diagnosis of Salmonella or enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Col 107-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Collinson SK,
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               AATACGGCGGTAATAACGCCGCGCGCTGGTTAATCAGACCGCATCTGATTC 398
                                                                         TCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCC
                                                                                                                       TTGCTCTGCAAAGCGATGCCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTA
                                                                                                                                                                                                                      ATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGC
                                                                                                                                                                                 TTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTA
                                                                                                          ACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTT
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/label= Primer_TAF6
complement(294..312)
/*tag= e
                                                                                                                                                                                                                                                                                                                                 94 A; 93 C;
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99.0%;
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Primer_TAF4
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Pred. No. 8.
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Search completed: March Job time : 246.684 secs 15, 2004, 17:51:59

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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                           28
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Match
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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  Length DB
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US-09-540-236-492
US-09-596-002-31
US-08-508-761B-1
US-08-916-421B-1
US-09-328-352-1775
US-09-328-352-1775
US-09-328-352-1006
US-09-139-802-200
US-09-659-786-200
US-09-659-786-200
US-09-659-786-200
US-08-443-104-5
US-08-248-130-6
US-08-442-859-5
US-08-442-859-5
US-08-9207-844-1
US-09-252-509-1
PCT-US95-5534-5
US-08-956-171B-54
US-09-557-884-1
US-09-659-388-3
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Sequence 31, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1775, Ap
Sequence 2055, Ap
Sequence 310, App
Sequence 200, App
Sequence 200, App
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Sequence 56, Appl
Sequence 3, Appli
Patent No. 5486473
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TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:

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383, App 1858, Ap		5 7 8 5 8

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; NAME/KEY:
; LOCATION:
US-08-233-788A-58
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 920043.403C2
REFERENCE/DOCKET NUMBER: 920043.403C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
Query Match
Best Local Similarity
Matches 423; Conserv
                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 58:
                                                                                                                                  FEATURE:
                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                    LENGTH: 456 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Seattle
STATE: Washing
                                                                                                                                                      TOPOLOGY:
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88.4%;
ilarity 92.8%;
Conservative
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Score 403.2; DB Pred. No. 5e-135; 0; Mismatches 3
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APPLICATION DAFA:
APPLICATION UNMBER: US/08/233
ELISIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35.570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELERAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
                                                                                                                                                                                                                                                        STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Karen S.
APPLICANT: Collinson, Marion C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION NUMBER OF SEQUENCES: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56, Application US/08233788A
Patent No. 5635617
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                               361 base pairs
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6300 Columbia Center,
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APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HARDLAM, JOHN M.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TITLE OF INVENTION: WWP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
CURRENT APPLICATION NUMBER: US/09/125,619
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin Ver. 2.1
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SEQ ID NO 3
LENGTH: 7766
TYPE: DNA
ORGANISM: Borrelia burgdorferi
FEATURE:
NAME/KEY: modified_base
OCCATION: (127)
                                                                                                                                                                                                                           ; OTHER INFORMATION: R = A OR US-09-125-619-3
                                                                                                                                                        Matches 100;
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Best Local Similarity
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APPLICANT: NORRIS, STEVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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Best Local Similarity 99.0%;
Matches 286; Conservative
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STRANDEDNESS: doub.
TOPOLOGY: linear
MOLECULE TYPE: DNA (
FEATURE:
VAME/KEY: CDS
LOCATION: 1..357
4492 ÁTTGCTGCTGCTÁTTGGGAAGGGTAATGAGGÁTGGTGCGGÁTTTTGGTÁAGGATGÁGATG
                                                                4432 GTTACGGCTGCGGCTGCTGGTGAGCAGGATGGAGAAGCCTGCAGAGGCTACAAATCCG
                                                       217
                                                                                               157 GCT-AACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAG
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5. 6437116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 ACGGCCCCATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTT 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170 TTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTA 229
                       AGCGGTTATGGTAACGCCCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 ATGCATCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGC 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATACGGCGGTAATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATACGGCGGTAATAACGCCGCGCGCTGGTTAATCAGACCGCATCTGATTC 335
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EDNESS: double
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                                                                                                                                                                  47.48;
                                                                                                                                    Score 33.4; DB 4; Length 7:
Pred. No. 0.33;
0; Mismatches III; Indels
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Pred. No. 2.9e-92;
0; Mismatches 3
                                                                                                                                                                       Length 7766;
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RESULT 2 US-08-233-788A-56

CITY: Seattle ADDRESSEE:

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US-09-540-236-492/c
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APPLICANT: FUKITA, HIROYUKI; YOSHIDA, IWAO; TAKAGI, MITSUO; MANABE, SADAO; FUKAI, KONOSUKE

TITLE OF INVENTION: A DNA CODING FOR A FLAVIVIRUS ANTIGEN NUMBER OF SEQUENCES: 16

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4
5486473-3/c
                                                                                                                                                           NUMBER OF SEQ ID NOS: 3840; SEQ ID NO 492; LENGTH: 2436; TYPE: DNA ORGANISM: M.catarrhalis
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                                                                                                                                                                                                                                                                                     Patent No. 6673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
                                                                                           Best
                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                               Sequence 492, Application US/09540236 Patent No. 6673910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                              -09-540-236-492
                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/540,236 CURRENT FILING DATE: 2000-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/:
FILING DATE: 09-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 809,255
FILING DATE: 18-DEC-1991
                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 279,685
FILING DATE: 05-DEC-1988
APPLICATION NUMBER: 932,419
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   1511
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                                 209 TTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 CATGITCATCATTTTGACATCAATGGTTGGCTTGTCTTTTGACATTATGGTCACACAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 CAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCC 237
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                                                                                      Similarity
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TTACCCACATTCATCATAATCTTAAAGGCAAGTTCGGGCATGGTGCTGATTGAATTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAGTCACTGACCGAAGCTAGGTAACAGTAACTGCGCACATCTGCGAGGTTGGCTGCTTC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTACTGTCGGCCAATACGGCGGTAATAACG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATGCCACCATCGACCAGTGGAACGCTAAAAACTCC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCGCCTTCCAGTACCAGATCAACCCATGTAGCTCC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTGCTGTGAAGAGTAATGATGGTGAGAAAG 4642
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                                                                                      6.8%;
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Pred. No. 0.77;
0; Mismatches 78;
                                                                     Score 31.2; DB 4;
Pred. No. 1;
0; Mismatches 73
                                                                 73;
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CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
SOPTWARE: PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PROCESSION OF THE PERL PR
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US-08-508-761B-1
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; OTHER INFORMATION: INCYTE template ID No.
; PUBLICATION INFORMATION:
US-09-596-002-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-596-002-31/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08508761B Patent No. 6027920
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LENGTH: 65792
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                        APPLICANT: Renaud, Michel
TITLE OF INVENTION: System for Protein Expression and
TITLE OF INVENTION: Secretion Especially in Corynebacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                 STREET: 400 Seventn s
                                                                                ZIP:
                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAACTTCATAATCCAAAAATGCCTTCATAAATAAAGCCAGTATCGCCCTCTGCACAAGAA 6700
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                                                                                                                                                                                   E: Jacobson, Pri
400 Seventh St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guyonvarch, Armel
                                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Duchiron,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purification, Relano
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Francis
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                                                                                                                                                                                          Price,
St. N.W.
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Pred. No. 7
                                                                                                                                                                                                                             Holman & Stern,
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

US/08/508,761B

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                                                                                                                                                                                                                                                                               SEQ ID NO 1
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APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
Patent No. 6503729
PILE REFERENCE: PB275
FILE REFERENCE: PB275
                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/916,421B CURRENT FILING DATE: 1997-08-22 PRIOR APPLICATION NUMBER: US 60/024,428 PRIOR FILING DATE: 1996-08-22 NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: 420..2390
US-08-508-761B-1
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Patent No. 6503729
                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
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Best Local Similarity 58.9%; Pred. No. 1
Matches 53; Conservative 0; Mismatch
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2547 base pairs
TYPE: nucleic acid
TYPE: single
                                                                          NAME/KEY: misc feature
OCATION: (28222)..(28
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PRIOR APPLICATION DATA;
APPLICATION UNMBER: FR
FILING DATE: 29-JUL-19
PRIOR APPLICATION DATA;
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FILING DATE: 02-AUG-1991
ATTORNEY/AGENT INFORMATION:
INFORMATION: n equals a, CEY: misc_feature
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LOCATION: (312993) ...(312993)
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LOCATION: (31926)
OTHER INFORMATION: n equals a, t NAME/KEY: misc\_feature
LOCATION: (234814) (234814)
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LOCATION: (309398) .. (309398)
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OTHER INFORMATION: n equals a, t,
LOCATION: (312993) .. (31293) NAME/KEY: misc feature LOCATION: (559167)...(559167) OTHER INFORMATION: n equals a, NAME/KEY: misc feature
LOCATION: (148948) ... (148948)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (163385) ... (163385)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (191989) ... (191989)
OTHER INFORMATION: n equals a, t LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a, LOCATION: (234187).. (234187)
OTHER INFORMATION: n equals a, NAME/KEY: misc feature OCATION: (191995).. (191995) THER INFORMATION: n equals a, LOCATION: (98343)...(>00THER INFORMATION: n equals a, NAME/KEY: misc feature rocation: (103598)...(103598) CATION: (231980). (231980). (231980). (231980) LOCATION: (103998)..(103998)
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; Sequence 1775, Application US/09328352
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GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID /
TITLE OF INVENTION: BAUMANNII FOR
FILE REFERENCE: GTC99-03PA
                                                                                           Sequence 2055, Application Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1775
SEQ ID NO 1775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
APPLICANT: GIVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LCCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc_feature
LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a, t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
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                                                                                                                                                                                                                                                                                                               139 ATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATCT 198
                                                                                                                                                                                                                                                                                                                                                   799 GATATTCGAGCAAATAATCAGCAATTGGCTTATGGATATGGCTATGACCAAACTTGGGTA 858
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Pred. No. 1
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Pred. No. 60;
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                    AND AMINO ACID
R DIAGNOSTICS AN
                                                                                                                                                                                                                                                                                                                                                                                                                           ed. No. 1.5;
Mismatches
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                                       RELATING TO ACINETOBACTER
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CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 SEQ ID NO 2055

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US-08-961-527-310
                                                                                                                        Matches
                                                                                                                                                Query Match
                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 310:
SEQUENCE CHARACTERISTICS:
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-2055
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                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                   Local
                                                                                                                                                                                           TOPOLOGY:
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TITLE OF INVENTION: Strep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: HP Vectra 486/3
OPERATING SYSTEM: MSDOS V
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678 AAGGTTCCTATCCTAGATAGAAGTACTGCTGAAAA 712
                         295 аатлатессассатевассавтеваасеставаа 329
                                                                      235 GCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGA 294
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Rockville
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                                                                                                                 Conservative
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                                                                                                           Score 29.4; DI
Pred. No. 4;
0; Mismatches
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Pred. No. 2.2;
0; Mismatches
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                                                                                                                                    DB 4;
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                                                                                                                                    Length 1939;
                                                                                                         Indels
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PRIOR APPLICATION NUMBER: 08/71(
PRIOR APPLICATION NUMBER: 08/71(
PRIOR FILING DATE: 1996-99-10
NUMBER OF SEQ ID NOS: 226
SOFTWARE: Patentin Ver. 2.0
JENGTUM. 200
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                                                                                                                                                              TITLE OF INVENTION: Same
FILE REFERENCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/09/659,786
CURRENT FILING DATE: 2000-09-11
PRIOR APPLICATION NUMBER: 08/926,914
PRIOR FILING DATE: 1997-09-10
                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
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                                                                                                                                                                                                                                                                                    APPLICANT: Pasqualini,
TITLE OF INVENTION: NG:
TITLE OF INVENTION: MO
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TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renate
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Anglogenic Vasculature Using
TITLE OF INVENTION: Same
                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 200, Application US/09139802
Patent No. 6180084
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EARLIER FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
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CURRENT APPLICATION NUMBER: US/09/139,802
CURRENT FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: 08/926,914
EARLIER FILING DATE: 1997-09-10
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LOCATION: (121)..(3024)
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ORGANISM: Homo sapiens
FEATURE:
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LENGTH: 3494
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o. 6491894
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                                                                                                                                                                                                                                                                                                                                          Ruoslahti, Erkki
                                                                                                                                                                                                                                                               NGR Receptor and Methods of Identifying Tumor Homing Molecules That Home to Angiogenic Vasculature Using
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                                                                                                                                       08/710,067
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Pred. No. 5.6;
0; Mismatches 131;
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US-09-023-655-1006/c
; Sequence 1006, Application US/09023655
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; LOCATION: (121)..(3024)
US-09-659-786-200
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                                                                                                                          TELEFAX: (650) 845-416
NPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tent No. 6607879
                                                                                                                                                                                       NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: STREET: STREET: STREET: PALO ALTO CITY: PALO ALTO CITY CALIFORNIA
                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT:
  LIBRARY:
CLONE: 9
                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: U
                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 6.4%;
Local Similarity 45.2%;
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                                                                                                                ENGTH:
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g178535
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                                                                                                                3494 base pairs
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                                                        linear
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                                                                        single
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US-08-443-104-5
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US-08-443-104-5/c
                              Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
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ADDRESSEE: No. 56911620 No. 5691162disk of ADDRESSEE: No. 56911620 No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRESSEE: No. 5691162disk of ADDRE
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     MOLECULE TYPE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Agris Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
                                                                                                                                                                                                                                                                                                                             ENGTH:
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ilarity 49.4%;
Conservative
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                                 Score 29.2;
Pred. No. 4.
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Pred. No. 5.6;
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                                                                   DB 1;
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                                                                       Length 2052;
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Matches

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Gaps

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Search comp Job time :	Db 4	Qy 4	Db 5	Qy 3	Db 5	φ, γ
Search completed: March 16, 2004, 04:37:30 Job time : 52.6647 secs	443 AGGAGAAGACCTCGCCGTCAGCGCCAATCTGTAT 410	420 TGGTTTTGGCAACAACGCCACGGCTAACCAGTAT 453	503 CTTTCTCGTCACGCTTGGTAAGAGGACCGGGAATCTTGCCCTCGTAGAAGCTGTTTCCGT 444	360 TAATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGT 419	563 TGTCAGCCTCAACGGGGAGAGAAAGAACATCAACGGTGTCCTTGAGAGCGTCGACGGGGT 504	300 TGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGG 359

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2432557 seqs, 1840798884 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY_NUC
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456
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                                                                                                                                                                                                                                                                                                                                                     Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
/Cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
/Cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/Cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/Cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
/Cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
/Cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
/Cgn2_6/ptodata/2/pubpna/US10C_NEW_PUB.seq:*
/Cgn2_6/ptodata/2/pubpna/US10C_NEW_PUB.seq:*
/Cgn2_6/ptodata/2/pubpna/US10C_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                              6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                           6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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4179.927 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIE

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
_	35.6	7.8	1965	ِ ا	US-09-815-242-6264	Sequence 6264, Ap
N	35.6	7.8	1965	12	US-10-282-122A-20532	Sequence 20532, A
w	34	7.5	2583	12	US-10-282-122A-19592	Sequence 19592, A
4	34	7.5	2886	9	US-09-801-368-131	Sequence 131, App
v	33.6	7.4	549	10	US-09-991-936-1800	Sequence 1800, Ap
6	33.4	7.3	7766	12	US-10-222-566-3	Sequence 3, Appli
7	33.4	7.3	7766	14	US-10-222-162-3	Sequence 3, Appli
œ	33.4	7.3	7766	14	US-10-143-024-3	Sequence 3, Appli
9	32.8	7.2	1059	9	US-09-738-626-482	Sequence 482, App
c 10	32.8	7.2	1113	9	US-09-738-626-481	Sequence 481, App
c 11	32.8	7.2	3309400	9	US-09-738-626-1	Sequence 1, Appli
12	32.2	7.1	568	14	US-10-333-631-1	Sequence 1, Appli
13	32.2	7.1	972	14	US-10-333-631-4	Sequence 4, Appli
C 14	32.2	7.1	1083	15	US-10-369-493-33133	Sequence 33133, A
c 15	32.2	7.1	4830	12	US-10-282-122A-27869	Sequence 27869, A

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29.8	29.8	29.8	29.8	30	30	30.2	30.2	30.2	30.2	30.2	30.2	30.4	30.4	30.6	30.6	30.6	30.8	30.8	30.8	30.8	31	31	31	31.2	31.2	31.2	31.8	31.8	
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US-10-213-821-13	US-10-283-423-13	US-10-424-599-72759	US-10-424-599-73842	US-10-282-122A-30822	US-10-156-761-2947	US-10-027-632-59064	US-10-369-493-24379	US-10-210-115-19	US-10-282-122A-6780	US-10-282-122A-24039	US-10-424-599-102524	US-09-984-429-364	US-10-282-122A-25231	US-09-815-242-9042	US-09-815-242-4844	US-10-355-956-3	US-10-086-510-1	US-10-369-493-43454	US-09-873-367C-255	US-10-424-599-10132	US-10-398-221-3563	US-10-424-599-88945	US-09-918-995-32144	US-10-156-761-1	US-10-282-122A-26837	US-10-156-761-687	US-10-369-493-24480	US-10-282-122A-20335	
13,		Sequence 72759, A	Sequence 73842, A	Sequence 30822, A	Sequence 2947, Ap	Sequence 59064, A	243	Sequence 19, Appl	Sequence 6780, Ap	Sequence 24039, A	Sequence 102524,	Sequence 364, App	Sequence 25231, A	Sequence 9042, Ap	Sequence 4844, Ap	Sequence 3, Appli	۳	Sequence 43454, A	Sequence 255, App		Sequence 3563, Ap		Sequence 32144, A	Sequence 1, Appli			Sequence 24480, A	Sequence 20335, A	Are tones accomme

## ALIGNMENTS

US-09-815-242-6264

Sequence 6264, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Ohlsen, Kari L.
APPLICANT: Yeskind, Judith W.
APPLICANT: Yeskind, Judith W.
APPLICANT: Yeskind, Judith W.
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APPLICANT: Yeskind, Judith W.
APPLICANT: Yeskind, Judith W.
APPLICANT: Yeskind, Judith W.
APPLICANTON: Prokaryotes
FILLE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/263,625
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/263,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-26
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/263,308
PRIOR FILING DATE: 2000-12-26
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PRIOR FILING DATE: 2000-12-27
PRIOR FILING DATE: 2001-02-16
NUMBER: 60/263,308
PRIOR FILING DATE: 2001-02-16
NUMBER: 60/263,308
PRIOR FILING DATE: 2001-02-16
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PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-0

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; LENGTH: 1965
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-282-122A-20532
                                                           Query Match
Best Local Similarity
                                                        Matches
                                                                                                                                                                                 Remaining Prior Application da
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 20532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...
US-09-815-242-6264
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAR. 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20532, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
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Best Local S
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APPLICANT:
APPLICANT:
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APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/267,636
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/257,931 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/230,347 FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                      41
                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 AGAACGTTCCTGCTCGTGACCTGGCCCCCCTGCTCCGC 447
TTTCTGGCAGTGCTCTGGCTGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 AAATGGCACATGCATCCGGCCCGGACTCAACGTTGAGC 138
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1 Similarity 60.2%;
59; Conservation
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Carr, Grant
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Carr, Grant
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Forsyth, R.
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Zyskind, Judith
Wall, Daniel
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Malone, Cheryl
Haselbeck, Robert
                                                                                                                                                                                                               Application data removed - See File Wrapper or PALM
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                                                             7.8%;
                                    Score 35.6; DB 12;
Pred. No. 0.26;
0; Mismatches 39;
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Pred. No. 0.26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
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   100
                                 0,
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FILLE OF INVESTION. Identification of Essential Genes in Mic:
FILLE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR PILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-16

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                                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEG ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEG ID NO 19592
LENGTH: 2583
                                                                                                                                                                                                                                                                                      Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohleen, Kari
APPLICANT: Ohleen, Kari
APPLICANT: Zyskind, Judith
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US-10-282-122A-19592
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                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19592, Application US/10282122A Publication No. US20040029129A1
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                         121
                                     188 CCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCC
                                                                                                                            128 CAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCCTCTGCAAAGCGATG
                                                                                                              61
                                                                                                                                                                                                              68 ATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGCCCCGGACT 127
                                                                                                                                                                                                                                                                                                h 7.5%;
Similarity 48.9%;
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CGCATCGÁCCGCÁGTAAGCTGCTGGGCCAGCCGGTCÁCGGTGÁCCATCCCGÁCGCÁGAGC
                                                                                    GGCCGCGAGGCGATGTCCGAGTCGTTTTGCGCTGACGCTGACCGTGCTCGGCACGGACGCG
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                                                                                                                                                                      ATGCTCAACCGAATTACCGTTCAGCTCCCGGTGGAGGGGCTTCTGTTCTGGAAACTGACG 60
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Forsyth, R.
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הים, Robert
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Pred. No. 1.1;
0; Mismatches 95; Indels
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TYPE: DNA
; ORGANISM: Saccharomycee cerevisiae
US-09-801-368-131
                                                                                                                                                                                                                                                                                         US-09-991-936-1800
                                                                                                                                                                                                                                                                                                                 RESULT 5
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US-09-801-368-131
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PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 131
                                                                                                                                                                                                                          Sequence 1800, Application US/09991936
Publication No. US20030073827A1
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/991,936
CURRENT FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US/09/543,668
PRIOR FILING DATE: 2000-04-07
                                                                          APPLICANT: Brandt, Kevin S.
APPLICANT: Gaines, Patrick J.
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Wisnewski, Nancy
TITLE OF INVENTION: FILEA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
TITLE OF INVENTION: MUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
FILE REFERENCE: FC-6-C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
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PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
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Local Similarity 50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 ACTATTGAACTGAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCT 324
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Silva, Jeff
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Milne, Todd
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No. US20020128250Alman,
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Madden, Kevin
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APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REM, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: BARBOUR, ALAN G.
APPLICANT: BENISTICK, GEORGE M.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BOR
FILE REFERENCE: UTSH:234USD3
CURRENT APPLICATION NUMBER: US/10/222,566
CURRENT PILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR TILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Ver. 2.1
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; ORGANISM: Ctenocephalides felis
US-09-991-936-1800
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; SEQ ID NO 3
· PMCTH: 7766
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SEQ ID NO 1800
LENGTH: 549
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NAME/KEY: modified base
LOCATION: (127)
R =
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PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 1959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 7766
TYPE: DNA
ORGANISM: Borrelia burgdorferi
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4612
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TTTGCTGTGAAGAGTAATGATGGTGAGAAAG 4642
                                                                                                                                                                                        AGCGGTTATGGTAACGGCCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTG 276
                                                                                                                                                                                                                              GTTACGGCTGCGGCTGCTGGTGAGCAGGATGGAGAGGCCTGCAGAGGCTACAAATCCG
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                                  ATTACTGTCGGCCAATACGGCGGTAATAACG
                                                                            AAGAAGGATGATCAGATTGCTGCTGCTATTGCTTTGAGGGGTGGCTAAGGATGGAAAG 461
                                                                                                            ACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGAT 336
                                                                                                                                                    ATTGCTGCTGCTATTGGGAAGGGTAATGAGGATGGTGCGGATTTTGGTAAGGATGAGATG
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Pred. No. 3.3;
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Pred. No. 0.66;
0; Mismatches 34;
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APPLICANT: NORRIS, STEVEN J.
APPLICANT: JING-REN, ZHANG
APPLICANT: HARDHAM, JOHN M.
APPLICANT: HOWELL, JERRILYN K.
APPLICANT: BABBOUR, ALAN G.
APPLICANT: BABBOUR, ALAN G.
TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA CURRENT FILIR APPLICATION NUMBER: US/10/143,024
PRIOR APPLICATION NUMBER: 2002-05-10
PRIOR APPLICATION NUMBER: 09/125,619
PRIOR PILING DATE: 1999-01-27
NUMBER OF 507
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APPLICANT: NORELS, STEVEN J.

APPLICANT: HARDHAM, JOHN M.

APPLICANT: HARDHAM, JOHN M.

APPLICANT: HOWELL, JERRILYN K.

APPLICANT: BARBOUR, ALAN G.

APPLICANT: BARBOUR, ALAN G.

APPLICANT: WEINSTOCK, GEORGE M.

TITLE OF INVENTION: VMP-LIKE SEQUENCES OF PATHOGENIC BORRELIA

CURRENT APPLICATION NUMBER: US/10/222,162

CURRENT APPLICATION NUMBER: 09/125,619

PRIOR APPLICATION NUMBER: 09/125,619

PRIOR PILING DATE: 1999-01-27

NUMBER OF SEO IT NOS. E.
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                                                                NUMBER OF SEQ ID NOS: 4:
SOFTWARE: PatentIn Ver.
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10143024 Publication No. US20030092903A1 GENERAL INFORMATION:
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Best Local Similarity
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TYPE: DNA
ORGANISM: Borrelia burgdorferi
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 7766
                                             LENGTH: 7766
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Publication No. US20030060618A1
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NAME/KEY: modified base
LOCATION: (127)
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LENGTH: 1059
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                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEG ID NOS: 7059
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                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 482, Application US/09738626
Publication No. US20020197605A1
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                                                                                                                                                                                                                                                                                             TYPE: DNA
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Best Local Similarity
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NAME/KEY: modified_base
'COATTON: (127)
'TON' R =
                                 136 GCCGGTGAAAAAGTAACCÁTCACCGTCTÁCACCTCTGÁGCCTGAGGAAAAGGTCGÁTGAG 195
304 ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAAT 363
                                                                  244 GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC 303
                                                                                                                               184 GATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGGTTATGGTAACGGCGCCGATGTA 243
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                                                                                                     GAGGACGTTTCCACCGCÁGAGÁCCÁCCACTGCAÁGCTCTTCCGCTÁÁCGCATCCGÁTGCÁ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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                                                                                                                                                                                 Conservative
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Pred. No. 3.3;
                                                                                                                                                                            ed. No. 1.8;
Mismatches 112;
                                                                                                                                                                                                             DB 9;
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                                                                                                                                                                                                             Length 1059;
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US-09-738-626-1/c
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US-09-738-626-481/c
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SEQ ID NO 481
LENGTH: 1113
                                                                                                             GENERAL INFORMATION:
                                                                                                                           Sequence 1, Application US/09738626
Publication No. US20020197605A1
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ORGANISM: Corynebacterium glutamicum
-09-738-626-481
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APPLICANT:
APPLICANT:
                 APPLICANT:
                                                    APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSI
APPLICANT: ANDO, SEIKO
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PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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   PPLICANT:
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Local Similarity 47.2%;
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
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               HAYASHI, MIKIRO
OCHIAI, KEIKO
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YOKOI, HARUHIKO
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o. US20020197605A1
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                                                                     HIROSHI
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Pred. No. 1.9;
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Query Match
Best Local Similarity
Thes 70; Conserve
                                                                                                 ; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (90) \( \). (90)
; OTHER INFORMATION: n=a,
US-10-333-631-1
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US-10-333-631-1
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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10333631
Publication No. US20030190651A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bayer AG
TITLE OF INVENTION: ENZYME
TITLE OF INVENTION: ENZYME
FILE REFERENCE: LIO121 Foreign Countries
CURRENT APPLICATION NUMBER: US/10/333,631
CURRENT FILING DATE: 2000-01-23
PRIOR APPLICATION NUMBER: US 60/221,917
PRIOR TILING DATE: 2000-07-31
PRIOR TILING DATE: 2000-07-31
PRIOR TILING DATE: 2000-07-31
                                                                                                                                                                                                                                                                     SEQ ID NO 1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/280,112
PRIOR FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.1
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                    LENGTH: 568
TYPE: DNA
ORGANISM: Homo sapiens
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OZAKI, AKIO
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ilarity 52.6%;
Conservative
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                 Score 32.2; DB Pred. No. 2.1; 0; Mismatches
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Pred. No. 1.3e+02;
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                                                          DB 14;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-333-631-4
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B WITH IMPROVED PROPERTIES
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                          Sequence 33133, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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US-10-333-631-4
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APPLICANT: BAYER AG
TITLE OF INVENTION: REGULATION OF HUMAN PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE
TITLE OF INVENTION: ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/10333631
Publication No. US20030190651A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: LIO121 Foreign Countries CURRENT APPLICATION NUMBER: US/10/333,631 CURRENT FILING DATE: 2003-01-23 PRIOR APPLICATION NUMBER: US 60/221,917 PRIOR FILING DATE: 2000-07-31 PRIOR APPLICATION NUMBER: US 60/280,112 PRIOR FILING DATE: 2001-04-02
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Pred. No. 2.8;
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; LENGTH: 4830
; TYPE: DNA
; ORGANISM: Mycobacterium leprae
US-10-282-122A-27869
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US-10-282-122A-27869/c
; Sequence 27869, Application US/10282122A
; Publication No. US20040029129A1
                 Matches
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APPLICANT: Wang, Lia:
APPLICANT: Zamudio,
APPLICANT: Malone,
APPLICANT: Haselbecl
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US-10-369-493-33133
                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                         Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR PRIOR PRIOR NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-03-21
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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TYPE: DNA
               Local Similarity
les 76; Conserv
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
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Malone, Cheryl
Haselbeck, Robert
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Yamamoto, Robert
Forsyth, R.
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Trawick, John
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Search completed: March 17, 2004, 08:16:08 Job time : 411.736 secs	4109 TCGGTCAAGACGATGTCAGCGGCTCCTCG 4081	344 TCGGCCAATACGGCGGTAATAACGCCGCG 372	4169 ACGCCTGCCCACATGCTGCGGCCTTCGACCAGGGCATCGACCAGTACACCCAGATCGTCG 4110	284 ATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTG 343	

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VERSION
KEYWORDS
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AUTHORS
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ORGANISM
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97391 BJ39739	39739	12	ω	•	33	ö
35378 8J33537	33537	12	N	٠	33	9
96922 BJ39692	39692	12	N	٠	33	æ
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## ALIGNMENTS

Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp The information of this clone URL. Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, v Tel: 81-59-81-6856 Expressed genes in X. laevis embryo Unpublished (2001) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.

1 (bases 1 to 680)

Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Xenopus laevis (African clawed frog) Xenopus laevis EST Xenopus laevis BJ618688 BJ618688
BJ618688 NIBB Mochii normalized Xenopus early gastrula library Xenopus laevis cDNA clone XL186b22 5', mRNA sequence. Kohara,Y BJ618688.1 GI:37256713 is available through the Japan EST 01-OCT-2003

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  Contact: Brika Asamizu
The First Laboratory for Plant
Kazusa DNA Research Institute
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                                                                                                                         Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                         AV430994 AV430994 Porphyra yezoensis TU-1 Porphyra yezoensis AV43094-1 S', mRNA sequence.

AV430994-1 GI:8586219
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Nikaido,I., Asamizu,E., Nakajima,M., Nakamura,Y., Saga,N.
                                                                                                                                                                                                                                                                                                Porphyra yezoensis
Porphyra yezoensis
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
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Location/Qualifiers
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/dev_stage="stage 10.5"
/clone_lib="NIBB_Mochii_normalized_Xenopus_early_gastrula
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/mol_type="mRNA"
/mb_tref="taxon:8355"
/clone="XL186b22"
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0; Mismatches 146;
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                                                                                                                                                                                                        High quality sequence start:
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                 Zea mays subsp. mays (maize)
Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sparmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 772)
Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,
Zohovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.
Unpublished (2003)
Communications of the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321
                                                                                                                                                                                                                                          Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                    University
                                                                                                                                                                                                                                                                                                                                             Dr.Joachim Messing's lab
The Plant Genome Initiative
                                                                                                                                                                                                                                                                                                                                                                              Contact: Bharti, A.K.
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ZMMBBc0273B12f ZMMBBc (ECORI) Zea mays subsp. mays
ZMMBBc0273B12 5', genomic survey sequence.
CG862779
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Email: asamizu@kazusa.or.jp,
Location/Qualifiers
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                                                                                                                                                                                                                                                                 bharti@waksman.rutgers.edu
                                                     /sub_species="mays"
/db_xref="taxon:4578"
/clone="maxbase0273B12"
/lab_host="E._coli DH10B"
/clone_lib="zMMBBC (EcoRI)"
/note="Vector: pTARBAC2.1; Si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                   /organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="B73"
8.2%;
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/clones"pL027e10 r"
/clone=lib="Porphyra yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Porphyra yezoensis"
|mol_type="mRNA"
|strain="TU-1"
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57.1%;
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Pred. No. 2
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URL:http://www.kazusa.or.jp/en/plant/.
                                                  Site_1:
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genomic clone
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Similarity 51.884; Conservative

Score 37.2; DB Pred. No. 3.6; 0; Mismatches

29; 78;

Indels Length 772;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 484)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, I Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y. Lai, Z., Church, S., Jackson, L. and Bradford, K. Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore
University of California at Davis (UCD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CF089570 484 bp mRNA linear EST QHM23E04.yg.ab1 QH M sunflower H.argophyllus Helianthus CDNA clone QHM23E04, mRNA sequence. CF089570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              belongs to contig
for details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu] belongs to contig QH_CA_Contig2049, see http://cgpdb.uc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CF089570.1 GI:33128637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: QHM23 row: E column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helianthus
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GATCCTACTGCCATACCGGCTAGCTCTCCTACGGCTTTAGAATCTGTAGCTACGGCTGAA 204
                                     GGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTG 177
                                                                                                                  GCTGGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCATCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAGCTGCATTTGAACATTCAGCAATGTAGTCCAGGAGAGAC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCGCTTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGAC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCAGGTGGTTCCGGCAAGGACACGCCGATGAGCATCTGTCGGTATGTTGGGCAGCTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTCCATCAGCTCGCCCCTGGTGGGGGGTCTTGCGTCCCAACTTGCTAACCAGGTCGC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-(530)-752-9659
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                        /clome lib="QH_M sunflower H.argophyllus"
/note="Vector: pBRcDNASfiAB; The library was constructed from three different sources (seedling, root and leaf) of RNA from a single genotype. cDNAs were pooled and directionally cloned into a custom medium-copy vector. Details of library construction can be obtained at http://cgpdb.ucdavis.edu/"
                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:73275"
/clone="QHM23E04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Helianthus argophyllus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  lab_host="E.coli"
                                                                                                                                                                             7.9%;
                                                                                                                                                        ; Score 35.8; DB; Pred. No. 7.4; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                DB
                                                                                                                                                          142;
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                                                                                                                                                                                                14;
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                                                                                                                                                                                             Length
                                                                                                                                                                                                484;
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argophyllus
                                                                                                                                                          Gaps
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TITLE
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AUTHORS
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Best Local Similarity
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  238 GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 AATGCCACCATCGACCAGTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 CAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 GATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                             94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Riggs.F., de Jong.P. and Fraser,C.M
Rat BAC End Sequences from Library
Unpublished (1999)
Other_GSSs: CH230-390D21.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Riggs, F., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BZ204853.1 GI:23862905
                                            CAAGGACCTCCACATCAAACCAGACACTCAAACTAATAGAAGAAAAACTAGGGAAGCA 607
                                                                                 CAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGCCAAGATGGACCCTGTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGAAGGCGTGGTTGTGCCTAGATTTGTTATTGGATCTAACATTATCCGTAGCGCAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer: T7
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BAC ends.
                                                                                                                                                                                                                              /cell_type="Brain"
/clone lib="CHORI-230 Segment 2"
/clone="Vector: pTARBAC1.3; Site 1: MboI; Site 2: Mt/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: Mt/CHORI-230 Rat (BN/S8NHsd/MCW) BAC library produced Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/mol type="genomic DNA"
/strain="BN/S8NH8d/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                        /clone="CH230-390D21"
/sex="Female"
                                                                                                                                                 49.0%;
                                                                                                                             0;
                                                                                                                                                 Score 35.2;
Pred. No. 16;
                                                                                                                             Mismatches
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Russell, D.,
                                                                                                                                                                       813;
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Matches 112;
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Best Local (
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          361 ARIAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                  305 GARÁATGCTGCACÁGAGCÁÁCACCÁACÁACAATGÁAÁACÁATARCAATGÁÁAÁTGCGGGT
                                                                                                                                                                                                              181
                                                                        GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
                                                                                                                                                                                                                           Similarity 46.5
12; Conservative
                                                                                                   ĠACAATGTAAAŤĠĊAAÁŤGÁAGAŤGTŤÁCŤCÁÁAAĠGAAAÁCÁÁCĠAŤŤCAÁĠŦTCAÁÁŤ 304
                                                                                                                          GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                                                      AACAATGACGGGAATGCGAATGGGAATGTTGGCAGCACAGACAATCAGAGCAACACCAAT 244
                                                                                                                                                                               AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: rwing@clemson.edu
Seq primer: TRATACCACTCACTATACGG
Seq primer: Gequence stop: 696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A. of the cotton fiber of the genetics, development, and evolution unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gossypium arboreum Gossypium arboreum Gossypium arboreum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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BG441624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATGCCACGATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATACGGC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41624
702 bp mRNA linear EST 15-MAR-2001
Ea0014A14f Gossypium arboreum 7-10 dpa fiber library Gossypium
CDNA clone GA_Ea0014A14f, mRNA sequence.
                                                                                                                                                                                                                                                                    /lab_host="E. coli"
/clone lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:29729"
/clone="GA_Ea0014A14f"
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                                                                                                                                                                                                                                                                                                                                                                                            /organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
                                                                                                                                                                                                                                                                                                                                                                                cultivar="8400"
                                                                                                                                                                                                                                       7.6%;
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Pred. No. 22;
0; Mismatches 129;
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ORIGIN

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365 CÁGGÁCGGGAAGAATGCCÁCTCÁGÁGTAACACTGACAACÁATGAÁAATGTGGGTCÁGAAT
                                                              361 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                               185 AACAÁTGACGGGÁATGCGAÁTGGGÁATGTTGGCAGCAGACAÁTCAGÁGCAACACACCAÁT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGGGT 240
                                                                                                                                          GAAĀATGCTGCAĆĀGAĞCĀĀĆAĆCĀĀCĀĀCĀATĞĀĀĀACĀATAĀČAATGĀĀĀĀĀTĞCGĠĠŢ 364
                                                                                                                                                                                                GCCACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATACGGCGGT 360
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Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 804.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An integrated analysis of the genetics, development, and evolution of the cotton fiber (2000) (Contact: Wing RA Clemson University Genomics Institute (Clemson University Genomics Stitute (Clemson University Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Genomics Ge
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
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Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,
Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gossypium arboreum
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/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:29729"
/clone="GA__Ea0023M14f"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Gossypium arboreum"
/mol_type="mRNA"
/strain="AKA"
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46.5%; Pred. No. 26;
ative 0; Mismatches 129;
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RESULT 9
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AV058630
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    BJ334624 523 bp mRNA linea BJ334624 Dictyostelium discoideum cDNA library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (1986)
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                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                            TCCAGTGAAGCACAAAAATGAAGAAGAAAATGATTACCCAAAAGTTGGAATTAAGGTAG
                                                                                                                                                                                                                                                                ACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCG 370
                                                                                                                                                                                                                                                                                                             GTGGAGACCACAGTTTTTTCTAGGTCACCAAGGCTGGGTAAAGAAAAAAAGAAGCATCAACTG
                                                                                                                                                                                                                                                                                                                                                      GTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCG
                                                                                                                                       AGATGCCAAAATAGA 147
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="1810054H02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="pancreas"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib="Mus musculus pancreas C57BL/6J adult'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'sex="male"
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C57BL/6J adult Mus musculus cDNA
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linear EST 05-MAK-20 rary, AF Dictyostelium
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                               EST 05-MAR-2002
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Matches 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    458
                                                                                                                                                                                  1 (bases 1 to 811)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Frai Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Other_GSSs: BOOAOS8TR
                                                                                                                                                                                                                                                                                                                                                                                                       BCAO58TF BO 1.6 2 KB tot genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
                                                                                              9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                      Brassica oleracea
Brassica oleracea
                                                                Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                            BZ469000.1
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                              Class: sheared ends
                                                Seq primer: TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2002)
Contact: Tadasu Sh
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BJ334624
BJ334624.1 GI:19164754
                                                                                                                                                                    Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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1 (bases 1 to 523)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                    Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Dictyostelium discoideum"
/mol type="mRNA"
/strain="AX4"
            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="Aggregation stage"
/clone_lib="Dictyostelium discoideum cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'sex="mat A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:44689"
/clone="dda47006"
                                                                                                                                                                                                                                                                                                                                                                            GI:26764546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H., Tanaka, Y., Kohara, Y. and Shin-i, T.
cDNA of Dictyostelium discoideum at the aggregation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34.2; D
Pred. No. 25;
O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica
                                                                                                                                  Rockville,
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                                                                                                                                                                                                                                                                                                                                                                                                                          linear GSS 13-DEC-200
a genomic clone BOOAO58,
                                                                                                                                                                                                                                      and Fraser, C.M
                                                                                                                                  USA
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FEATURES
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CF372418/c
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VERSION
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                                                                                                                                                                                                                                                                                                       PO Box 350, Glen Osmond, SA, 5064, A
Tel: 61 8 83038600
Fax: 61 8 83038601
Email: Mark.R. Thomas@csiro.au
Seq primer: CCCAGTCACGACGTTGTAAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 CCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 TGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCG 235
                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2003)
Contact: Mark R. Thomas
CSIRO Plant Industry
CSIRO
                                                                                                                                                                                                                                                                                                   POLYA=Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expressed sequence tags from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vitis vinifera
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
rosids; Vitaceae; Vitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Iocco, P., Hua, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF372418 480 bp mRNA linear EST 27-AUG-2003 CSECS052808 FLON0012 CabSau Normalised Flower Stage 12 (FLOn0012) Vitis vinifera cDNA clone CSECS052808 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 480)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
           /sex="Hermaphrodite"
/dev_stage="12 - modified E-L system"
/dev_stage="12 - modified E-L system"
/clone_lib="cabSau Normalised Flower Stage 12 (FLOn0012)"
/note="Organ; Inflorescence including flowers; Vector:
/normalised cDNA library from immature inflorescences
at stage 12 of the modified E-L system. Tissue collected
from field grown plants. A description of the modified E-L
system can be found in the paper by B. G. Coombe 'Adoption
                                                                                                                                                                 /organism="Vitis vinifera"

/mol type="mRNA"

/culfivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="CSECS052B08"
                                                                                                                                                                                                                                                                               .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="BOOAO58" '
/clone lib="BO_1.6 2 KB tot"
/note="Vector: pHOS1; SIte 1: BstXI; 1.6-2 kb sheared total DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3712"
/clone="BOOAO58"
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/mol_type="genomic_DNA"
/strain="TO1000DH3"
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e tags from the grapevine cultivar Cabernet
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Pred. No. 37;
0; Mismatches 95
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                                                                                                                                                                                                                                                                                                           Forward)
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CF414539/c
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                                                                 Local
94 ACCCATGAAATGGCACATGCATCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGT 153
                                                                Similarity
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밁 S В Ś 밁 Ś 8 Ş

COMMENT

Conservative

87;

Indels

0,

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 тесестваесствесствестествевальнее поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий поставляющий постав
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Mark.R.Thomas@csiro.au
Seq primer: CCCAGTCACGACGTTGTAAAACG
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Fax: 61 8 83038601
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Contact: Mark R. Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PO Box 350, Glen Osmond,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSIRO Plant Industry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sauvignon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; rosids; Vitaceae; Vitis.

1 (bases 1 for interpretation)
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Vitis vinifera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Dases 1 to 481)
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                                                                                                                                                                               /note="Organ: Fruit with seeds removed; Vector: pZL; A CDNA library from postveraison fruit at stage 36 of the modified E-L system. Tissue collected from field grown plants. A description of the modified E-L system can be found in the paper by B. G. Coombe 'Adoption of a system for identifying grapevine growth stages' (1995) Aust. J. Grape and Wine Res. 1: 104-110."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="Hermaphrodite"
/dev_stage="36 - modified E-L system"
/clone_lib="CabSau Normalised Berry Postveraison Stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Vitis vinifera"
/mol type="mRNA"
/cultivar="Cabernet Sauvignon"
/db xref="taxon:29760"
/clone="CSECS071B09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POSn0036) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                               7.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davies, C. and Thomas, M.R.
Score 33.8; DE
Pred. No. 31;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratorio di Genetica Molecolare Istituto Agrario di San Michele all'Adige (IASMA) via E. Mach 1, San Michele all'Adige (TN), I-3801 Tel: 0039-0461-65314 Fax: 0039-0461-650956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequencing work has been funded Risparmio di Trento e Rovereto'. High quality sequence stop: 509.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
CF605114
CF605114.1 GI:37185761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: claudio.moser@ismaa.it
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                                                          CAGAAAGAATCAAGGCTTGGAAGCAGCAGTAGCCGGGATCAGGATGATTCTCC
                                                                                       CAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTAC 266
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                                                                                                                                                                                                                                                                                                                        /lab_host="DH108"
/clone_lib="Grape Root pSPORT1 Library"
/clone_lib="Grape Root pSPORT1; Site_1: Not1;
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/sex="Hermaphrodite"
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/lab_host="DH10B"
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Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540,
                                                                                                                                                                                                                                                                       Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium. 1 (bases 1 to 653)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the
                                                                                                                                                                                                                                                                                                                                                                                                                                         BJ336964 EST 05-MAR-20 BJ336964 Dictyostelium discoideum cDNA library, AF Dictyostelium discoideum cDNA clone dda55e20 5', mRNA sequence.
BJ336964
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                                                                                                                                                                                                             Unpublished (2002)
Contact: Tadasu Shin-i
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Dictyostelium discoideum
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Full length cDNA of Dictyostelium
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BJ335653.1 GI:19165783
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Fax: 81-559-81-6855
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1 (bases 1 to 594)
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                                                              tshini@genes.nig.ac.jp.
Location/Qualifiers
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Location/Qualifiers
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/organism="Dictyostelium
/mol_type="mRNA"
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/mol_type="mRNA"
/strain="AX4"
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clone_lib="Dictyostelium discoideum"
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Search completed: March 16, 2004, 04:29:07 Job time: 2232.91 secs Ş 밁 Ś 밁 망 ORIGIN Query Match 7.4%; Score 33.6; DB 12; Length 653; Best Local Similarity 53.9%; Pred. No. 43; Matches 69; Conservative 0; Mismatches 59; Indels 0; Gaps 307 AATAAAAA 314 358 GGTAATAA 365 ||| || 298 AATGCCACCATCGACCAGTGGAACGCTAAAAACTCCCGATATTACTGTCGGCCAATACGGC 357 /strain="AX4"
/db xref="taxx0:44689"
/clone="da45620"
/sex="mat A"
/dev stage="Aggregation stage"
/clone\_lib="Dictyostelium discoideum cDNA library, AF"

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a

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J. Clin. Microbiol. 31 (9), 2263-2273 (1993)
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                                                         Salmonella enteritidis
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                                                                              Kay, W.W
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Salmonella enteritidis
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2067 bp DNA linear BCT 14-
Salmonella enteritidis agfBAC operon: fimbrin-like protein
precursor (agfB), thin aggregative fimbriae precursor (agff
AgfC (agfC) genes, complete cds.

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                                                    agfBAC operon encoding
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                                                                              Doran, J.L.,
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1.9e-103;
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1352. 1645
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/note="thin aggregative fimbrin subunit; major fimbrial subunit of thin aggregative fimbriae"
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.710. .2036
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LSIYQYGSANAALALOSDARKSETTITQSGYGNGADVGQGADNSTLELTQNGFRNNAT
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(Jenne-WagfA)
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696. .752
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/note="putative signal sequence of 21
fimbrin-like protein"
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Best Local Similarity

89.1%; 93.2%;

Score 406.4; DB 1; Pred. No. 2.1e-103;

Length 2067;

Query Match

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MEDLINE
PUBMED
                                                                                                                                                                                                                                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella typhimurium
Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ002301
AJ002301.1 GI:2739232
csgA gene; csgB gene; csgC
csgG gene.
                                                                                                                                                                                                               Submitted (29-OCT-1997) Romling U.,
Karolinska Institute, MTC, Box 280,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           Romling, U., Bian, Z., Hammar, M., Sierralta, W.D. and Normark, S. Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cegC genes.
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                                                                                                                                                                                                                                                                                              Romling, U.
                                                                                                                                                                                                                                                                               Direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCCACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATACGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCGATGCCCGTAAATCTGAAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGCGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                                                                                                                                                                         Bacteriol. 180 (3),
                                                                                                                                                                                                                                                                                                              (bases 1 to 5103)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; csgD gene; csgE gene; csgF gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ďď
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                                                                                                                                                                                                                                   Department Stockholm,
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                                                                                                                                                                                                                                   of Bacteriology,
S-17177, SWEDEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       csgA, and
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                                                        -10_signal
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gene

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mat_peptide
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gene CDS

gene Sg

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Query Match
Best Local Similarity
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The Salmonella typhimurium Genome Sequencing Project Direct Submission
Submitted (29-MAR-2001) Genome Sequencing Center, Department of
                                                                                                                                                                                       1 (bases 1 to 22411)

McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W.,

McClelland, M., Sanderson, K.E., Spieth, J., Clifton, S.W.,

Latreille, Courtney, L., Porwollik, S., Ali, J., Dante, M., Du, F.,

Hou, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes, A.,

Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Miller, W.,

Stoneking, T., Nhan, M., Waterston, R. and Wilson, R.K.

Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                             Salmonella typhimurium LT2
Salmonella typhimurium LT2
                                                                                                                                                     Nature 413 (6858),
21534948
                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
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Salmonella typhimurium
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AE008749 AE006468
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CDISTHAENI"
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Pred. No. 1.4e-101;
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gene CDS		gene RBS CDS	)	COMMENT
YDVLLKRLGASFMQYCLRPEIGKVEIAPFAYMRGRTFENAVVILDEAQNVTAAQMKMF LTRLGENVTVIVNGDITQCDLPRGVRSGLSDALERFEEDEMVGIVHFNKDDCVRSALC QRTLHAYS"  complement (14142303) /gene="STM1127" complement (14142295) /gene="STM1127" /pene="STM1127" /note="similar to E. coli orf, hypothetical protein /note="similar to E. coli orf, hypothetical protein /note="similar to E. coli orf, hypothetical protein /note="similar to E. coli orf, hypothetical protein /note="similar to E. coli orf, hypothetical protein /note="similar to E. coli orf, hypothetical protein /note="similar to E. coli orf, hypothetical protein /AAC75480.1; Blastp hit to AAC75480.1 (285 aa), 29\$ identity in aa 15 - 264" /codon_start=1 /trans[ table=11 /product="putative transcriptional regulator" /protein_id="AAL20058.1" /protein_id="AAL20058.1" /db_xref="GI:16419643" /translation="mepoppprLKPGKILDTLGAMOKSLTRASQRIAQYILAFPRQVTQ SSIADLSRETQAGEATVLTRFCRTLGYKGFQDFKWDLAIELATTESDDSSPLLDAEVSE SDDAHAIGLKLQNTISNYLSETLNLLDMQQVLGYVDALRHCHSVYIFGVGSSGITALD MKHKLMRIGLRGDAVSNNHFMYMQATLLKAGDVAMGVSHSGTSPETVHSLRLARQAGA	/gene "pnoh" /note="similar to E. coli phoB-dependent, ATP-binding pho /note="similar to E. coli phoB-dependent, ATP-binding pho regulon component; may be helicase; induced by P starvation (AAC74105.1); Blastp hit to AAC74105.1 (354 aa), 92% identity in aa 71 - 354" /codon starte1 /trans1_table=11 /product="phoB-dependent ATP-binding pho regulon component" /protein_id="AAL20057.1" /protein_id="AAL20057.1" /db_xref="GI:16419642" /trans1ation="MCAHRRYQENAGDVYLQLKYLSMGRQKAVIKARREAKRYLRRDS /SHKQREEESVTSLVQMGGVEAIGMARDSRDTSPVKARNEAQAHYLNAIDSKQLIFAT GEAGCGKTWISAAKAAEALIHKDVERIIVTRPVLQADEDLGFLPGDIAEKFALYFRPV	/organism='Salmonella typhimurium LT2" /organism='Salmonella typhimurium LT2" /mol_type="genomic DNA" /strain="LT2; SGSC 1412; ATCC 700720" /db_xref="ATCC:700720" /db_xref="taxon:99287" /note="LT2" 4341308 /gene="phoH" /note="synonym: STM1126" 434439 /gene="phoH" /note="putative RBS for phoH; RegulonDB:STMS1H001398" /500 "phoH"	EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EccCyc; http://ecccyc.PangeaSystems.com/ecccyc/  The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence than one ml3 subclone.  Location/Qualifiers	Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 AI43283  Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
gene	RBS gene CDS	gene CDS		RBS gene
(AAC77266.1); Blaidentity in aa 4(codon start=1) (codon start=1) (transl_table=1) (product="putatity") (product="qutatity") (product="qutatity") (product="qutatity") (product="gutatity") (product="g	/db xref="G1:1643" /trānslation="MSI AGAVAVRIEGISULITY AFDASFRSRPVDIDSLI ITPMEPDLAWVTQLSH WFSHAVKR" Complement (5094. /gene="STM1129" /note="putative F 5599. 6759 /gene="STM130" /gene="STM130" /gene="STM1130" /note="sim1130"		YGVI YGVI YGVI YGVI YGVI YGVI YGVI YGVI	TTVAITHNLGSPLCEE, QARESKLRTMMALDMTI Complement (2298. /gene="STM1127" /note="putative l complement (2580. /gene="STM1128" /complement (2580.

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astp hit to AAC76255.1 (229 aa), 70% identity in aa 1 -
6"
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ene="STM1129"
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ote="similar to E. co
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99. .6759
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RESKLRTMNALDMTK"
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RBS for STM1131; RegulonDB:STMS1H001402"

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RESULT 5
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                          AL627269 254050 bp
Salmonella enterica serovar Typhi
complete chromosome; segment AL627269 AL513382 AL627269.1 GI:16502231
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ieklemgigfyudasvksggvdgeqdkhlsdlvanaielgvsynykvtunfvlgpgfi
fesgpdtsiykpylrggynfdsgvymagrykvdyarktanysddektnrfdtyigyvf
DELKLEYNFTMMDSDQIKfDNKKTNYEHNVALAWKLNKSFTPYVEVGNVAVRNNTDER
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(AAC77235.1); Blastp hit to AAC77235.1 (425 aa),
identity in aa 25 - 418"
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/protein_id="AAL20062.1"
/db_xref="GI:16419647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to E. coli orf, hypothetical protein (AAC77267.1); Blastp hit to AAC77267.1 (241 aa), 26% identity in aa 4 - 239"
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/transl_table=11
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92.3%;
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0; Mismatches 35;
                                        (Salmonella typhi) strain
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) strain CT18,
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Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Details of S. typhi sequencing at the on the World Wide Web.
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Parkhill, J.
Direct Submission
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Salmonella enterica subsp.
Bacteria, Proteobacteria, C
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Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                            /db_xref="Gripambi.gaztto"
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//db_xref="Gripambi.gaztto"
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//translation="mtoopoaxxrhdyrapdyoitdieltfdldaektyvytaisqavr
HGAPDAPLIRLDGEDLTLVSIHVNDAP mytaytarettkii addlereftlikingn
NTALEGLYOSGDALCTQCEASGGRHITMYLDREDYLARETTKII TADDLEREFLISNGN
RIVAGELENGRHHVOWODPFEKECYLFALVAGDFDVLRDTFTTRSGREVALELYVDRG
RIVAGGELENGRHHVOWODPFEKECYLFALVAGDFDVLRDTFTTRSGREVALELYVDRG
NLDRAPMAMTSILNSKWADETREGLEYDLDI YMIVAVDFFNMCAMENKGLNIFNSKYV
LARTDTATDGVLLEKVGHREVFHNMTGNRVYCTAPFOLSIKEGLTVUPRODEFSSDL
SGRAVNRISNVRTMGGLOFADDAS PMAHPIRDEDAVVLLSHFERRWSQSCTPIVTV
SGRAVNRISNVRTMGGLOFADDAS PMAHPIRDEDASVDLSHFERRWSQSCTPIVTV
KDDYNPETEQYTITISORTPATADQAEKQPHIPFALELYDMEGNUPFOKARNDFSRWD
TLLGEERBLAVGKGWLYFERHDGSAATCDDFVARAVLLDELSHFRRWSQSCTPIVTV
KDDYNPETEQYTITISORTPATADQAEKQPHIPFALELYDMEGNUPFOKARNDFSRWD
AAQSILATYYIKUNVARHOQGQPLSLPVHVADAFRAVLLDEKIDPALAREILTJESANE
AAQSILATYYIKUNVARHOGGOPLSLPVHVADAFRAVLLDERVDHGDIGKRTLNA
AAQSILATYYIKUNVASHOOGOPLSLPVHVADAFRAVLLDERVDHGDIGKRTLNA
ACKIRFTIFGETELANTILVSKOYRDANMTDALAALSAAVAAQLPCRDTLMGEYDDKMH
ODGSTVORFIVENDETVASILKHRSFSMSDNARRSLIGAFAGSSNDAAFH
ANDRGGVORFIVENDETVASILKHRSFSMSDNARRSLIGAFAGSSNDAAFH
ANDRGGVORFIVENDETVASILKHRSFSMSDNARRSLIGAFAGSSNDAAFH
ANDRGGVORFIVENDETVASILKHRSFSMSDNARRSLIGAFAGSSNDAAFH
ANDRGGVORFIVENDETVASILKHRSFSMSDNARRSLIGAFAGSSNDAAFH
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Location/Qualifiers
/gene="STY1078"
/note="Pfam match
family M1, score;
                                                                                                                                                            LSGDLYEKITKALA"
                                                                                                                                                                                AQDGSGYQFLVEMLTDLNSRNPQVASRL1EPL1RLKRYDDKRQEKMRAALEQLKGLEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="aminopeptidase
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/db_xref="GOA:Q8Z7TO"
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/transl_table=
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Typhi"
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/strain="CT18"
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    entry PF01433 Peptidase_M1,
.10, E-value 1.9e-84"
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94% identity in 869 aa overlap"
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                                                                        RCPAGVQMEQFRPNLVVSGVAAWEEDSWKVLRIGDVIFDVVKPCSRCIFTTVSPEKGQ
KHPSGEPLATLQAFRTAQDNGDVDFGQNLIARNSGVIRVGDEVEILATAPAKAYGATT
LDDSVTPEKHPDGSVTIDWQGQTFCGNNQQVLLEQLENQGIRIPYSCRAGICGCCRIR
                                                                                                                                                                                translation="MATLSRLFIHPVKSMRGIGLTHALADISGLAFDRIFMVTESDGTFITARQPPQMVRFTPSPLHDGLHLTAPDGSSALVRFTDFTPQDAPTEVMGNHFTARVAPTAINQMLSGFFSRDVQLCMVGPQLTRRVKRHNAVPLGFADGYPYLLTNEASLRDLQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (4716. .5825)
/gene="STY1081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mmrikpddnwrwyydbehdrmmldlangmlfrsrfsrkmltpda
FCPTGFCVDDAALYFSFBEKCRDFBLTKEQRABLVLNALVAIRYLKPQMPKSWHFVAH
GEMMTPGTGDAASVWLSDTAEQVNLLVVPBGENAALCLLAQPGVVIAGRTMQLGDAIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVDAEGLINRMGFNNLGVDNLVENVKKAHFDGILGINIGKNKDTPVENGKDDYLICME
KVYAYAGYIAINISSPNTPGLRTLQYGDALDDLLTAIKNKQNDLQVIHHKYVPVAVKI
APDLCEEELIQVADSLLRHNIDGVIATNTTLDRSLVQGMKNCQQTGGLSGRPLQLKST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="dihydroorotate dehydrogenase"
/protein id="CAD08184.1"
/db_xref="G1:16502233"
/db_xref="GACA:08759"
/db_xref="SWISS-PROT:0827S9"
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/translation="MYYPFVRKALFQLDRDEGENEGGYPTFR"/"MYYPFVRKALFQLDRDEGENEGGYPTFR
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/translation="MYYPFVRKALFQLDRDGGYPTFR"/"MYYPFTR
/translation="MYYPFVRKALFQLDRDGGYPTFR"/"MYYPFTR
/translation="MY
complement (4737.
                                      LLEGEVSPLKKSAMGDDGTILSCSCVPKTALRLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="STY1080"

/note="Orthologue of E. coli YCBW ECOLI; Fasta hit to YCBW ECOLI (192 as), 90% identity in 180 as overlap. If the discrepancy in position of translational start site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="STY1079"
/note="PS00912 Dihydroorotate dehydrogenase signature
4174. .4719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Pfam match to entry PF01180 DHOdehase, Dihydroorotate dehydrogenase, score 563.50, E-value
                                                                                                                                                                                                                                                                                       /product="conserved hypothetical protein"
/protein id="CAD08186.1"
/db_xref="G1:16502215"
/db_xref="GOA:082757"
/db_xref="SPTREMBL:082757"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="STY1080"
4174. .4719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="PS00911 Dihydroorotate dehydrogenase signature 3874. .3936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Orthologue of E.
to PYRD_ECOLI (336 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PS00142 Neutral zinc metallopeptidases, zinc-binding region signature"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              producT="conserved hypothetical protein"
protein id="CAD08185.1"
db_xref="GI:16502234"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Orthologue of E. coli P75863; Fasta hit 369 aa), 86% identity in 367 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="SPTREMBL:Q8Z7S8"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lement (4716. .5825)
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95% identity in 336 aa overlap"
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Best Local (
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89146 GTAGGCCAGGGTGCGGATAACAGTACTATTGAACTGACTCAGAATGGTTTCAGAAACAAT 89205
                                                                                                                                                                                                                                                                                                                                                                       GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
                                            GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                                                                                                                                                                                 CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCACTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                                                                                                                                                   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
                                                                                                                                                                                                                            CCGGATTCCACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                                                                                                                                                          GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGG
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HRGHWGFSGWAQHDEAIWQEWKAEAQTRARKCLAEYSSHFYGSDSDARVIERARSNAR
RAGIGELITFEVKDVAQLSNPLPKGPYGTVISNPPYGERLDSDPALIALHSLLGARTMK
NQPGGWNLSLFSASPDLLGSLQLRADKQFKARNGPLDCVQKXYHIAETTADSKEATVA
EDYANRLRKNLKKLEKWARQEGIECYRLYDADLPEYNVAVDRYGDWAVIQEYAPPKTV
DAQKARQRLEDIIAATLSVLGIPPNKLVLKYTBERQKGRNQYQKWSEKGEFLEWSEYNA
RLWWLTDYLDTGLFLDHRIARRMLGEMSKGKDFLNUFSYTGSASVHADLGGARNTTT
VDMSRTYLEWAERNILALNGLSGRAHRLIQADCLGWLRRANBQFDLIFIDPPTENSKR
MEESFDVQRDHVALMKDLKRLLRKGGTIMFSNNKRGFRMDLEGLAELGLTAQEITQKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E-value 3.7e-231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Pfam match to entry PF00111 fer2, 2Fe-2S
iron-sulfur cluster binding domains, score 55.90,
8.5e-13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fasta hit to YJJK_ECOLI (554 aa), 34% identity in 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         526 aa overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8045. .9952
/gene="STY1083"
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YQSLMWSRLASRIILPMGECKVYSDLDLYFGVQAINWTEIFNPGATFAVHFSGLNDTI
RNSQYGANKVKDAIVDAFTRKNLPRPNVDRESPDLRINVWLNKETASIALDLSGDGLH
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/db_xref="GI:16502236"
/db_xref="GOA:Q827S6"
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/transl_table=
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product="conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Fasta hit to YBIT_ECOLI (530 aa), 32% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9952
gene="STY1083"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="Pfam match to entry PF01170 UPF0020,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="SPTREMBL:Q827S6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87.4%;
92.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 398.4; DB 1;
Pred. No. 5.2e-101;
D; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein"
37.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family UPF0020, score 781.30,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 254050;
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Salmonella enterica subsp. er
16 of the complete genome.
AE016840 AE014613
AE016840.1 GI:29137797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmonella enterica subsp. enterica serovar Typhi Ty2 Salmonella enterica subsp. enterica serovar Typhi Ty2 Bacteria; Proteobacteria; Gammaproteobacteria; Enterol Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deng,W., Liou,S.-R., Plunkett,G. III, Mayhew,G.F., Rose,D.J., Burland,V., Kodoyianni,V., Schwartz,D.C. and Blattner,F.R.
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                                                                                                                 / LYANS at ion="Modeks.LAHTRWNCKYHIVFAPKYRRQAFYGEKRRAVGSILRKLCEWKNVRILEAECCAHIHMLLEIPPKWSVSSFMGYLKGKSSLMLYEQPGDLKFKYRNREWCRGYYVDTVGKWTAKIQDYIKHQLEEDKMGEQLSIPYPGSPFTGKK"

Complement (844 . . . 1797)
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                                                                                                                                                                                            /protein_id="AAO69359.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'mol_type="genomic DNA"
'strain="Ty2"
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Yyphi Ty2"
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                                                                                    _tag="t1736"
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VAQGNLSVTVNRQLNVNQPNTPPGGGGTVVTPQTQIDLRQSGGSLQSVRSSANLNSVV
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Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (4488.
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DVEKEKAAAAAIDKTNRGLKUSLNNVLTVRABIGTQLSELSTLDSLGSDRALGQKLQMS
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Query Match
Best Local Similarity
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Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VETSNVNVAEELVMMIQVQRAYEINSKAVSTTDQMLQKLTQL"
complement(7146...7901)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / translation="MISSLMIAKTGLDAQQTMMDVIANNLANUSTNGFRRQRAUFEDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tränslation="MOKYALHAYPVMALMVATLTGCAWIPAKPLVQGATTAQPIPGPV
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SFGFDTVPRYLQGLFGASKADMEASGGNSFNGKGGANASNTFSGTLTVYTQVLANGU
LHVVGEKQIAINQGTEFIRFSGVVNPRTISGSNSVPSTQVADARIEYVGNGYINEAQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="t1740" complement (5597. .6295)
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complement(5597. .6295)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus_tag="t1741"
/note="distal rod protein; corresponds to STY1218
Accession AL513382: Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /locus_tag="t1741"
complement(6350. .7132)
                                                                                                                                                                                                                                                        /gene="flgE"
/locus_tag="t1743"
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/protein id="AAO69366.1"
/db_xref="GI:29137805"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGWLQRFFLNLSPM"
                                                                                                                                       codon_start=
table
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/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="flgF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 locus_tag="t1742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="flagellar basal-body rod protein
/protein_id="AAO69365.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="flgG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="flagellar L-ring protein
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 87.4%;
92.1%;
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   Score 398.4; DB 1; Pred. No. 5.3e-101;
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                 Length 301983;
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Sukupolvi,S., Lorenz,R.G., Gordon,J.I.,
Normark,S.J. and Rhen,M.
Expression of thin aggregative fimbriae
Salmonella typhimurium SR-11 with mouse
                                                                                                                                                                                                                                                                                 Submitted (14-JUL-1997) Sukupolvi S.S., Medical Biochemistry, University of Turku, Kiinanmyllynkatu, 20520, FINLAND
                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to
Sukupolvi, S.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    agfA gene; agfB gene.
Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella typhimurium agfB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
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/transl_table=11
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                                                                                                                                gene="agfB"
                                                                                                                                                                                                   organism="Salmonella typhimurium"
|mol_type="genomic DNA"
                                                                                                                                                                          db_xref="taxon:602"
                                                                                                                                                                                                                                                 . .1048
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         1 (bases 1 to 361)
Doran, J.L., Kay, W.W., Collinson, S.Ka
Methods and compositions comprising
Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             416;
Patent: US 5635617-A 56 03-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                               Sequence 56 from patent I44908
                                                                                                           Unknown.
                                                                               Unclassified
                                                                                                                                             I44908.1
                                                                                                                                                                                                                                                                 GGTTTTGGCAACAACGCACCGGCTAACCAGTATAA 1047
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LSIYQYGSANAALALQSDARKSETTITQSGYGNGADVGQGGNNAFANQYN"
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REFERENCE AUTHORS

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Citrobacter sp. Fec2
Bacteria; Proteobacteria; Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (11-NOV-2002) Romling U., Microbiology and Tumorbiology Center, Karolinska Institute, Box 280, S-17177 Stockholm, SWEDEN
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                                                                                                                                                                          /db_xref="toxon:213763"
/country="Germany"
complement (or o
                                                                                  complement (212. .862)
                                                                                                                                                                 complement (212.
        /gene="csgD"
/function="necessary
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Citrobacter sp.
/mol type="genomic DNA"
                                                                                                                                gene="csgD"
                                                                                                                                                                                                                                                                                 /isolation_source="faeces"
/specific_host="Homo sapie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                    'isolate="Fec2"
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/mol_type="unassigned DNA"
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Pred. No. 1.9e-68;
0; Mismatches 33;
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        transcription
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                                                                      GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                               AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                                                GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
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                                                                                                                                  CATAACGCCGCACTGGTGAACCAGACTGCGTCCGATTCCAGCGTTCTGGTGCATCAGGTT
                                                                                                                                                                                                                         GCCACCATCGATCAGTGGAACGGCAAAAATTCGGACATTACTGTGAGCCAGTATGGTGGA
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2119. .2571
/gene="csgA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKLLQVAAFAAIVVSGSALAGSVPQWGGGGGGGGGGSSSGPESTL
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DQWNGKNSDITVSQYGGHNAALVNQTASDSSVLVHQVGFGNNATANQY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="nucleation component of curlin monomers"
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/db_xref="GI:31790493"
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SISQSNYGNTAMIIQKGSGNKANITQYGTQKTAVVVQRQSQMAIRVIQR"
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/brotein id="CAD56670.1"
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1623. .2078
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/db_xref="GI:31790494"
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/transl_table=11
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/transI_table=
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/gene="csgB"
/function="nucleator"
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Pred. No. 9e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        csgA gene; csgB gene; csgD gene; curlin-csgA protein; component of curlin monomers; regulatory protein. Citrobacter freundii
Citrobacter freundii
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Production of Cellulose and Curli Fimbriae by Members of the Fami
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract
Infect. Immun. 72 (7), 4151-4158 (2003)
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QWNAKNADISVTQFGGRNGALVNQTASDSNVLIQQVGFGNNATANQH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="csgB"
1624. .2082
/gene="csgB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="Menevasihghtllltykpsloatlohkkoslaltgkhnio
RSLDDISSCIVLLDMMEADKKLIHYMODNLSRKNNNIKTLLLHTPDDYPYRDIENWP
HINGVFYATEDEORVVSGLOGVLRGECYFSOKLASVLIHYGGNYRYNSTESALLTHRE
KEILNKLRIGASNIEIARSLFISENTVKTHLYNLFKKIAVKNRTQAVSWANDNLRR"
                                                                                                                                                                                                                                                          'gene="csgA"
                                                                                                                                                                                                                                                                                                             ASIKQGSYGNTAVIIQKGSGNKANITQYGTQKTAVVVQRQSQMAIRVTQR'
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                                                                                                                                                                                                                                                                                                                                                                          /codon start=1
/transl_table=11
/product="nucleation component of curlin
/protein id="CAD56674.1"
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/transI_table=11
/product="putative regulatory protein"
/protein_id="CAD56673.1"
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complement(211.
                                                                                                                                                                                               gene="csgA"
function="curli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /isolation_source="faeces"
/specific_host="Homo_sapiens"
/db_xref="taxon:546"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        624
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function="necessary for transcription of the csgBA
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isolate="Fec4"
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                                                                                                                                                                                                                                                                                                                                                       translation="MKNKLLFMMFTMLGVPGIAAATTSYDLANSEYNFAVNELSKSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function="nucleator"
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                                                                                                                                                                       Submitted (11-AUG-1995) M. Hammar, Karolinska Institutet, Microbiology and Tumorbiology Center, Box 280, S-171 77 Stockholm,
                                                                                                                                                                                                                     Direct Submission
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                                                                                                                                                                                                                                                                                                              Mol.
                                                                                                                                                                                                                                                                                                                           Hammar,M., Arnqvist,A., Bian,Z., Olsen,A. and Normark,S. Expression of two cg operons is required for production of fibronectin- and congo red-binding curli polymers in Escherical vers
                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                            8817489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                csgA gene; csgB gene; csgD gene; csgE gene; csgF orfC gene.
                                                                                                                                                                                                                                                                                           96414468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X90754.1 GI:1147558
                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X90754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ĠĠĊŤŤŤĠĠŦĀĀĊĀĀĊĠĊŦĀĊĀĠĊŤĀĀĊĊĀĀĊĀĊŤĀĀ 2572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTTTTGGCAACAACGCCACGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCAACGGTGCGTTGGTTAATCAGACAGCCTCTGACTCCAATGTGCTGATTCAGCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCACCATCGACCAGTGGAAACGCTAAAAACTCCGGATATTACTGTCGGCCAATACGGCGGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCACTATÓGATCAGTGGAÁTGCAÁAÁÁÁTGCTGÁTÁTTÁGCGTGACCCÁAGTTCGGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTGGCCÁGGTGCTGÁTGACAGTÁCCÁTTAGCCTGÁAACÁGACCGGCTTCCCAGÁACAGT
                                                                                                                                                                                                                                                       (bases 1 to 4680)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCAGACTCTTCACTGAGTATCTACCAATATGGGTCAAACAACTCTGCAAATGCTCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCACTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTGATGCGCGTAAATCAGATGTCACCÁTCACACAACACGGGCGTGGCAÁCGGAGCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTGTTGTTCCGCAATGGGGCGGC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGAĀĀCTTTTĀĀĀĀGTGGCĀGCĀTTCGCĀGCĀATCGTĀGTTTCTGGCĀGTGCTCTGGCT 2182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
                                                                                                                                                                                                                                                                                                  Microbiol. 18 (4), 661-670 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    li csgG, csgF, csgE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                 organism="Escherichia coli"
                                                                                   /mol_type="genomic DNA"
/strain="K12"
                                                                                                                                                   Location/Qualifiers
                                                     map="23.15 minutes"
                                                                   db_xref="taxon:562"
                                                                                                                 organism="Escherichia coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 245.2; DB 1;
Pred. No. 5.8e-58;
0; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4680 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cagD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  csgB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -AATCATCATGGTGGCAGTAATTATGGC 2236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
JB, csgA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear BCT 07-JUL-2002 and orfC genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene;
                                                                                                                                                                                                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cagG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2476
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misc_feature
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KEILNKLRIGASNNEIARSLFISENTVKTHLYNLFKKIAVKNRTQAVSWANDNLRR"
                                                                                                                                                                                                                                complement (1828.
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IQTEEALNRRQINQALLSTGDLAHDEF"
                                                                                                                                                                                                                                                            complement (1828. .2478)
                                                                                                                                                                                              'note="necessary
                                                                                                                                                                                                                  /gene="csgD"
                                                                                                                                                                                                                                                /gene="csgD"
                                                                                                                                                                                                                                                                                                                                                                                  production"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (1434. .1823)
/gene="csgE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(1434. .1823)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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/product="assembly /
production"
                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
/product="assembly
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VGYTSNEPVMLCLMSAIETGVIFLINDGIDRGLMDLQNKAERQNDILVKYRHMSVPPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="csgF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product≃"assembly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="csgF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /insertion seq="IS2 (partial)"
complement(133..966)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:562"
<1. .>4680
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3141. .4680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Escherichia
mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain="W3110"
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_xref="GI:1147561"
                                                                                                                                                                                                                                                                                                                                                                                                                                  _start=1
                                                                                                                                                                                     for transcription of the csgBA operon"
                                                                                                                                                                                                                              .2478)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .1409)
                                                                                                                                                                                                                                                                                                                                                                                         /transport component in curli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           component in curli
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Matches 316;
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Best Local Similarity
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GTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTCGGTAACAGC 4028
                                     GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                            AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
                                                                                                                                                                                                      ccegaciaicaicaecreciiacccereriacccargaaareccarecacrecaa 180
                                                                                                                                                                                                                                                     GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC
                                                                                                                                                                                                                                                                                 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
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                                                                                                                                                                                                                                                                                                                                                              ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                                                                                                                                                 CCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transI_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="orfC"
4243. .4575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="transcriptional start site for csgBA operon" 3233. .3688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="csgA"
4243. .4575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SISQGAYGNTAMIIQKGSGNKANITQYGTQKTAIVVQRQSQMAIRVTQR"
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/transI_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="major subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MKNKLLFMMLTILGAPGIAAAAGYDLANSEYNFAVNELSKSSFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="orfC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="GOA: P39828"
                                                                                                                                                                                                                                                                                                                                                                                                                                            50.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 232; DB 1;
Pred. No. 3.1e-54;
0; Mismatches 140
                                                                                                                                                                                                                                                                                                                                                                                                                          140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4680;
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note="transcriptional start site for csgDEFG operon"
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AUTHORS
TITLE
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AUTHORS
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AUTHORS
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AE000205
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Direct Submission

AL Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli K12 strain MG1655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 3032 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG Site Nos., unique ID nos. for the genes in the E. coli Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli Genome Project's World Wide Web Site (http://www.genetics.wisc.edu). *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications
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Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
608-263-7459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecol@genetics.wisc.edu Phone: 608-262-2534 Fax:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The complete genome sequence of Escherichia coli K-12 Science 277 (5331), 1453-1474 (1997) 97426617
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Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F. Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
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Plunkett, G. III.
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Direct Submission
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                            note="factor Sigma70;
                                                                                                                                                            note="No predicted"
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                                                                                                                                                            promoter"
predicted
                            predicted +1
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                  start at 1096049"
                                                                                                                                                                                                                                                                                                                                                                            promoter: -104"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at 1094983"
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Query Match
Best Local Similarity
Matches 316; Conserv
                                                                                                                                                    promoter
                                                                                                       promoter
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          Conservative
                                                                                                                                                                                                                                                                                               /codon_start=1
/transI_table=11
/product="putative debydrogenase"
/protein_id="AAC74117.1"
/protein_id="AAC74117.1"
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LEDTGWGEQWGEYAVSQVLHWFRRFDDFTGTONSSHWQFLEEYHREDFTIGIGAGVU
                                                                                                                                                                                                                                  GSKVAQSLQTWRFPLRCWSRTRKSWPGVQSFÄGRBELSAFLSQCRVLINLLPNTPETV
GIINQQLLEKLPDGAYLLNLARGVHVVEDDLLAALDSGKVKGAMLDVFNREPLPDESP
LWQHPRVTITPHVAAITRPAEAVEYISRTIAQLEKGERVCGQVDRARGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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SNWLSPVVEPRSGLLIPPVCAIYEKKARTFYRALL"
complement(2111. .2198)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SW: P45637"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="ycdW"
/function="putative enzyme; Not classified"
/note="0325; This 325 aa ORF is 32 pct identical (2 gaps)
to 177 residues of an approx. 312 aa protein YPRA_CORGL
                                                                                                                                                                      'note="factor Sigma70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: b1032"
complement(2111. .2198)
                                                                                                                      note="factor Sigma70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="factor Sigma70; predicted +1 start at 1097049"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="factor Sigma70; predicted +1 start at 1096980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /function="putative structure; Not classified" (note="0137; This 137 aa ORF is 27 pct identical (1 gap) to47 residues of an approx. 80 aa protein RS37_YEAST SW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="orf, hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="synonym: b1033"
393. .3370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="anticodon: GGA;
/function="RNA; tRNA"
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/function="orf; Unknown"
/note="083; This 83 aa ORF i
to81 residues of an approx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="serX"
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transl_table=
                           50.9%;
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     0;
Score 232; DB 1;
Pred. No. 3.3e-54;
0; Mismatches 140
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                                                                                                                                                                      predicted +1
                                                                                                                      predicted
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     140;
                                          Length 10346;
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Gaps
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                                                                                                                                                Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, S., Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yamamoto, Y., and Yano, M.
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Direct Submission
Submitted (29-JUL-1996) Hirotada Mori, NARA Institute and Technology, Res. & Edu. Center for Genetic Info.;
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Complete and shotgun sequencing; csgG; csgF; csgE; csgA; ycdE; cls; nov; mdoG.
Escherichia coli K12
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Bacteria; Proteobacteria;
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D90741 AB001340
                                                                    Mori, H.
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                                                                                                         Unpublished
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The Japan F
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Collaboration Information:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Headed by:
Name: Takashi Horiuchi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Aiba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, S., Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kimura, S., Kitagawa, M., Kitakawa, M., Makino, K., Kimura, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampei, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yamamoto, Y. and Yano, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Address: NARA Institute of Science Ikoma, 630-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name: Hirotada Mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E-mail: kishori@nibb.ac.jp
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                                                                                                                              /codon_start=
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                                                                                                                                                                                                                                                                                                                                                   intergenic region."
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transl_table=11
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complement (5812.
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CsgF precursor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="csgF"
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imilar to SwissProt Accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MNEFSILCRVLGSLYYROPODPLLVPLFTLIREGKLAANWPLEQDELLTRLQKGCDMTQVSADYNALFIGDECAVPPYRSAWVEGATEAEVRAFLSERGMPLADTPADHIGTLLLAASMILEDOSTEDESSALETLFSEYLLPWCGAFLGKVEAHATTPFW
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Hansa Medical Research Aktiebolag
Location/Qualifiers
1. .456
                                                                                                               Escherichia coli
Escherichia coli
Escheria, Proteobacteria, Gammaproteobacteria,
                             Patent: WO 03064446-A 15 07-AUG-2003;
Patent: WO 03064446-A figure (SE)
                                                                           Bjoerck, L., Olsen, A.,
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7217. .7672
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Rslddissgsiilldmmeadkklihymqdtlsrknnnikilllntpedypyrdienwp
Hingvfysmedqervvnglqqvlrgecyftqklasylithsgnyrynstesallthre
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transl_table=
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db_xref="GI:4062613"
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Pred. No. 3.4e-54;
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SOURCE
ORGANISM
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ECOCSGAA
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On Jun 11, 1993
Original source
K-12) (library:
                                                                       1 (bases 1 to 648)
Olsen, A., Arnqvist, A., Hammar, M., Sukupolvi, S. and Normark, S.
The RpoS sigma factor relieves H-NS-mediated transcriptional repression of csgA, the subunit gene of fibronectin-binding c in Escherichia coli
no., Microbiol. 7 (4), 523-536 (1993)
                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                               cegA gene; curli organelle;
Escherichia coli
                                                                                                                                                                                                  Escherichia coli
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/codom_start=1
/trans[_table=1]
/protein_id="CAE83541.1"
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LDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQVGFGNNATAHQY"
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/db_xref="taxon:562"
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           this sequence version replaced gi:145630.
text: Escherichia coli (sub_strain W3110,
 Kohara) DNA
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                                          GGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT
                                                                                   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                    GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
                                                                                                                                                                                                                    GTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTCGGTAACAGC
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  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
                                                                                                                              GCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGTGGT
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83. .538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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db_xref="taxon:562"
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Aac64617 Salmonell
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î f		andard		7.6	7.6	7.8	7.8	7.8	•		٠		÷	8.1	÷	o		თ	8.6	8.9				9.5	10.5
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irst entry)		BP.	ALIGNMENTS	AAC64620	ADA71938	AAS89144	AAS88526	ABS67377	ADA71938	ACA25910	ACA45315	ACA42270	- 1	9	AAA81482	AAS76745	AAF21612	AAA81489 S	AAA81465	AAC64605	ACD68809	AAC64606	ACD68808	AAC64616	AAC64621
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                                                                        WPI; 2000-672631/65.
                                                                                 White AP,
                                                                                                   05-APR-1999;
                                                                                                             05-APR-2000; 2000WO-CA000356
                                                                                                                               WO200060102-A2
                                                                                                                                        Synthetic.
                                                                                                                                            Escherichia coli.
                                                                                                                                                 Salmonella enteritidis.
                                                                                                                      12-OCT-2000.
                                                                                          (UYVI-) UNIV VICTORIA.
                                                                                 Doran JL,
                                                                                                   99US-0127888P
                                                                                 Collison SK,
                                                                                 Kay ww;
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Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen; ds.

The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 136; 139pp; English.

8888888888888888888

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CC back into the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or polymer into the animal in conjunction with a carrier or diluent. (1) is CC polymer into the expression of recombinant AgfA protein for the expression of recombinant AgfA protein for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for CC system the heterologous antigens are presented in high numbers (up to conjunctive, the heterologous antigens are presented in high numbers (up to vaccine, the carrier fimbrial subunit protein sere usually strong CC immunogenicity and adhesion properties relevant for an efficient live communogens, which may be important for directing an immune response cc inexpensive to purify in large amount. The present sequence is given in XX the exemplification of the present invention
                                                             25-MAR-2003
26-JUN-1995
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Best Local :
     Salmonella; AgfA;
                                   AgfA sequence.
                                                                                                        AAQ87467;
                                                                                                                           AAQ87467 standard; DNA; 456 BP
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                                                                                                                                                                                                      GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
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100.0%; Pred. No. 1.3e-135;
tive 0; Mismatches 0;
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    genetic
immunization;
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RESULT 3 AAT74142

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Matches 425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 456 BP; 117 A; 112 C; 122 G; 105 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
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GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                         GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                   GCCACCATCGACCAGTGGAAAGCTTAAAAACTCTCGGATATTACTGTCGGCCAATACGGCGGT
                                                            AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
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/*tag= a
/note= "AgfA"
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Pred. No. 9.9e-120;
0; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 456 BP; 117 A; 112 C; 122 G; 105 T; 0 U; 0 Other;
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29-SEP-1997
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GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
                                                                         AGCGATGCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCCGAT
                                                                                                                                              CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTGCAA
                                                                                                                                                                                    CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCACTGCAA
                                                                                                                                                                                                                                           GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
                                                                                                                                                                                                                                                                            GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
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                                                                                                                                                                                                                                                                                                                                            ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                                AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
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/label= agfA gene_fragment
/transl_except= (pos:367. .369,aa:Pro)
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0; Mismatches
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       CC The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombinant on a recombination of a recombinant gene contained the chromosome of the homologous species, replacing the native CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising asperating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the CC useful for the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant. TafA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation on System the heterologous antigens are presented in high numbers (up to companioty and adhesion properties relevant for an efficient live
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                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA seq which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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P-PSDB; AAB36341.
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esponse; immunogen; ds.
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Best Local Sim
Matches 425;
                    White AP,
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Escherichia coli.
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Pred. No. 9.9e-
0; Mismatches
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2000-672631/65. DB; AAB36350.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 137; 139pp; English.

CC Regment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative finbriae (SER17/TAF) nucleation depended CC assembly system of strains of Salmonella, Bacherichia coli and CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) cc homologous species; (3) directing recombinant gene into the chromosome of the back into the chromosome of the homologous species, replacing the native comprising separating an amino acid polymer comprising a recombinant gene copy of that gene; and (4) eliciting an immune response in an animal, cc protein containing a replacement segment or segments of foreign amino acid polymer comprising a recombinant epine comprising separating an amino acid polymer comprising a recombinant coli acid sequence or sequences grown on a Salmonella, E. coli or polymer into the animal in conjunction with a carrier or diluent. (1) is certain for the expression of recombinant AgfA protein which is useful for South and adhesion properties are presented in high numbers (up to comprisine the heterologous antigens are presented in high numbers (up to comprise the laterologous antigens are presented in high numbers (up to comprise the heterologous antigens are presented in high numbers (up to compresent the laterologous antigens are presented in high numbers (up to compresent the inserted epitope, and hybrid fimbrin are usually strong compressive to purify in large amount. The present sequence is given in the exemplification of the present invention

Sequence 456 BP; 116 A; 111 C; 120 G; 109 T; 0 U; 0 Other;

밁 Ş Ъ Ś 밁 Ş Б Ş 밁 δ Query Match Best Local S Matches 398 421 361 361 301 301 241 181 181 121 121 61 398; 61 μ, ь GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA AATAACCCCGCGCTCGTTAATCAGACCGCATCTGATTCCAGCCTAATGGTGCCTCAGGTT GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT AATAACGCGGGCTGGTTAATCAGACGGCATCTGATTCCAGGCGTAATGGTGCGTCAGGTT GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT AGCGÁTGCCCGTAÁÁTATGÁTCAGCTGGTTÁCCCGTGTTGTTACCCATGÁAATGGCACÁT AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGAT CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGGCTAACGCTGCGCTTGCTCTGCAA 180 CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGCAA 180 Similarity Gécercerrecakáreseseseseseseses a rearrando de construcción de GGCGTCGTTCCACAATGGGGCGGCGGCGGCGATAATCATAACGGCGGCGGCAATAGTTCCGGC ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTTCTGGCT ATGAAACTTTTAAAAGTĞGCAĞCATTCĞCAĞCAATCĞTAĞTTTCTĞĞÇAĞTĞCTĞTĞĞÇT Conservative 79.6%; Score 363.2; DB 3; Pred. No. 6.9e-106; 0; Mismatches 58; Indels <u>.</u> 420 360 300 240 300 240 120 120 60

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421

GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456

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assembly system of strains of Salmonella, Escherichia coli and
Enterobacteriaceae for the production of fimbriae comprising recombinant
Agfa, CsgA and Agfa-homologue fimbrin subunits, respectively; (2)
Cdirecting recombination of a recombinant gene into the chromosome of the
CC homologous species; (3) directing recombinant gene into the chromosome of the
CC back into the chromosome of the homologous species, replacing the native
CC copy of that gene; and (4) eliciting an immune response in an animal,
CC comprising separating an amino acid polymer comprising a recombinant Agfa
CC comprising separating an amino acid polymer comprising a recombinant Agfa
CC comprising separating an emino acid polymer comprising a recombinant Agfa
CC protein containing a replacement segment or segments of foreign amino
CC acid sequence or sequences grown on a Salmonella, E. coli or
CC Enterobacteriaceae host cell, from the host cell and introducing the
CC useful for the expression of recombinant Agfa protein which is useful for
CC eliciting an immune response in an animal. In a fimbrial presentation
CC system the heterologous antigens are presented in high numbers (up to
CS 100,000 copies/cell), the hybrid fimbrial subunit protein possesses both the
CC vaccine, the carrier fimbrial subunit protein are usually strong
Query Match
Best Local Similarity
Matches 393; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant agfA gene (I) where a geneent of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                         Sequence 456
                                                                                                                         immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-672631/65
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                                                                                                              exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doran JL,
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 Conservative
                                                                       BP; 119 A; 110 C; 120 G; 107 T; 0 U; 0 Other;
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                                                                                                          of the present
               77.9%;
86.2%;
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Score 355.2; Pred. No. 2.5e
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                                                                                                              invention
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; DB 3;
.5e-103;
lea 63;
 Indels
                                  Length 456;
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so described
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                                               Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                WPI; 2000-672631/65.
P-PSDB; AAB36346.
                      Disclosure; Page 135; 139pp; English.
                                                                                                                                                                                         05-APR-1999;
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                                                                                                                                                                                                                                                                     WO200060102-A2
                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                            Escherichia
                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                              vaccine; immune response; immunogen; ds.
                                                                                                                                                                                                                                                                                                                                                           Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                      Agfa::PT3#1 DNA sequence SEQ ID NO:11.
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                                                                                                                                         Doran
                                                                                                                                                                                                                                                                                                            coli.
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                                                                                                                                       JĽ,
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The present invention describes a recombinant agfA gene (I) where a

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RESULT 8
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ID AAC6
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AC AAC6
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XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC directing recombination of a recombinant gene into the chromosome of the copy of that gene, and (4) eliciting recombination of a recombinant gene copy of that gene, and (4) eliciting an immune response in an animal, where the copy of that gene, and (4) eliciting an immune response in an animal, or comprising separating an amino acid polymer comprising a recombinant gene comprising separating an amino acid polymer comprising a recombinant AgfA carrier ontaining a replacement segment or segments of foreign amino comparations are replacement segment or segments of foreign amino computation of the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for compungation antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to compungation) and adhesion properties relevant for an efficient live considered phicope, and hybrid fimbrial presentation compungation, which may be important for directing an immune response companies the inserted epitope, and hybrid fimbriae are usually strong consists the inserted epitope, and hybrid fimbriae are easy and the exemplification of the present invention
                                                             AAC64629 standard; DNA; 456
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                                           AAC64629
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(1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant
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                                                                                                                                                                                  AATAACGCCGCGCTGGTTÄÄTTÄTGATCAGCTGGTTÄČCCGTGTTGTTACCCATGÄAATG 420
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86.2%;
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                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred. No. 2.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5e-103;
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26-FEB-2001

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                 CC AgfA, CsgA and AgfA-homologue fimbrin subunite, respectively; (2) directing recombination of a recombinant gene into the chromosome of the CC homologous species; (3) directing recombinant gene into the chromosome of the CC back into the chromosome of the homologue species, replacing the native comprising separating an amino acid polymer comprising a recombinant AgfA (2) eliciting an immune response in an animal, CC protein containing a replacement segment or segments of foreign amino acid polymer comprising a recombinant AgfA (2) eliciting an immune response in an animal, CC acid sequence or sequences grown on a Salmonella, E. coli or polymer into the animal in conjunction with a carrier or diluent. (1) is CC eliciting an immune response in an animal. In a fimbrial presentation or Sol,000 copies/cell), the hybrid fimbrin protein which is useful for Sol,000 copies/cell), the hybrid fimbrin protein possesses both the carrier fimbrial subunit proteins are usually strong companies the inserted epitope, and hybrid fimbriae are usually strong consensive to purify in large amount. The present sequence is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                             Matches 393;
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are:

(I) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant and the production of strains of Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 138; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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P-PSDB; AAB36353.
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121 CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCACTGCAA 180
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                                                                              61 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC
                                                                                                                                                              61
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                                                                                                                                                                            GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
                                                                                                                                                                                                                                                                                                     Conservative
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86.2%;
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Pred. No. 2.
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1.5e-103;
1es 63;
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           The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene homologous species; (3) directing recombination of a recombination of a recombination the chromosome of the homologous species; (3) directing species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal,
                                                                                                                                                                                                                            Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                                                                                                                                                                                                         White AP,
                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine; immune response; immunogen;
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DB; AAB36347.
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 separating an
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 polymer comprising
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recombinant AgfA
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RESULT 10
AAC64624
ID AAC644
XX AAC64
AC AAC64
XX 26-FE
CT 26-FE
CX ASAlmo
KW Vaccii
XX Vaccii
XX Salmo
OS Salmo
OS Salmo
OS Synth
XX WO200

AAC64624 standard; DNA; 456

26-FEB-2001 AgfA::PT3#3 Salmonella; vaccine; im

immune

response;

immunogen;

agfA; chromosomal gene replacement;

fimbrin;

DNA sequence SEQ ID NO:15.

(first entry)

Synthetic. WO200060102-A2

Salmonella enteritidis. Escherichia coli.

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                                                                                                                                                                             GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
                                                                                                                                                                                                                                                                                                           AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
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                                 GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                     CTGGTTACCCGTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
                                                                                                        AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
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                                                                                                                                            GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
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86.2%;
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Pred. No. 2.5e-103;
D; Mismatches 63;
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12-OCT-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA-homologue fimbriae comprising recombinant CC directing recombination of a recombinant gene into the chromosome of the back into the chromosome of the homologus species; (3) directing recombinant gene into the chromosome of the homologus species, respectively; (2) back into the chromosome of the homologus species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, cc protein containing a replacement segment or segments of foreign amino acid polymer comprising a recombinant AgfA acid sequence grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the useful for the expression of recombinant AgfA protein which is useful for grown in an animal. In a fimbrial presented in concisting an immune response in an animal. In a fimbrial presentation cc system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live communogenicity and adhesion properties relevant for an efficient live immunogenicity and adhesion properties relevant for an efficient live capainst the inserted epitope, and hybrid fimbriae are usually strong consensive to purify in large amount. The present sequence is given in the present invention consensive to purify in large amount. The present sequence is given in the present invention in the present invention consensive to purify in large amount. The present sequence is given in the present invention in the present sequence is given in the present invention.
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Best Local S
Matches 392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a recombinant segment of the gene has been replaced by a segment of the gene has been replaced by a segment of the gene has been replaced by a segment of the general segment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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CC Regment of the gene has been replaced by a segment of a foreign DNA CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation described are: (2) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) CC homologous species; (3) directing recombinant gene into the chromosome of the homologous species, (3) directing a recombinant gene into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, CC protein containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (1) is CC eliciting an immune response in an animal. In a fimbrial presentation celicity and adhesion properties replacement suseful for celiciting an immune response in an animal. In a fimbrial presentation conjunction, the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation conjunction, the expression of properties relevant for an efficient live immunogenicity and adhesion properties relevant for an efficient live immunogenicity and be immortant for directing an enuminal strong cimmunogens, which may be immortant for directing an enuminal strong
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Escherichia coli.
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                                                                                                               99US-0127888P
                                                                                                                                                                                                                                                                                                                                 response; immunogen;
                                                                                                                                                                                                                                                                                                                                                  chromosomal gene replacement; fimbrin; epitope;
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85.7%;
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                                      SK,
                                      Kay ww;
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P-PSDB; AAB36351

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 137; 139pp; English.

The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF1/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene CC composes species; (3) directing recombination of a recombinant gene CC composes pecies; (3) directing an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA composition or the containing a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC Enterobacteriaceae host cell, from the host cell and introducing the useful for the expression of recombinant AgfA protein which is useful for polymer into the animal in conjunction with a carrier or diluent. (I) is CC useful for the expression of recombinant AgfA protein which is useful for system the heterologous antigens are presented in high numbers (up to CC 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live capainst the inserted epitope, and hybrid fimbriae are usually strong communogens, which may be important for directing an immune response constitute of the present of the present sequence is given in the exemplification of the present invention

Sequence 456 BP; 112 A; 113 C; 125 G; 106 T; 0 U; 0 Other;

Best Local Sim Matches 391; Query Match Best Local 361 361 301 301 241 241 181 181 121 121 61 61 1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT Similarity GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACCGCCGGCGGCGATAGTTCCCGGC GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA AATAACGCCGCGTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT GCCACCATCGACCAGTGGAACGCTAAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT GTAGGCCAGGGTGCGGATAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT AGCGATGCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCGAT 240 CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGCAA 180 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC **AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT** ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA Conservative 77.2%; 85.7%; 0, Score 352; DB 3; Pred. No. 2.7e-102; Mismatches 456 Length 456 Indels <u>,</u> Gaps 360 420 420 360 300 240 180 120 60 120 60

GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA

240 240 180

120 120 60

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RRESULT 13
ID AAC64631
ID AAC64631
XX AAC64631
AX AAC64631
AX AAC64
AX AAC64
AX AAC64
AX Salmo
KW Salmo
KW Vacci
XX Salmo
OS Esche
OS Synth
XX WO200
PD 12-OC
PF 05-AF
XX WO200
PF 05-AF
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                                                                               Matches 389;
                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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P-PSDB; AAB36355.
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Escherichia coli.
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1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
                                                                                                                                                                                        456
                                                                         Conservative
                                                                                                                                                                                BP; 113
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                                                                                                76.5%;
                                                                                                                                                              A; 110 C; 124 G; 109 T; 0 U; 0 Other;
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                                                                                          Score 348.8;
Pred. No. 2.8
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                                                                    Mismatches
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                                                 26-APR-1994;
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25-MAR-2003
26-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella; AgfA; vaccine; genetic immunization;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AgfA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ73066 standard; DNA; 361 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ73066;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ĢССАССАТСФАССАФТФФААСФСТАЛАЛАЛСТССФАТАТТАСТФТСФФССАЛТАСФФСФФТ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ccesactcaacettsagcatttatcagtacsgttccsctaacectscscttsctciscaa
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93US-00054452
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/note= "TAF5 primer (pair with
52. .69
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                                                                                                                                                                                                                                                                                                                                              /note= "TAF3
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/note= "AgfA"
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DT 30-SE
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The DNA encodes the Salmonella enteritis27655-3b TnphoA mutant strain agfA gene cloned into pUC19. The DNA and isolated proteins are used in genetic immunization and vaccine compositions, respectively, to elicit immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WYVI-)
                   primer_bind
                                                                                  Salmonella enteritidis
                                                                                                     Enteropathogenic bacteria;
                                                                                                                           Salmonella
                                                                                                                                               25-MAR-2003
30-SEP-1997
                                                                                                                                                                              AAT74141;
                                                                                                                                                                                                   AAT74141 standard; DNA; 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 361 BP; 94 A; 93 C; 94 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eliciting an immune response to Salmonella - using attenuated Salmonella strains, vector constructs, or compsns. contg. fimbrial type proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              124 GACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGCAAAGC
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                                                                                                                                                                                                                                                                           AACGCCGCGCTGGTTAATCAGACCGCATCTGATTC
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                                                                                                                         enteritidis 27655-3b TnphoA mutant agfA gene fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                              (revised)
(first entry)
         /label= agfA_gene_fragment
16. 60
/*tag= b
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                                                              Location/Qualifiers
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Primer_TAF5
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                                                                                                      enterobacteria;
                                                                                                                                                                                                   ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 282.2; DB 2
Pred. No. 5.6e-80;
0; Mismatches 33
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Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from Salmonella enteritidis 27655-3b TnphoA mutant strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 9% of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Col 107-110; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                  GACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCACTGCAAAGC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCGGCAATAGTTCCGGCCCG
                                                                                                                                                                                              GCCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 BP;
                                   AACGCCGCGCTGGTTAATCAGACCGCATCTGATTC 398
                                                                                                                        ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAAT
                                                                                                                                                                    GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC
                                                                                                                                                                                                                                                     GATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTA
                                                                                                                                                                                                                                                                                                                                     GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC
AACGCCGCGCTGGTTAATCAGACCGCATCTGATTC
                                                                            ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAAT
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/label= Primer_TAF6
complement(294..312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-00054452
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/label= Primer_TAF3
complement(103. .128)
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Primer_TAF4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 282.2; DB 2
Pred. No. 5.6e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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Job time : 246.684 secs

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Database
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: LEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version
CURRENT APPLICATION LOADA
APPLICATION NUMBER: US/08/233,788A
FILING DATE: 26-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 920043.403C2
REFERENCE/DOCKET NUMBER: 920043.403C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEG ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
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Patent No. 5635617
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APPLICANT: Doran,
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APPLICANT: Kay, William W.
APPLICANT: Collinson, Karen S.
APPLICANT: Clouthier, Sharon C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION
TITLE OF INVENTION: OF SALMONELLA
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; APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NO 13717
SEQ ID NO 13717
SEQ ID NO 13717
TYPE: DNA
COGANISM: Pseudomonas aeruginosa
US-09-252-991A-13717
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                                                                                                                                                                                       Query Match 8.0%; Score 36.4; DB Best Local Similarity 47.4%; Pred. No. 0.04; Matches 109; Conservative 0; Mismatches
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GENERAL INFORMATION:
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Best Local Similarity
Matches 302; Conserv
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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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LOCATION: 1..
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                                   210 redecedecererrececiaerrececierecereciaecaecreceaecaecaeceaecearerre 151
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                                                                     77 GGGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGCCCGGACTATGATCAGC 136
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Conservative
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Pred. No. 2.5e-83;
0; Mismatches 33
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
US 60/094,190
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION UNMBER: US 60
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13820
LENGTH: 2748
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US-09-252-991A-13820/c
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                                                            PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13627
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Patent No. 6551795
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-09-252-991A-13627
                                                                                                                                                                                          FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                       APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
            TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
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US-09-103-840A-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09103840A Patent No. 6294328
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SOFTWARE: PatentIn Ver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DNA SEQUENCES TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FLEISCHMAN, Robert D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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GCCACCCCGTGCGGATCGTTGAAGCTGGCGTGGCGTGATGGTGACGGCGCCG 1093736
                                                              TGGTTACCCGTGTTGCTTACCCATGAAATGGCACATGCACTGCAAAGCGATGCCCGTAAAT 196
                                                                                                                                                                                                                                                           GCGGTGCCGACGGTGATGGGGGAGCCGGTGACGGTGTTGGTGGTCGGGTCGATCACCGAC
                                                                                                                                                                                                                                                                                          GGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGCCCCGGACTATGATCAGC 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGCCCGGACTATGATCAGC 136
                            GGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCG
                                                                                                                                                             CTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGG 256
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                                                                                            ataatagtactattgaactgactcagaatggtttcagaaataatgccaccatcgaccagt
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                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 0.087
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Pred. No. 3
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US-09-621-976-2574
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US-09-621-976-2574
/ Sequence 2574, Application US/09621976.
/ Patent No. 6639063
/ GENERAL INFORMATION:
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LENOTH: 834

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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OTHER INFORMATION: H37Rv
US-09-103-840A-1
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TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET. 0545PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILLING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y.
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NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
PROPERTY OF SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SER
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Best Local Similarity 44.6%;
Matches 131; Conservative
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APPLICANT: WHITE, OWEN R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM FILE REFERENCE: 24456-20007.00
FILE REFERENCE: 24456-20007.00
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Patent No. 6294328
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                              l Similarity 14.
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      7.2%; Score 33; DB
14.9%; Pred. No. 0.54
tive 64; Mismatches
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Pred. No. 31;
0; Mismatches 163;
                                               DB 4; Length 834;
0.54;
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US-08-469-412A-8
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LENGTH: 332 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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OTHER INFORMATION:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: The ERF Genetic Locus and Its Products
NUMBER OF SEQUENCES: 16
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107 GCAATAGTTCCGGCCCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGG 166
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Athanasiou, Meropi A.
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Blair, Donald G.
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Pred. No. 0.53;
0; Mismatches 111;
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; Sequence 8, Application US/09021715
; Patent NO. 6194547
; GENERAL INFORMATION:
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                                                                                                                                                                  Local Similarity
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,715
FILING DATE: 10-Feb-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  LOCATION: 1..332
OTHER INFORMATION: /note= "human ERF gene promoter region"
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sgouras, Dionyssios N.
TITLE OF INVENTION: The ERF Genetic Locus
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 015280-229000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       FEATURE:
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                 180
                                             107 GCAATAGTTCCGGCCCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGG 166
                                                                                   120
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                                                                                                               47 GCAGTGCTCTGGCTGGCGTTCCTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCG 106
                                                                                                                                                  99;
               GGGCGTGGGCGTCCCGGCCCCGGAGTGCGATATTAACCCCGGGAGGCGGCGGCGGGGAGGG
                                                                                                                                                                                                                                                                                                                                      LENGTH: 332 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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N FOR SEQ ID NO: 8:
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                                                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                7.1%;
ilarity 47.1%;
Conservative
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Athanasiou, Meropi A.
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                                                                                                                                                Score 32.4; DB 3; Length 3 Pred. No. 0.53; Indels
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                                                                                                                                                                                Length 332;
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                                                                                                                                               Gaps
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US-09-480-884A-153/c
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                                                                                                                                               Sequence 153, Application US/09480884A Patent No. 6482597 GENERAL INFORMATION:
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            APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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CURRENT APPLICATION NUMBER:
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; LENGTH: 2007
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-643-597-153
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SOFTWARE: FABL
SEQ ID NO 153
FUGTH: 2007
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Best Local Similarity

Matches 101; Conserv
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CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
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APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE:
1257 ATCTGCCCTCCCATTAGTGGTAGGAGAGGAGGTCCAA 1221
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o. 6426072
                                                                                         GCCTAGGGGAATTTCAGCATTAGGGCTTGAAATTACTCACCCAGGAGAAATCCCAGTATA 1256
                                                                                                                                  ATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATA 298
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                                         ATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGA 335
                                                                                                                                                                                AGTTAAAAGTACTTAAAAGTTCACTGGGAATTTTGCAATGCAGTTGAGAAAACTGGAGCT 1318
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Fanger, Gary I
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Fan, Liqun
Kalos, Michael D.
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Pred. No. 2.8;
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US/09/480,884A

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APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Honger, Chaitanya S.
APPLICANT: Honger, Nancy A.
APPLICANT: Honger, Gary R.
ITITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
ITITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455CB
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 153
LENGTH: 2007
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US-09-542-615A-153/c
; Sequence 153, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
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Best Local Similarity 46.5%;
Matches 101; Conservative
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ORGANISM: Homo sapien
-09-542-615A-153
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; ORGANISM: Homo sapien
US-09-480-884A-153
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Best Local Similarity 46.1
Matches 101; Conservative
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NUMBER OF SEQ ID NOS: 330
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 153
LENGTH: 2007
1257 ÁTCTGCCCTCCCÁTTAGTGGTÁGGAGAAGCTCCAÁ 1221
                                                                                                                    1317 GCCTÁGGGGÁATTŤCAGCÁTTÁGGGCTTGÁAATTÁCTCÁGCCÁGGÁGAAAATCCCCAGTÁTÁ 1258
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; TYPE: DNA
; ORGANISM: Human
US-09-221-107-153
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ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

CURRENT APPLICATION NUMBER: US/09/606,421B

CURRENT FILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 2007

TYPE: DNA

ORGANISM: Homo sapien
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US-09-221-107-153/c
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                 Matches 101;
                                 Query Match
Best Local Similarity
                                                                                                                                         SOFTWARE: PatentIn Ver.
SEQ ID NO 153
LENGTH: 2007
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                                                                                                                                                                                                                                                                                                          Sequence 153, Application US/09221107
Patent No. 6660838
GENERAL INFORMATION:
                                                                                                                                                                             APPLICANT: WAIG, TONGTONG
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455C2
CURRENT APPLICATION NUMBER: US/09/221,107
CURRENT FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 161
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Best Local Similarity 46.5%; Pred. No. 2.8;
Matches 101; Conservative 0; Mismatches 116;
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US-09-606-421B-153/c
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Patent No. 6531315
GENERAL INFORMATION:
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APPLICANT:
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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             Conservative
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Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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                           6.9%;
46.5%;
Score 31.4; DB 4; Length 2
Pred. No. 2.8;
0; Mismatches 116; Indels
                                   Length 2007;
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119 GCCCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGC 178

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Gaps

Searc Job t	DЬ	ફ	В	ફ	ф	ફ	DЬ
Search completed: March 16, 2004, 04:37:43 Job time : 60.6647 secs	1257 ATCTGCCCTCCCATTAGTGGTAGGAGAGGAGCTCCAA 1221	299 ATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGA 335	1317 GCCTAGGGGAATTTCAGCATTAGGGCTTGAAATTACTCACCCAGGAGAAATCCCCAGTATA 1258	239 ATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATA 298	1377 AGTTAAAAGTACTTAAAAGTTCACTGGGAATTTTTGCAATGCAGTTGAGAAAACTGGAGCT 1318	179 AAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCG 238	

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_NEW PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08_NEW PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

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19: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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456
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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13 14 15	10 12 12	വേഷസര	Rebult No.
32.3 22.8 8 8 2		3 3 3 5 4 4 8 5	Score 36.4
7.3 7.2 7.2	777777	77.55	Query Match 8.0
992 568 718	2886 2301 2301 3140 3485 493	954 1355 2547 1878	Query Match Length DB
12 14 15	122	15	12 12 18
US-10-425-114-31747 US-10-333-631-1 US-10-027-632-26874	US-09-801-368-131 US-09-815-242-4844 US-09-815-242-9042 US-10-425-114-29450 US-10-424-99-64614 US-10-282-122A-26087	US-10-282-122A-13780 US-10-045-674-593 US-10-282-122A-36154 US-10-369-493-43934	ID US-10-282-122A-30140 US-10-282-172A-33185
Sequence 31747, A Sequence 1, Appli Sequence 26874, A	Sequence 131, App Sequence 4844, Ap Sequence 9042, Ap Sequence 29450, A Sequence 64614, A Sequence 26087, A		Description Sequence 30140, A Semison 31185 A

C 45	C 44	C 43	C 42	C 41		39		c 37	36		c 34	33	32	31	c 30	29		c 27	26	c 25	c 24	23	22		c 20				16
31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.6	31.6	31.6	31.8	31.8	31.8	31.8	31.8	31.8	32	32	32	32	32.2	32.2	32.2	w	ω	32.4	ω			32.8
6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	6.9	7.0	7.0	7.0	7.0	7.0	7.0	7.0 9	7.0	7.0	7.0	7.1	7.1	7.1	7.1	7.1 9	7.1	7.1	7.2	7.2	7.2
2007	2007	2007	1833	1467	1320	734	1642	1338	951	2766	978	930	930	930	678	9025608	1152	1001	669	4830	1083	1015	972	9025608	789	960	3309400	1113	1059
9 1	9 U	9	9 0	12	10	12	9	15	15	12	15	15	12	9	14	14	14	12	12	12	15	14	14	14	14	12	9	9	9
US-09-897-778-153	US-09-850-716A-153	US-09-735-705-153	US-09-989-920-87	US-10-282-122A-25701	US-09-738-630-70	US-10-425-114-566	US-09-887-576-469	US-10-369-493-37494	US-10-369-493-43201	US-10-282-122A-42042	US-10-369-493-24265	US-10-369-493-24480	US-10-282-122A-20335	US-09-815-242-6028	US-10-156-761-1219	US-10-156-761-1	US-10-156-761-303	US-10-425-114-14270	US-10-282-122A-31444	US-10-282-122A-27869	US-10-369-493-33133	US-10-198-846-4377	US-10-333-631-4	US-10-156-761-1	US-10-156-761-2022	US-10-282-122A-11889	US-09-738-626-1	US-09-738-626-481	US-09-738-626-482
153,	153,		Sequence 87, Appl	2570	Sequence 70, Appl	•	Sequence 469, App	Sequence 37494, A					Sequence 20335, A	Sequence 6028, Ap	Sequence 1219, Ap	e 1,	Sequence 303, App	1427	31444,			43	`~	m	202	116	e 1, A	•	Sequence 482, App

## ALIGNMENTS

RESULT 1

		PRIOR
	FILING DATE	PRIOR
	APPLICATION N	PRIOR
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	OR APPLICATION NUMBER: 60/230,347	PRIOR
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	OR FILING DATE: 2000-05-26	PRIOR
	OR APPLICATION NUMBER: 60/207,727	PRIOR
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	PRIOR APPLICATION NUMBER: 60/191,078	PRIO
	CURRENT FILING DATE: 2003-02-20	CURR
122A	CURRENT APPLICATION NUMBER: US/10/282,122A	CURR
	FILE REFERENCE: ELITRA.034A	FILE
Essential Genes in Microorganisms	ication of	TIIL
		APPL
	APPLICANT: Forsyth, R.	APPL
	APPLICANT: Yamamoto, Robert	APPL
	APPLICANT: Carr, Grant	APPL
	APPLICANT: Trawick, John	APPL
	APPLICANT: Wall, Daniel	APPL
	APPLICANT: Zyskind, Judith	APPL
	APPLICANT: Ohlsen, Kari	APPL
	APPLICANT: Haselbeck, Robert	APPL
	APPLICANT: Malone, Cheryl	APPL
	APPLICANT: Zamudio, Carlos	APPL
	APPLICANT: Wang, Liangeu	APPL
	ENERAL INFORMATION:	ENER
	ublication No. US20040029129A1	ubli
A	ence 30140, Application US/10282122	eque
	10-282-122A-30140/c	10-2

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US-10-282-122A-33185/c

/ Sequence 33185, Application US/10282122A

/ Publication No. US20040029129A1
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Identification of Essential Genes
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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Matches 1
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 30140
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Pseudomonas aeruginosa
LENGTH: 2610
                                        APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
                                                                                               APPLICATION NUMBER: 60/230,347
FILING DATE: 2000-09-09
APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
                                                                                                                                                                                               FILING DATE: 2000-03-21
APPLICATION NUMBER: 60/206,848
FILING DATE: 2000-05-23
APPLICATION NUMBER: 60/207,727
                                                                                                                                                             APPLICATION NUMBER: 60/230,335
FILING DATE: 2000-09-06
                                                                                                                                                                                      FILING DATE: 2000-05-26
                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/191,078 FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 GTGGCTTCGCCCTTGACGÁTGGCGGAAÁGGAATCCGGCCTTGÁCGTÁGGC
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Malone, Cheryl
Haselbeck, Robert
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Grant
היים, Robert
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Pred. No. 0.21;
0; Mismatches
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LENGTH: 2667
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Remaining Prior Application data
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
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GGCG 108
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Pred. No. 0.3;
0; Mismatches :
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    See File Wrapper or PALM

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APPLICANT: XU, H.

TITLE OF INVENTION: Identification of Essential General Reference: ELITEA.034A

CURRENT APPLICATION UNMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/291,078

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-05-23

PRIOR PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/2030,335

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-05

PRIOR PRIOR PRIOR DATE: 2000-09-05

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PRIOR PRIOR DATE: 2000-09-05

PRIOR PRIOR PRIOR DATE: 2000-09-05
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US-10-282-122A-13780/c
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APPLICANT: Zamudio, Carl
APPLICANT: Malone, Chery
                                                                                                                                                                                                                                                                                              APPLICAN'
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                Ohlsen, Kari
Zyskind, Judi
Wall, Daniel
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Zamudio, رمان
zamudio, رمان
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                                                                                                                                                                                                                                                                                                                                                                                                                               Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                        Judith
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in Microorganisms

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US-10-045-674-593
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; ORGANISM: Burkholderia mallei
US-10-282-122A-13780
                                                                                                                                                          SEQ ID NO 593
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Best Local :
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Publication No.
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CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 60/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                  APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FF
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVE
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
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FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
EQ ID NO 13780
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                                                     OTHER INFORMATION:
                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                        FEATURE:
                                                                                                                                          ENGTH: 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR APPLICATION NUMBER: 60/253,625
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/257,931
OR FILING DATE: 2000-12-22
OR APPLICATION NUMBER: 60/267,636
OR APPLICATION NUMBER: 60/269,308
OR APPLICATION NUMBER: 60/269,308
OR FILING DATE: 2001-02-16
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(1) ... (1305)
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, EDWARD H.
I, HORACIO G.
Y, KRISTIN L.
                                                   Description of Arti
nucleotide sequence
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Pred. No. 0.2;
0; Mismatches
                                                                      of Artificial Sequence: M13-III
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Best Local
Remaining
NUMBER OF
                                             PRIOR APPLICATION NUMBER: 60/257,931
PRIOR TILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR
                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
                                    PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                    APPLICATION NUMBER: 60/242,578
FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                        APPLICATION NUMBER: 60/230,347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
 Prior Application data removed SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYGGYGAYGTYWSYGGYCTKGCTAAYGGYAAYGGWGCYACYGGWGAYTTYGCWGGYTCKA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANACGACCATTACCCAGAGCGGTTATGGTAACGGCCCGATGTAGGCCCAGGGTGCGGATA 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zamudio, Carlo
Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wall, Daniel
Trawick, John
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                                                                                                                                                                                                             2000-09-09
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                  See File Wrapper or PALM
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
CURRENT FILE OF 10(52052)B
CURRENT FILING DATE: 2003-02-08
PRIOR APPLICATION NUMBER: US 50/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
RIOR APPLICATION NUMBER: US 60/360,039
RIOR APPLICATION NUMBER: US 60/360,039
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LENGTH: 1388
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; ORGANISM: Streptococcus mutans
US-10-282-122A-36154
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LENGTH: 2547
                                                                                                                                                                                                                                                                                                                                               Local Similarity
336 TATTACTGTC 345
                               373 GTCCCTGCCACGGTTGAGTAATGAGATTACCTTGTAGATCCCATAAACACAAAATTCCGT 314
                                                           276 GAÇTÇAGAATGGTTTCAGAAATAATOCCAÇÇATCGACCAGTGGAACGCTAAAAACTCCGA 335
                                                                                                  216 GAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACT
                                                                                                                                                                  493 CTTGTÄÄÄŤCCCÁCÁAACÁCACCGTTCCGTCAAAACCÄÁCACTGÁCÁATGCTTACCCCAG 434
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                                                                                                                                                                                                                                       TAAAAGCCGACGGAAATAACTCCTTCCTTGTGTCCGCGCCAAGGTTGAGTAATGGCGTTAC 494
                                                                                                                                                                                                                                                                      TAACGGCGGCAATAGTTCCGGCCCGGACTATGATCAGCTGGTTACCCGTGTTGTTAC 155
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46.0%;
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                                                                                                                                                                                                                                                                                                                                               Length 1878;
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APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xyamamoto, Robert T.
APPLICANT: Xyamamoto, Robert T.
APPLICANT: Xyamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Ger
TITLE OF INVENTION: Prokaryotes
FILE REFERENCES: ELITAN.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
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US-09-801-368-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4844, Application US/09815242
Patent No. US20020061569A1
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TITLE OF INVENTION: Methods for Improving Selection of Invention of Inv
                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                   APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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SEQ ID NO 131
LENGTH: 2886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 ACCATTACCCAGAGCGGTTATGGTAACGGCGCCCATGTAGGCCAGGGGTGCGGATAATAGT 264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 CAATACTGCC 304
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Salama, Sofie
Sherman, Amir
Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US200
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Milne, Todd
No. US20020128250Alman,
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Holtzman, Doug
Madden, Kevin
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FILE REFERENCE: ELITA. 011A
CURRENT APPLICATION NUMBER: U5/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
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US-09-815-242-9042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version SEQ ID NO 4844
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TYPE: DM: Staphylococcus aureus
ORGANISM: Staphylococcus aureus
-09-815-242-4844
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PRIOR
PRIOR
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                OR APPLICATION NUMBER: 60/191,078
OR FILING DATE: 2000-03-21
OR APPLICATION NUMBER: 60/206,848
OR FILING DATE: 2000-05-23
OR APPLICATION NUMBER: 60/207,727
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: 60/242,578
OR FILING DATE: 2000-10-23
OR FILING DATE: 2000-11-27
OR APPLICATION NUMBER: 60/253,625
OR APPLICATION NUMBER: 60/257,931
OR APPLICATION NUMBER: 60/257,931
OR APPLICATION NUMBER: 60/257,931
OR APPLICATION NUMBER: 60/257,931
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APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/253,625
FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
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Xu, H. Howard
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Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari L.
Zyskind, Judith W.
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60/269,308
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Pred. No. 1.8;
0; Mismatches 109; Indels
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; NAME/KEY: CDS
; LOCATION: (1)...(2301)
US-09-815-242-9042
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29450, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 29450
LENGTH: 3140
                                                                                                                                                                                                                                              Matches 115;
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B FILE REFERENCE: 38-21(53313)B CURRENT APPLICATION NUMBER: US/10/425,114 CURRENT FILLING DATE: 2003-04-28 CURRENT FILLING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 73128
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                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Clone
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Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                                                                                                     GTTACCCATGAAATGGCACATGCACTGCAAAGCGATGCCCGTAAATCTGAAACGACCATT
TCAGATAGTAGTTCTGCAAAAGGAAAGAATGTTGTTGATAATATGGATAATGGAGAGCTT 1980
                                                                                                                                                          AATCAAGGCAAGGGCCTAAATAGGCTAAATCAGGTAGATAAAAGGCATAGCTGGTAAA 1860
                                ACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCCAGGGTGCGGATAATAGTACTATT
                                                                             ACTGCATCTGGAGGAGCTAGAGAAATGGACAAGGATGCTCAGAATGTTGAAACAAGTGGT
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                                                                                                                                                                                                                                              Conservative
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Pred. No. 2
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Pred. No. 1.8;
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RESULT 12
US-10-282-122A-26087/c
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                                            APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Cari
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judit
APPLICANT: Wall, Daniel
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US-10-424-599-64614
Sequence 64614, Application US/10424599
; Publication No. US20040031072A1
                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                 Sequence 26087, Application US/10282122A Publication No. US20040029129A1
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Best Local Similarity
Matches 115; Conserv
                       APPLICAN
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LENGTH: 3485
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APPLICANT: Kovalic David
APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_29358C.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                     2326
                                                                                                                                                                                                                                                                                            2386 ATTGAACTTTC 2396
                                                                                                                                                                                                                                                                                                                                                                                                                                      2266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2206 ACTGCATCTGGAGGAGCTAGAGAAATGGACAAGGATGCTCAGAATGTTGAAACAAGTGGT
                                                                                                                                                                                                                                                                                                                           331 TCCGATATTAÇ 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 GTTACCCATGAAATGGCACATGCACTGCAAAGCGATGCCCGTAAATCTGAAACGACCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2041 ATTGAACTTTC 2051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91 AATCATAACGGCGGCGAATAGTTCCGGCCCGGACTATGATCAGCTGGTTACCCGTGTT 150
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                                                                                                                                                                                                                                                                                                                                                                                  GAACTGACTCAGAATGGTTTCAGAAATAATGCCCACCATCGACCAGTGGAACGCTAAAAAC 330
                                                                                                                                                                                                                                                                                                                                                                                                                     TCAGATAGTAGTTCTGCAAAAGGAAAGAATGTTGTTGATAATATGGATAATGGAGAGAGCTT
                                                            Ohlsen, Kari
Zyskind, Judith
                                                                                               Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
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Yamamoto, Robert
                             Wall, Daniel
Trawick, John
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            Grant
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Pred. No. 2.7;
0; Mismatches 136;
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APPLICANT: APPLICANT: APPLICANT:

APPLICANT: Kovelic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

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RESULT 13
US-10-425-114-31747/c
Sequence 31747, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
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; ORGANISM: Mycobacterium
US-10-282-122A-26087
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 26087
LENGTH: 493
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Best Local
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PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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TITLE OF INVENTION: Identification of Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                               168
                                                                                                                                                                                                                                       317
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                                                                                                                                                                                                                                                                                                                                                                                                         197
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                                                                                                                                                                                                                   ATCACCGACACCGTGCCGCTGCCGAAATTGGTGACGTAGACGTTGCCGCCCCGGGTTGACC 169
                                                                                                                                                                                                                                                                                                                                                                                       CTGAAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                ACCGTGTTGCTGTCGAAGTTGGTCACGAAGACCAGGCCGGTGACGGGGCTGACCGGCACC 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n 7.3%;
Similarity 44.6%;
31; Conservative
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                                                                                                                                                                                                                                                                                                                                               CCGCTTGGACCGTTGCCGATGGTGATGGGGGAGCCGGTGACGGTGTTGGTGGCGGGGTTTG
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Pred. No. 1.1;
0; Mismatches 163;
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, NAME/KEY: misc feature
; LOCATION: (90) . (90)
; OTHER INFORMATION: n=a,
US-10-333-631-1
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US-10-333-631-1
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 568
TYPE: DNA
ORGANISM: Homo sapiens
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Publication No. US20030190651A1
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Best Local S
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LENGTH: 992
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CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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                                     259 AATAGTACTATTGAACTGACTCAGAATGG 287
                                                                                                            199 GANACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGAT 258
                                                                                                                                                                                             139 GTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGCAAAGCGATGCCCGTAAATCT 198
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                                                                                                                                                                                                                                                        Similarity
CCTGGATCTGCGGATAGCCCACATGCTGG 235
                                                                             GAAATGGTCCGTCACCCAGGCACTGGACGTCACAGAGCAGCTGGATGCCGGGGTGCGGTA 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGGAGGCGGATCAGGCCTTGGTGGCGGGTCAGGTCTCGGCGGCCTTGGTGGTCTCGGC
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Conservative
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Pred. No. 1.6;
0; Mismatches
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Pred. No. 1.6;
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                                                                                                                                                                                                                                                                            DB 14; Length 568;
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; TYPE: DNA
; ORGANISM: Human
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PRIOR FILLING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILLING DATE: 2000-04-20
PRIOR FILLING DATE: 2000-03-29
PRIOR FILLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILLING DATE: 2000-02-24
PRIOR FILLING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILLING DATE: 1999-11-23
PRIOR FILLING DATE: 1999-11-23
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SEQ ID NO 26874
LENGTH: 718
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 85; Conser
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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CURRENT FILING DATE: 2002-04-30
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                                          138 GGTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGCAAAGCGATGCC 189
                                                                                           574
                                                                                                                                                                                                                                      18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 4.0
                                                                                                                                        GGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCCGGACTATGATCAGCT 137
                                                                                                                                                                                       GGAAGCATCCACAGCACAAGGTGCCGCTCGCCCTCGTGTGCCCGGGGTGGCCTGCCCAGGG
                                                                                                                                                                                                                                   TGTGTTCCCTGAAGGCAGACATGACTGGGCACAGGCACGGGGGTTCTATGCC
                                                                                         GCTGGCAGCGTCCCCACGTGTCGGGGCTGGCCTGAGTTCCGTGTCCCCTGGGATCTACAGC
                                                                                                                                                                                                                                                                                  Conservative .
                                                                                                                                                                                                                                                                                                      7.2%;
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Pred. No. 1.9;
                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                               DB 15;
                                                                                                                                                                                                                                                                                  87;
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Search completed: March 17, 2004, 08:16:20 Job time: 413.736 secs

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Perfect score:
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Maximum DB seq
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                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  232.6
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length: 2000000000
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456
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Maximum Match 100%
Listing first 45 summaries
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 51.0
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AV430994
CF848025
CF842541
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BJ618688 BJ618688
AV430994 AV430994
CF848025 psMA003xI
CF842541 psHB020xG
                                           Description
                                                                     TITLE
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                         Expressed genes in X. laevis embryo Unpublished (2001)
Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Jaj Tel: 81-559-81-6855
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                          BJ618688 680 bp mRNA linear EST 01-OCT-BJ618688 NIBB Mochii normalized Xenopus early gastrula library Xenopus laevis CDNA clone XL186b22 5', mRNA sequence.
BJ618688 BJ618688.1 GI:37256713
         Email: tshini@genes.nig.ac.jp
The information of this clone
                                                                                               Xenopus laevis
Eukaryota; Metszoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 680)
Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
Kohara, Y.
                                                                                                                                                                        EST
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BZ568375
FR0020317
BZ469000
BZ204853
CA588919
AU085223
AU085223
AU041511
BJ006097
BJ001420
BJ004146
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AV058630
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CA731849
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CNS02GQP
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AA746477
CA711477
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CC333807
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CC961526
BH663951
BH651371
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          is available through the following
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ALD1202 F.rubripe
BZ469000 BOOADSBTF
BZ204853 CH230-390
CA588919 hab51c12.
AU085223 AU085223
AU241511 AU241511
BJ006097 BJ001629
BJ001426 BJ001426
BJ001406 BJ001416
BJ010763 BJ0010653
BJ0012818 BJ011653
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BJ012818 CF402142 RTWW1_200180
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BG444255 GA_Ea00180
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CA711477 wd62c.pk0
BH438448 BGVQ226TR
AV058630 AV058630
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AQ33823 mgxb0001F
BJ335653 BJ335653
BJ335653 BJ335653
BJ335653 BJ335653
BJ335653 BJ335653
BJ335653 BJ33694
CR333807 CGMBC13TV
CA26630 ACUIRT307
AU177600 AU177600
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CC961526 BOIGS10TF
BH663951 BOMBL85TR
BH651371 BOHXV71TF
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BZ568375 pacs2-164
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Matches 316; Conserv
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Contact: Erika Asamizu
The First Laboratory for Plant
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                          173
                                                                                                                                                                                                                                                                                                                                                                                                   421
                                                                                                                                                                                                                                                                                                                                                                                                                               361 AATAACGCCGCCGCGTGATTCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                     Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
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                                                      10907854
                                                                                                                                                              Porphyra yezoensis
Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      413
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Nikaido,I., Asamizu,E., Nakajima,M., Nakamura,Y., Saga,N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473
                                                                                                                                                                                                       Porphyra yezoensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCGGATAGTTCCGGC 120
                                                                                                                                                                                                                                                                                                                                                                               GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                            GGCĂĂČGGTĞCTGCAĞTTGÁCCÁĞÁČTĞCĂTČTAÁCTČĆTCĆĞTCÁACĞTĞACTCÁĞĞTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCTÁCTCTTGÁTCÁGTGGÁÁÁCGGCÁAÁAÁTTTCTGÁAÁTGÁCGGTTAAACÁGTTCGGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="whole embryo"
/dev_stage="stage 10.5"
/clone_lib="NIBB Mochii normalized Xenopus early gastrula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
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Pred. No. 4.7e-54;
0; Mismatches 140;
               Gene Research
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CDNA clone
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Seq primer: BK reverse primer
High quality sequence stop: 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             441
                                                                                                                                                                                                                                                                              BACKWARD: BK reverse primer plate: 003 row: I column:
                                                                                                                                                                                                                                                                                                                                      Email: bmtyler@vt.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         321
                                                                                                                                                                                                                                                                                                          FORWARD: BK reverse primer
                                                                                                                                                                                                                                                                                                                              PCR PRimers
                                                                                                                                                                                                                                                                                                                                                           1880 Pratt Dr., Blacksburg,
Tel: 540-231-7318
                                                                                                                                                                                                                                                                                                                                                                                                        Tyler lab
                                                                                                                                                                                                                                                                                                                                                                                                                                 Tyler, B. Not Published Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phytophthora sojae
Phytophthora sojae
                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Tyler B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CF848025.1 GI:38063679
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       psMA003xI14f USDA-IFAPS:Expression of Phytophthora sojae genes during infection and propagation sMA Phytophthora sojae cDNA clone CF848025 mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 590)
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/db_xref="taxon:67593"
/clone="sMA003114"
/tissue_type="myycelium"
/cell_line="p6497"
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/lab_host="synthetic medium"
/clone_lbb="USDA-IFAFS: Expression of Phytophthora sojae
genes during infection and propagation sMA"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xho1"
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/clone="pI027e10 r"
/clone=lib="Porphyra yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1:
   8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Porphyra yezoensis"
/mol_type="mRNA"
/strain="TU-1"
 Score
Pred.
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Pred. No. 15;
 37;
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DB
21;
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           14;
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       Length 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACKWARD: BK reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bmtyler@vt.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; stramenopiles; Phytophthora.
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GTGTTGTTACCCATGAAATGGCACATGCACTGCAAAGCGATGCCC
                                                           CCGTTGATGAGCACGACGCCCCACAAAGGCCGTGGCCGCGATGATGGCCAGGCGCTCG
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                                                                                              GCGGTAATCATAACGGCGGCGAATAGTTCCGGCCCGGACTATGATCAGCTGGTTACCC
                                                                                                                                       TTGTAGCGGTAGTCCTTGATGTCCGTGAGCTTGGGGGAAGTCGCCGATGAAGTAGCCGGCG
                                                                                                                                                                          TCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCTGGCGTCGTTCCACAATGGGGCGGCG 85
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                                                                                                                                                                                                                 8.1%;
larity 51.5%;
Conservative
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                                                                                                                                                                                                                                                                                                     /dev stage="48 hr. post infection stage"
/lab_host="Soybean plant"
/clone lib="USDA-IFAFS:Expression of Phytophthora sojae
/clone during infection and propagation sHB"
/note="Vector: pBK-CMV; Site_1: EcoR1; Site_2: Xho1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Phytophthora
/mol_type="mRNA"
/db_xref="taxon:67593"
/clone="sHB020G21"
                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="mycelium"
/cell_line="P6497"
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                                                                                                                                                                                                               Score 37; DB Pred. No. 22; O; Mismatches
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                                                                                                                                                                                                                 51
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This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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141G11 of
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Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
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                                                           TGCACTGCA 179
                                                                                                                  TAGTTCCGGCCCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACA 170
                    CGCTCTGCA
                                                                                                                                                                            TGTCCTGCCGGGCGTAGGGGAWGCAGGGGATGACGGCGTKACGCGTGACGAGGAGGCGW 378
                                                                                                                                                                                                   TGCTCTGGCTGGCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAA 110
                                                                                                TCTTGCAGGCGTTGWTYATGWTCAGCTGCTCCWTCAWGTTGTCGTTAWTTTCGCCGCAGC 318
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                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="141G11"
                                                                                                                                                                                                                                                                                                                                                                         note="Genoscope sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Tetraodon nigroviridis"
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51.2%;
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GSS; genome survey sequence.
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
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AL013202
AL013202.1 GI:2679570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      University of Washington
Box 352145, Seattle, WA:
Tel: 2062216954
Fax: 2066857244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                      TTGGCGCGCTCGGCGACGTCGTGGAAGGCGTCGAACATCAGCAGGGTGTGCTTCAGCTGT
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Pseudomonadaceae; Pseudomo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:287"
/clone="pacs2-164 7503"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Pseudomonas
/mol_type="genomic DNA"
/strain="2-164"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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Pred. No. 36;
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                                                                                                                                       genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
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                                                                                                                                                     Email: cdtown@tigr.org
DNA is from a_doubled
                                                                                                                                                                                                                                                           Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
Cther GSSs: BOOAO58TR
                                                                                                                                                                                                                                               Contact: Chris
                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosida; eurosida II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                               Brassica oleracea
Brassica oleracea
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BCOAOS8TF BO 1.6 2 KB tot Brassica
genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l (bases 1 to 417)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
Direct Submission
Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
V_type: phagemid
PRIMMER: KS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTCNGÉCTGTGTTCACACGCCTGTGTTCTTCATTTGGACTCCAAGGACTCTAATACNTG 135
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                                                                                                                                             primer: TF
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                                                                                                                                                                                                            Medical Center Drive,
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                                                                                                                            sheared ends.
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/clone_lib="BO_1.6_2_KB_tot'
                      /organism="Brassica oleracea"
/mol type="genomic DNA"
/strain="TO1000DH3"
/db xref="taxon:3712"
/clone="BOOA058"
                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db xref="taxon:31033"
/clone="040D20bD10"
/clone_11b="cosmid 040D20"
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                                                                                                                                               haploid provided by
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                                                                                                                                                                                                          Rockville,
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Length

813;

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607

727 357 667

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Riggs,F., de Jong,P. and rraser,.....
Rat BAC End Sequences from Library CHORI-230 Mbol segment
Unnublished (1999)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                  Email: Bzhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tbb/bac_ends/rat/bac_end_intro.html
plate: 390 row: D column: 21
Seg primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Other_GSSs: CH230-390D21.TJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BZ204853.1 GI:23862905
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301 838 0208
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                                                                                                                                                                                                                                                                                                                                                   BAC ends.
     /cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
CHORI-230 Rat (BN/S8NH8d/MCW) BAC library produced by
                                                                                                                                                                         /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pHOS1; Site_1: BstXI; 1.6-2 kb sheared
total DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                           'sex="Female"
                                                                                                                                                     clone="CH230-390D21"
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Pred. No. 78;
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Russell,D.,
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1 (bases 1 to 490)

2 Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

Waterston, R. and Wilson, R.

Washu Zebrafish EST Project 1998

L. Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 GGTAATAACGCC 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA588919 490 bp mRNA linear EST 19-NOV-ZUU.
hab51c12.yl Fugu UT7 adult skin Takifugu rubripes cDNA clone
hAb51c1265′ similar to SW:CLD4_MOUSE 035054 CLAUDIN-4;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94;
                                                                                                                                                                                                                                                                                                                                     Email: zbrafish@watson.wustl.edu
Library materials provided by G. Elgar (UK MRC HGMP-RC) Library
constructed by Drs. K. Kawakami, M. Sasaki, S. Sugano, K. Kikuchi
and S. Watabe (University of Tokyo, Institute of Medical Science
and Laboratory of Aquatic Molecular Biology and Biotechnology) DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution: Fugu clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL, send email to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Stephen L. Johnson washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takifugu rubripes (Fugu rubripes)
Takifugu rubripes
                                                                                                                                                                                                                                                                                    info@image.llnl.gov
Seq primer: T3 ET f1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
CA588919
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/tissue_type="skin"
/lab_host="DH10B (T1
/clone_lib="Fugu UT7
                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:31033"
/clone="IMAGE:6352126"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pieter de Jong
                                                                                                                                                                                                   organism="Takifugu rubripes"
                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                              sex="female"
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                                                                                                                                                                                                                                                                                       from Amersham
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Pred. No. 78;
0; Mismatches
           phage-resistant)"
adult skin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Louis,
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EST 19-NOV-2002

8

REFERENCE AUTHORS

COMMENT

TITLE JOURNAL

FEATURES

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VERSION KEYWORDS

ORGANISM

ACCESSION

DEFINITION BZ204853 RESULT 9 ঠ 밁 श् 밁 ફ 밁

460 326 520

988

206 640 146

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Matches 103; Query Match

Local

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AUTHORS
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AU085223
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                             Query Match
Best Local (
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Matches 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307
                                                                                                                                                                                                                                                                             Bio-resources Technology Division
Forestry and Forest Products Research Institute
Matsunosato 1, Kukizaki, Ibaraki 305-8687, Japan
                                                                                                                                                                                                                 Email: udino@ffpri.affrc.go.jp;
URL:http://www.ffpri.affrc.go.jp/labs/cjgenome/database/cjdatae.htm
1.
                           Similarity
                                                                                                                                                                                                                                                                                                                                 Contact: Tokuko Ujino-Ihara
                                                                                                                                                                                                                                                                                                                                                                       Expression analysis of ESTs derived from Cryptomeria japonica Plant Mol. Biol. 43 (4), 451-457 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 480)
Ujino-Ihara,T., Yoshimura,K., Ugawa,Y., Yoshimaru,H., Nagasaka,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cryptomeria japonica (Japanese cedar)
Cryptomeria japonica
Cryptomeria japonica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                                                                                                                                           and Tsumura, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU085223 Cryptomeria japonica i
clone CC2407 5', mRNA sequence.
AU085223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cryptomeria.
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80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGCACTGCATCTGACCTGTGCTCTGCACCACGCAGTTCATCCAGATCCCTTCCCAAGTG
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             Conservative
                                                                                                                                                                                                                                                        81-298-73-3211 (ex.444)
81-298-73-3795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescript-FL; Site 1: pflM I (CCANNINNTGG); Site 2: pflM I (CCANNINNTGG); BamHI-SmaI sites were converted to BamHI-PflMI-Sfil-PflMI sites (SmaI is destroyed). Other part of the vector is untouched. The CDNA is inserted between two PflMI sites in T3 (5') to T7 (3') direction. Library materials provided by G. Elgar (UK Kawakami, M. Sasaki, S. Sugano, K. Kikuchi and S. Watabe (University of Tokyo, Institute of Medical Science and Biotechnology)."
                                                                                 /tissue_type="inner bark"
/clone_lib="Cryptomeria ja
                                                                                                               /organism="Cryptomeria japonica"
/mol_type="mRNA,"
/db xref="taxon:3369"
/clone="CC2407"
                                                                                                                                                                                               Location/Qualifiers
                        7.6%;
51.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.7%;
      Score 34.8; DI
Pred. No. 81;
0; Mismatches
         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 1
Pred. No. 72;
0; Mismatches
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a inner bark Cryptomeria japonica cDNA
                                                                                 japonica
                                     BB
    77;
                                   9;
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                                  Length 480;
                                                                                inner bark"
    Indels
                                                                                                                                                                                                                                                                                Japan
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    0,
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RESULT 13
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AU241511/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                            173
                                                                                                                              171
                                                                                                                                                                     233
                                                                                                                                                                                                         111
                                                                                                                                                                                                                               293 TETRCTTGCCGGGCGTACGGGAAGCAGGGGATGACGGCGGTGACCCGGGGACGACGAGGCGA
                                                                                                                                                                                                                                                                                51
BJ006097
                                                                                                                                                                                                                                                                                                                    70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: naruse@biol.s.u-tokyo.ac.jp
This clone was isolated from UV irradiated OLHNI
library (OLc) 5' end sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Alyona Pepartment of Biological Sciences
Department of Biological Sciences
Graduate School of Science, University (
Anno 7-3-1. Bunkyo-ku, Tokyo 113-0033,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Naruse, K., Mitani, H. and Tanaka, M.
Medaka EST Project in University of Tokyo (2001)
Unpublished (2001)
Contact: Kiyoshi Naruse
                                                                                                                                                                                                                                                                                                                               7.6%;
Similarity 54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                     TAGTTCCGGCCCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 81-3-5841-4443
Fax: 81-3-5841-4410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryzias latipes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU241511 406 bp mRNA linear EST 15-JAN-: AU241511 UV irradiated OLHNI cell line cDNA library (OLC) Oryzii latipes cDNA clone OLC53.01d similar to pir T16763 hypothetical protein R151.2 - Caenorhabditis elegans, mRNA sequence.
AU241511
                                                                                                                              TGCACTGCA
                                                                                                                                                      TCTTGCAGGCGTTGATCATGATCAGCAGCTCCATCAGGTTGTCGTTGATCTCACCGCAGC 174
                                                                                                                                                                                                                                                            TGCTCTGGCTGGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryzias latipes (Japanese medaka)
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(OLc)"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:8090"
/clone="OLc53.01d"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryzias latipes"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    strain="HNI"
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Pred. No. 86;
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                                                                                                                                                                                                                                                                                                                                             Length 406;
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                                                    Kohara,Y., Shin-i,T., Kimura,T., Narita,T., Jindo,T. Medaka BST Project in Takeda's lab Unpublished (2001)
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
                                                                                                                                                                                                  Oryzias latipes (Japanese medaka)
Oryzias latipes
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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BJ006097.1 GI:17359814
EST.
Center For Genetic Resource Information National Institute of Genetics
                 Contact: Tadasu Shin-i
Center For Genetic Res
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BJ001420.1 GI:17361687
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Kohara,Y., Shin-i,T., Kimura,T., Narita,T.,
Medaka EST Project in Takeda's lab
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Acanthomorpha; Acanthopterygii; Percomorpha; Atheri
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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Contact: Tadasu Shin-i
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Location/Qualifiers
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/clone_lib="MF01SSA cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="MF01SSA088D11"
/sex="mixture of female and
/tissue_type="whole embryo"
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/strain="Hd-rR"
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Pred. No. 94;
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Medaka EST Project in Takeda's lab
Unpublished (2001)
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Oryzias latipes
Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Teleostei; Euteleostei; Neoteleostei;
Actinopterygii; Neopterygii; Teleostei; Atherinomorpha;
Acanthomorpha; Adarianichthyidae; Oryziinae; Oryzias.
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70; Conserv
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                       Center For Genetic Resource Information National Institute of Genetics
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Location/Qualifiers
                                                                                                                                                                                                                                                                                           Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                 Contact: Tadasu Shin-i
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                                                                                                                                                                                                                                      tshini@genes.nig.ac.jp
Location/Qualifiers
                                                    /sex="mixture of female and
/tissue_type="whole embryo"
/dev_stage="segmentation sta
/clone_lib="MF01SSA cDNA"
                                                                                                                                                              /mol_type="mRNA"
/strain="Hd-rR"
                                                                                                                          clone="MF01SSA014A01"
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(rissue type="whole embryo"
dev stage="segmentation stage 20
(clone_lib="MFO1SSA cDNA"
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(mol_type="mRNA"

(strain="Hd-rR"
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Pred. No. 98;
O; Mismatches
   Score 34.6;
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Search o	В	γŞ	DЬ	Ş	DЪ	Ş	Matches
Search completed: March 16, 2004, 04:29:12 Job time : 2235.91 secs	267 CGCTCTGCA 259	171 TGCACTGCA 179	327 TOTTGCAGGCGTTGATCATGATCAGCAGCTCCATCAGGTTGTCGTTGATCTCACCGCAGC 268	111 TAGTTCCGGCCCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACA 170	387 TOTCCTGCCGGCGTACGGGAAGCAGGGGGATGACGGCGGTGACCGGGGACGACGAGGCGA 328	51 TGCTCTGGCTGGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCAA 110	Matches 70; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

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Minimum
Maximum
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10077.856 Million cell updates/sec
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## REFERENCE AUTHORS TITLE VERSION KEYWORDS SOURCE ORGANISM RESULT 1 I44909 LOCUS DEFINITION ACCESSION Result No. JOURNAL 238.4 238.4 238.4 238.4 237.2 237.2 237.2 236.8 236.8 228.6 228.6 228.6 228.6 228.6 228.6 228.6 228.6 228.6 228.6 236.8 216.8 412 412 404 404 403 403 397 288 Unknown. Unknown. 1 (bases 1 to 456) Doran, J.L., Kay, W.W., Collinson, S.Karen. and Clouthier, S.C. Methods and compositions comprising the agfA gene for detection Salmonella Patent: US 5635617-A 58 03-JUN-1997; I44909 49 Sequence 58 from patent US I44909 Unclassified. I44909.1 90.5 2067 88.8 5103 88.8 22411 88.4 301983 87.1 1048 63.3 1468 52.3 15046 52.3 15046 52.3 15046 52.3 17046 52.3 15047 52.0 2920 51.9 648 51.9 648 50.1 1711 50.1 1711 50.1 3273 49.8 306358 42.8 2883 42.8 2883 42.8 292504 37.2 292504 37.2 292504 37.2 292504 37.2 10370 37.2 10370 37.2 10370 37.2 10370 37.2 10370 37.2 10370 Match 9.2 2000 9.2 112243 7.9 114866 7.9 298900 7.8 153232 7.8 185224 7.8 186228 7.8 2916 7.8 2926 7.8 3315 7.7 5014 7.7 12641 7.7 12641 7.7 149980 7.6 301727 7.6 301725 10.6 GI:2469622 Length 1 CSP515700 ECCSGABDG AE000205 D90741 CFR515701 AX814811 ECCCSGAA AF275733 AE005315 AP002554 AP002554 AP002554 AP002559 SEU5320 AE016759 ESA515702 SEU53207 AE016981 AF237726 D90742 ECC131756 AX814809 AX814809 AX814798 AX814809 AX814798 AX814798 AX814809 AX814798 AX655393 AC146945 OSJN00093 AC024086 AC009358 AC009358 AC009358 AC009358 AC009358 AC009358 AC009358 FAU26221 PFPFPRNA AE014731 AX492785 AX553952 AE016960 BX248356 AE008749 AL627269 AE016840 STAGFBA I44908 SEU43280 STAJ2301 **I44909** 456 bp | US 5635617. ALIGNMENTS DNA linear AJ515701 Citrobact AX814811 Sequence L04979 Escherichia AF275733 Escherich AE005515 Escherich AE005515 Escherich AE016759 Escherich AE016759 Escherich AE016759 Escherich AE015131 Shigella AE015131 Shigella AE015131 Shigella AE015131 Shigella AE015131 Shigella AE015131 Shigella AE015131 Shigella AE016981 Shigella AE01742 Escherichia AU131756 Escherichia AU131756 Escherichia AU131756 Escherichia AU131756 Escherichia AU131758 Equence AX814798 Sequence AX814798 Sequence AX814798 Sequence AX814606648 Oryza sat AL606648 Oryza sat AL606648 Oryza sat AL0009358 Human Chr AC014084 Homo sapi AC014084 Homo sapi AC014084 Fowl aden AJ554049 Fowl aden AJ554049 Fowl aden AJ554049 Fowl aden U43280 Salmonella AJ002301 Salmonell AE008749 Salmonell AL627269 Salmonell AL627269 Salmonell AJ000514 Salmonell I44908 Sequence 56 AJ515700 Citrobact X90754 E.coli csgG AE000205 Escherichia U26221 Fowl adenov X63648 P.falciparu AE014731 Bifidobac AX492785 Sequence I44909 Sequence Description PAT 07-OCT-1997 Sequence Coxiella of.

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                                                                        Salmonella enteritidis agfBAC operon encoding
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J. Clin. Microbiol. 31 (9), 2263-2273 (1993)
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1 (bases 1 to 2067)
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, Clouthier,S.C.,
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Collinson, S.K., Doran, J.L., Banser, F.A. and Any, ......
Direct Submission
Submitted (13-DEC-1995) S. Karen Collinson, Biochemistry and Microbiology, University of Victoria, P.O. Box 3055 Petch Bldg., Victoria, BC VBW 3P6, Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium
Salmonella typhimurium
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                             Submitted (29-OCT-1997) Romling Karolinska Institute, MTC, Box : Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Romling, U., Bian, Z., Hammar, M., Sierralta, W.D. and Normark, S. Curli fibers are highly conserved between Salmonella typhimurium and Escherichia coli with respect to operon structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cegA gene; cegB gene; cegC gene; cegD cegG gene.
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AJ002301
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Salmonella typhimurium
cegC genes.
                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 5103)
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:sgG, csgF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                         mling U.,
Box 280,
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                                                                                                                                                                                                                                                                                                                         of Bacteriology,
S-17177, SWEDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCT 15-NOV-2000
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                                                                                 complement (2869. .2874)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALAQTEEALNRRQIDQTLLSTSDLARDEF" complement (2064. . . 2714)
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                                                                                                                                   complement (2869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (2064. .2714)
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transl_table=11
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                                                                                                                                                                                                                                                                            Bacteria; Profeobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriacee; Salmonella.

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                                        The Salmonella typhimurium Genome Sequencing Project Direct Submission
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Salmonella typhimurium LT2
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AE008749.1 GI:16419641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGGATTCCACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
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(29-MAR-2001) Genome Sequencing Center, Department of
                                                                                                                                                                                                                                       (6858), 852-856 (2001)
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                                                                                                                                                to 22411)
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Pred. No. 1.6e-105;
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of 220 of the complete
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	gene CDS			CDS	RBS	gene		Bource	PRATTIBES	~~~~	70 mm	2222	COMMENT
/gene="similar to E. coli orf, hypothetical protein /notes "similar to E. coli orf, hypothetical protein (AAC75480.1); Blastp hit to AAC75480.1 (285 aa), 29% identity in aa 15 - 264" /codon_start=1 /codon_start=1 /transI table=11 /transI table=11 /producE="putative transcriptional regulator" /producE="putative transcriptional regulator" /protein_id="AAL20058.1" /db_rotein_id="AAL20058.1" /db_xref="Gi:16419643" /translation="MEPQOPPLKPGKILDTLGAMQKSLTRASQRIAQYILAFPRQVTQ SSIADLSRETQAGEATVIRFCRTUGYKGFQDFKMDLAIELATTESDDSSPLLDAEVSE SDDAHAIGLKLQNTISNVLSETLANLLDMQQVLGVVDALRHCHSVYIFGVGSSGITALD MKHKLMRIGLRGDAVSNNHFMYMQATLLKAGDVAMGVSHSGTSPETVHSLRLARQAGA	complement (14142303) /gene="STM1127" complement (14142295)	Component " /protein_id="AAL20057.1" /protein_id="AAL20057.1" /protein_id="AAL20057.1" /db_xref="GI:16419642" /db_xref="GI:16419642" /translation="MCAHRRVQEHAGDVYLOLKYLSMGRQKAVIKARREAKRVLRRDS /translation="MCAHRRVQEHAGDRYLOLKARNEAQAHYLNAIDSKQLIFAT RSHKQREEESVTSLVQMGGVEAGMARDSRDTSPVKARNEAQAHYLNAIDSKQLIFAT GEAGCGKTWISAAKAAEALIHKDVERIIVTRPVLQADEDLGFLPGDIAEKRAPYFRPV YDVLLKRLGASFMQYCLRPEIGKVEIAPPAYMRGRTFENAVVILDEAQNVTAAQMKMF LTRLGBNVTVIVNGDITQCDLPRGVRSGLSDALERFEEDEMVGIVHFNKDDCVRSALC ORTLHAYS"	/gener product   PhoB-dependent, ATP-binding pho / notes "similar to E. coli PhoB-dependent, ATP-binding pho regulon component; may be helicase; induced by P starvation (AAC74105.1); Blastp hit to AAC74105.1 (354 aa), 92% identity in aa 71 - 354" / codon starte1 / transI table=11 / transI table=11 / product= "PhoB-dependent ATP-binding pho regulon	/gene="puon" /note="putative RBS for phoH; RegulonDB:STMS1H001398" 4541308	/note="synonym: STM1126" 434439	/note="LTZ" 434. 1308 /gene="phoH"	/organism="Salmonella typhimurium LT2"  /mol_type="genomic DNA"  /strain="LT2; SGSC 1412; ATCC 700720"  /db_xref="ATCC:700720"  /db_xref="taxon:99287"	122411	This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one mil subclone.	The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and ReguonDB; http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset	EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EcoCyc; http://ecocyc.PangeaSystems.com/ecocyc/	Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/	Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 AI43283
gene RBS		gene CDS	RBS				gene	RBS				gene · cDS	RBS

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/note="putative RBS for STM1128; RegulonDB:STMS1H001400"
complement(4413. .5099)
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Blastp hit to AAC76255.1 (229 aa), 70% identity in aa 1 -
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/gene="STM1129"
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AFDASFRSRPVDIDSLLTRIRLHGLLAMADCSTVNEGISCHQKGIEFIGTTLSGYTGP
AFDASFRSRPVDIDSLLTRIRLHGLLAMADCSTVNEGISCHQKGIEFIGTTLSGYTGP
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/gene="STM1128"
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db_xref="GI:16419646"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AAC77266.1); Blastp hit to AAC77266.1 (404 aa), 41% identity in aa 40 - 403" (codon start=1 table=11
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;599. .6759
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transl_table=11
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6793. .6798 /gene="STM1131" /note="putative

RBS for STM1131; RegulonDB:STMS1H001402"

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ACCESSION
VERSION
                                                                                                                                                                RESULT 5
AL627269
                                                                                                                 DEFINITION
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Best Local
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                        Salmonella enterica serovar Typhi complete chromosome; segment 5/20, AL627269 AL513382
AL627269.1 GI:16502231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGTCAATACGGCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTAGGCCAGGGTGCGGATAACAGTACTATTGAACTGACTCAGAATGGTTTCAGAAACAAT 18068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCGTČGTTČCAČAATGGGGGGGGGGGGGGGAAATCATAACGGCGGCGGCAATAGTTČCGGC 17888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to E. coli putative transport protein (AAC77235.1); Blastp hit to AAC77235.1 (425 aa), 57% identity in aa 25 - 418" /codon_start=1 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative sugar transport protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="putative RBS for STM1132; RegulonDB:STMS1H001403"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="STM1132"
7768. .7773
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ieklengigfyvdasyksggvdgeqdkhlsdlvanaielgvsynykyvdnfvlqpgfi
fesgpdtsiykpylrggynfdsgvymagryrydyarktanysddektnrfdtyigyvf
Delkleynfimmdsdqikfdnkktnyehnvalawklnksftpyvevgnvavrnntder
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/protein_id="AAL20062.1"
/db_xref="GI:16419647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="STM1132"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
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Pred. No. 1.
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                                                                                   DNA linear BCT 04-JUL-20
(Salmonella typhi) strain CT18,
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nes 32;
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Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebahia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Stevens, K., Whitehead, S. and Barrell, B.G., Skelton, J., Complete genome sequence of a multiple drug resistant Salmonella Nature 413 (6858), 848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CBIO 18A, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (URL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E-mail: parkhill@sanger.ac.uk
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Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Location/Qualifiers
                      /note="Pfam match
family M1, score 2
1060. 1089
gene="STY1078"
                                                                                                gene="STY1078"
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/db_xref="GI:16502232"
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to AMPN_ECOLI (869 aa),
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/transT_table=
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Typhi"
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strain="CT18"
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                                   h to entry PF01433 Peptidase_M1,
245.10, E-value 1.9e-84"
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94% identity in 869 aa o
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/translation="MMRIKPDDNWRWYYDEEHDRMMLDLANGMLFRSRFSRKMLTPDAFCPTGFCVDDAALYFSFEEKCRDFELTKEQRAELVLNALVAIRYLKPQMPKSWHFVAHGEMMTFGTGDAASVWLSDTAEQVNLLVVEPGENAALCLLAQPGVVIAGRTMQLGDAIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Orthologue of E. coli YCBW_ECOLI; YCBW_ECOLI (192 aa), 90% identity in 180 discrepency in position of translational
                                                             RCPAGVQMEQFRPNLVVSGVAAMEEDSWKVLRIGDVIFDVVKPCSRCIFTTVSPEKGQ
KHPSGEPLATLQAFRTAQDNGDVDFGQNLIARNSGVIRVGDEVEILATAPAKAYGATT
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                                                                                                                                                                                                                                                                                                                                                                                                      complement (4716. .5825)
/gene="STY1081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (4716. .5825)
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                                            LLEGEVSPLKKSAMGDDGTILSCSCVPKTALRLEN"
                                                                                                                                                                                                                   /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMNDRLKPQVHCHSFSLEQAV"
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/protein_id="CAD08185.1"
/db_xref="GI:16502234"
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4174. .4719
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3874. .3936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Pfam match to entry PF01180 DHOdehase, Dihydroorotate dehydrogenase, score 563.50, E-value
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KVYAYAGYIAINISSPNTFGLRTLQYGDALDDLLTAIKVKQNDLQVIHHKYVPVAVKI
APDLCEEELIQVADSLLRHNIDGVIAINTTLDRSLVGMKNCQOTGGLSGRPLQLKST
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                         /note="Orthologue of E. coli P75863; Fasta hit
(369 aa), 86% identity in 367 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="STY1079"
/note="PS00912 Dihydroorotate dehydrogenase
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co PYRD_ECOLI (336 aa), 95% identity in 336 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="STY1079"
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                     .4955)
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D aa overlap. N
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Query Match
Best Local Similarity
89146 GTAGGCCAGGGTGCGGATAACAGTACTATTGAACTGACTCAGAATGGTTTCAGAAACAAT 89205
                                                                                                                                                                                                                                                                              CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCGCTCTGCAA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                            GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                     AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
                                                                                                                                                                               AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT 240
                                                                                                                                                                                                                                           CCGGATTCCACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                                                                                                                                                                                    GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCCGGG 89025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Fasta hit to YBIT_ECOLI (530 aa), 32% identity in 526 aa overlap Fasta hit to YJJK_ECOLI (554 aa), 34% identity in 524 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Pfam match to entry PF01170 UPF0020, Uncharacterized protein family UPF0020, scc E-value 3.7e-231"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRGYRDRTGLAPIKETLAAAIVMRSGWQPGTPLLDPMCGSGTLLIEAAMWATDRAPGL
HRGHWGFSGWAQHDBAIWQBYWAEAQOTRARKGLAEYSSHFYGSDSDARVIERARSNAR
RAGIGELITPEVKDVAQLSNPLPKGPYGTVISNPPYGERLDSDPALIALHSLLGFTMR
KOPGGWNLSLFSASPDLLGSLQLRADKQPKAKNGPLDCVQKNYHIAETTADSKPATVA
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DAQKARQRLFDIIAATLSVLGIPPNKLVLKTRERQKGKNQYQKMSEKGEFLEVSEYNA
RLWYNLTDYLDTGLFLDHRIARMLGEMSKGKDFLNLFSYTGSASVHAGLGGARNTTI
VDMSRTYLEWAERNLRLINGLSGRAHRLIQADCLGWLREANBORDLIFIDPFTENSKR
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5924. .8032
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/gene="STY1083"
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/gene="STY1083"
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yQSLmmsrlasriilpmgeckvysdldlyfgvqainmteifnpgatfavhfsglndti
RNSQYGamkvkdaivdaftrknlprpnvdrespdlrinvmlnketasialdlsgdglh
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/db_xref="GI:16502236"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-SEP-2002) Laboratory of Genetics, University of Wisconsin - Madison, 445 Henry Mall, Madison, WI 53706, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salmonella enterica subsp. enterica serovar Typhi Ty2
Balmonella enterica subsp. enterica serovar Typhi Ty2
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.

1 (bases 1 to 301983)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 of the complete genome. AE016840 AE014613 AE016840.1 GI:29137797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGTCAATACGGCGGT 89265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATACGGCGGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 301983)
                                                                                                                                                                                                                                                      /transl tart=1
                                                           complement (844. .1797)
                                                                                                               complement (844. .1797)
                                                                                                                           REFWCRGYYVDTVGKNTAKIQDYIKHQLEEDKMGEQLSIPYPGSPFTGRK"
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Salmonella typhi CT18"
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/note="corresponds to STY1223 from Accession AL513382:
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IS200"
                                                                                                                                                                                                                                                                                                                                                         gene="tnpA"
                                                                                                                                                                                                                                                                                                                                                                                                                              complement (164. .622)
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                                                                                                                                                                                                                                                                                                                                                                                                             gene="tnpA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mol_type="genomic DNA"
strain="Ty2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .301983
                                                                                                                                                                                                                                                                                                                                       _tag="t1735"
                                                                                                                                                                                                                                                                                                                                                                                          _tag="t1735"
                                                                                                                                                                                                                                                                  _table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sm="Salmonella enterica subsp. enterica serovar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301983 bp
                                                                                                                                                                                                                                     insertion sequence
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                                                                                                                                                                                                                                                                                                            Accession AL513382:
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                                                                                                                                                                                                                                         element
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Salmonella typhi CT18"
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Salmonella typhi CT18"
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TGSLGGLLTFRSQDLDQTRNTLGQLALAFADAFNAQHTKGYDADGNKGKDFFSIGSPV

VYSNSNNADKTVSLTAKVVDSTKVQATDYKIVFDGTDWQVTRTADNTTFTATKDADGK

VYSNSNNADKTVSLTAKVVDSTKVQATDYKIVFDGTDWQVTRTADNTTFTATKDADGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="flgI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="fl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEIDGLKVTVGTGAQKNDSFLLKÞVSNAIVDMNVKVTNEAEIAMASESKLDÞDVDTGD
SDNRNGQALLDLQNSNVVGGNKTFNDAYATLVSDVGNKTSTLKTSSTTQANVVKQLYK
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                                                                                                                                                                                                                                                                                                                                                                                                                    locus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="flagellar hook-associated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MRISTQMMYEQNMSGITNSQAEWMKLGEQNSTGKRVTNPSDDPI
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/salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (1812. .3473)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein_id="AA069361.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="flgK"
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                                                                                                                                                                                                                                                                                                                                                                                                             _tag="t1739"
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                                                                                                                                                                                                                                      protein
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CDS

gene CDS

VAQGNLSVTVNRQLNVNQPNTPFGGGQTVVTPQTQIDLRQSGGSLQSVRSSANLNSVV

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                               gene
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Salmonella typhi CT18"
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VETSNVNVAEELVNMIQVQRAYEINSKAVSTTDQMLQKLTQL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trānslation="MOKYALHAYPWALMVATUTGCAWIPAKPLVQGATTAQPIPGPVPVANGSIFQSAQPINYGYQFLEFDRRPRINTGDTLITULOENVSAKSSSANASROGKTSFQFTGTVAPVARGIVARVATUTGGLFGARSAGRASAROGKTSGANASAUTFSGTTLTTVDQVILARULLAVVGEKQIAINAGCTEFIRFSGVVNPRTISGSNSVPSTQVADARIEYVGNGYINEAQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="corresponds to salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (7146. .7901)
/gene="flgF"
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Accession AL513382: Salmonella typhi CT18"
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Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RALNALGATPMDLMSILQSMQSAGCLRAKLEII"
complement(5597. .6295)
                                                                                                                                                                                                                                                                                                 complement (7922. .9133)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGWLQRFFLNLSPM"
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transl_table=11
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88.4%;
92.8%;
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Score 403.2; DB 1;
Pred. No. 5.8e-105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STY1217
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                Length 301983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        precursor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
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STAGFBA
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VERSION
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MEDLINE
PUBMED
                                                                                                                                                                                                                                                             AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
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                                                                                     SGS
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Submitted (14-JUL-1997) Sukupolvi S.S., University of Turku, Kiinanmyllynkatu,
                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1048)
Sukupolvi, S.S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Normark, S.J. and Rhen, M.

Expression of thin aggregative fimbriae Salmonella typhimurium SR-II with mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agfA gene; agfB gene.
Salmonella typhimurium
Salmonella typhimurium
Bacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STAGFBA
Salmonella typhimurium
AJ000514
AJ000514.1 GI:2275119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sukupolvi,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Infect. Immun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 36891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCACCATCGACCAGTGGAACGCTAAAAACTTCCGATATTACTGTCGGCCAATACGGCGGT_360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTAGGCCAGGGTGCGGATAACAGTACTATTGAACTGACTCAGAATGGTTTCAGAAACAAT 37011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGGATTCCACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGG
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                                                                                                                                                                                                                                                                                ocation/Qualifiers
                                                                                            gene="agfB"
                                                                                                                                   gene="agfB"
                                                                                                                    . 553
                                                                                                                                                                                                                                                          .1048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gordon, J.I.,
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                                                                                                                                                                                                                                                                                                                              Medical Biochemistry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promotes interaction of small intestinal epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bian, Z.,
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gene

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Query Match Best Local ! Matches

419;

Conservative

0

Similarity

87.1%; 92.1%;

Score 397.4; Pred. No. 1.9e 0; Mismatches

No. 1.9e-103

Indels Length

0;

Gaps

60

DB 1;

1048;

653 121

CCGGATTCCACGTTGAGCA

TTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA

ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTGGCT ATGAAACTTTTAAAAGTGGCAGCAATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT

593

61

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CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
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AUTHORS
TITLE
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
CSP515700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
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Best Local S
Matches 306
                                                                                                  gene
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                                                                                                                                                                                                                                                                                                                                Zogaj,X., Bokranz,W., Nimtz,M. and Romling,U.
Production of Cellulose and Curli Fimbriae by Members of the Fami.
Enterobacteriaceae Isolated from the Human Gastrointestinal Tract
Infect. Immun. 72.(7), 4151-4158 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                               Citrobacter sp. Fec2
Citrobacter sp. Fec2
Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AJ515700.1 GI:31790491 csgA gene; csgB gene; csgD gene; curlin-csgA protein; csgA gene; csgD gene; curlin-csgA protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306;
                                                                                                                                                                                                                                          Direct Submission
Submitted (11-NOV-2002) Romli
Center, Karolinska Institute,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                          Romling,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSP515700 2889 bp
Citrobacter sp. Fec2 csgB gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteriaceae; Citrobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACGCCGCGCTGGTTAATCAGACCGCATCTGATTC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCATCGACCAGTGGAACGCTAAAAACTCCCGATATTACTGTCGGCCAATACGGCGGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTA
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                                                                                                                                                                                                                                                                                                                          (bases 1 to 2889)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
operon"
/codon_start=1
                                                               complement (212.
                                                                                             complement (212.
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                                                                                                            country="Germany"
                                                                                                                                                                               /isolate="Fec2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Pred. No. 4.5e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                   Romling U., Microbiology and Tumorbiology inte, Box 280, S-17177 Stockholm, SWEDEN
                                                                                             .862)
                         for transcription of the csgBA
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AUTHORS
                                                                                                                                         RESULT
144908
                                                                                                                             Locus
    JOURNAL
                        TITLE
                                                                 ORGANISM
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                 1 (bases 1 to 361)
Doran, J.L., Kay, W.W., Collinson, S.Ka
Methods and compositions comprising
                                                                                                      Sequence
I44908
                                                     Unclassified
                                                                          Unknown.
                                                                                                                             I44908
 US 5635617-A 56
                                                                                                               56 from patent
                                                                                             GI:2469621
              Collinson, S.Karen. and Clouthier, S.C.
03-JUN-1997;
                                                                                                               361 bp
US 5635617.
                                                                                                                        DNA
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                for detection
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421 953 361 893 301 833 241 773 181 713

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GGTTTTGGCAACAACGCACCGGCTAACCAGTATAA 1047 GGTTTTGGCAACAACGCCACGGCTAACCAGTATTA 455 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT

420

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360 952

892 300 832

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gtaggeeaggeteeggataacagtaetattgaaetgaeteagaatgettteagaaacaat

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                                                                  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                     GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
                                       GGTTTTGGCAACAACGCCACCGCTAACCAGTACTAA 2571
                                                                                                                                                    AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                           GCCACCATCGATCAGTGGAACGGCAAAAATTCGGACATTACTGTGAGCCAGTATGGTGGA
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                                                                                                                           CATAACGCCGCACTGGTGAACCAGACTGCGTCCGATTCCAGCGTTCTGGTGCATCAGGTT
                                                                                                                                                                                                                                                                                               GTGGGCCAGGGCTCAGATAACAGCACCATCGATCTGACTCAAAAACGGCTTCAAAAACAAC 2415
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                                                                                                                                                                                                                                                                                                                                                                                AGCGACGCTCGTAAATCTGATACGACCATTCATCAGAATGGCTTTGGTAACGGCGCAGAC
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1623. .2078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MKLLQVAAFAAIVVSGSALAGSVPQWGGGGGGGGGGSSSGPESTL
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DQWNGKNSDITVSQYGGHNAALVNQTASDSSVLVHQVGFGNNATANQY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="mfnefhsihghtlllitkpslqatallqhlkqslalsgklhniq
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HINGVYYVADDEERVNNGLQGILRGECYFSQKLASYLITHSGNYRYNSSESALLTHRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hammar,M.
Direct Submission
Submitted (11-AUG-1995) M. Hammar, Karolinska Institutet,
Microbiology and Tumorbiology Center, Box 280, S-171 77 Stockholm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol.
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Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hammar, M., Arnqvist, A., Bian, Z., Olsen, A. and Normark, S. Expression of two csg operons is required for production
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                                                                                                                                             complement (993.
                                                                                                                                                                                                                                                / translation="Morlfilvavmilsgcitapperbaarptimpraggykdlthlpa
ptgkifysvyniqdetgqfkpypasnestavpgatamlvtalkdsrwifiplergglq
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igadtgyqldqiavnlrvvnvstgeilssvntsktilsyevqagvfrfidygrllege
                                 production"
                                                                                                                                                                                     complement (993.
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                                                         /codon_start=1
/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Escherichia/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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| db_xref="GI:1147560"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          product="assembly
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strain="MC4100"
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strain="K12"
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and orfC
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IQTEEALNRRQINQALLSTGDLAHDEF"
IQTEEALNRRQINQALLSTGDLAHDEF"
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729. .4184
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                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="GOA:P39828"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="transcriptional start site for csgDEFG operon"
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                                         GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
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CDS

Direct Submission Submitted (16-JAN-1997) Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

1 (Dases 1 to 10346)

Blattner,F.R., Plunkett,G. III, Bloch,C.A., Perna,N.T., Burland,V Riley,M., Collado-Vides,J., Glasner,J.D., Rode,C.K., Mayhew,G.F., Gregor,J., Davis,N.W., Kirkpatrick,H.A., Goeden,M.A., Rose,D.J., Mau,B. and Shao,Y. Escherichia coli K12 Escherichia coli K12 Blattner, F.R. 97426617 The complete genome sequence of Escherichia coli K-12 Science 277 (5331), 1453-1474 (1997) (bases 1 to 10346) Guy Plunkett III, Laboratory of Genetics, Burland, V.,

10346 bp | K12 MG1655 section

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL Submitted (13 -OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA This sequence was determined by the E. coli Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIH grants HG00301 and HG01428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from E. coli K12 strain MG1655 Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 (e-mail: mark@amber:gatech.edu). Open reading frames that have been correlated with genetic loci are being annotated with CG Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berlyn. A public version of the database is accessible (http://cgsc.biology.yale.edu). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the E. coli (http://www.genetics.wisc.edu): *** The E. coli K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein- or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoll@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459
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Plunkett, G. III.
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                                                                                                                                                                                                                                                                 /translation="mcnirkkspyfrtssslnmavrggltrfarpagspltaftvcpt
gcrqlstpgrgfssprcvqytkkkpvlsyelffkyggeggidslrspcgqpahcvhgl
snwlspvveprsgllippvcaiyekkartfvrall"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MIPDYLTFIRFQDKRNLIYIXAIGLILIGFYWKNAGFTFPSEDI
GVVSGILALVLYNFIEDLKAXWAYKCVTKNIDPSWFKKKQNHKIELFITQDLVAGFLS
LIMLSAMSWGLYQLLPSLYALFLISLLGPLVIELLFRHIRTSYVKQVAISVAKKVKK
SLTRYVLLSVGISTVVNLLTISPLRNSDSFVTEGQWLTFKSIIALLILGGVVLAKIVKY
FLRFSKRYAFLGRLFIQEIDLFFSSENALSTFPAKPLWLRLFILLVIEVMWITLVSVL
ATLYEWRIWFEAYFLLCYVPCLIYYFFYCRFLWHNDFMMACDMYFRWGHFNK"
                                                                                                                                                /note="synonym: b1032"
complement(2111. .2198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /function="putative structure; Not classified"
/note="0137; This 137 aa ORF is 27 pct identical (1 gap)
/1047_residues of an approx. 80 aa protein RS37_YEAST SW:
                                                                                                                                                                                                                                     complement (2111. .2198)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  389. .137
                                                                                                                                                                                                                                                                                                                                                      /product="putative ribosomal protein"
/protein_id="AAC74116.1"
/db_xref="GI:1787269"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VHGLSNWLSPVVDPRSGLLIPPVCAIHEKKARTFVRALL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="orf, hypothetical protein'
/protein id="AAC74115.1"
/db xref="GI:1787268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1494.
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/transl_table=11
/product="orf, h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SW: P47562"
                     note="anticodon: GGA; CG Site No. 17878" (function="RNA; tRNA"
                                                                                       product="tRNA-Ser"
                                                                                                                    gene="serX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="ycdV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MGGGTRCVQYTKKKPVLSYBLFFKYGGEGGIDSLRSPCGQPAHC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="orf; Unknown"
/note="083; This 83 aa ORF is 25 pct identical (7 gaps)
.081 residues of an approx. 616 aa protein ALBU_RABIT SW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="No predicted promoter"
bound_moiety="DeoR predicted site"
1337. _1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="ycdU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="ycdU"
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/db_xref="GI:1787267"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="ycdV"
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product="orf, h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bound_moiety="DeoR predicted site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="central position to predicted promoter: -104"
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0 191 residues of an approx. 288 aa protein Y320_MYCGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="synonym: b1029"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="factor Sigma70; predicted +1 start at 1096049"
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RESULT
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Best Local
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              D90741 15047 bp
Escherichia coli K12 genomic DNA.
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                                                                                                                                          GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                   GGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT
                                                                                                                                                                                                                   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
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                                                                                                                  GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 9448
                                                                                                                                                                                                                                                      GCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGTGGT
                                                                                                                                                                                                                                                                                       GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
                                                                                                                                                                                                                                                                                                                          GTTGGTCAGGCTCAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTCGGTAACAGC
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                                                                                                                                                                                                                                                                                                                                                                                               ACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGCAGAT
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Ksgdndsadyalwhppyemlagrdlkavfalgagvbsilskloahfemlingsvplfr
Ledtgweegodyavsgovlhwperfddyrigonsshwopleyhpethedftigiigagvl
GSKVAQSLQTWRFPLRCWSRTRKSWPGVQSFAGREELSAFLSQCRVLINLLPNTPETH
GIINQOLLEKLEDGAYLLNLARGVHVVEDDLLAALDSGKVKGAMLDVPNREPLPPESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="factor Sigma70; predicted +1 start at 1097992"
3383. .3410
/note="factor Sigma70; predicted +1 start at 1098094"
3396. .3423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LWQHPRVTITPHVAAITRPAEAVEYISRTIAQLEKGERVCGQVDRARGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative dehydrogenase"
/protein_id="AAC74117.1"
/db_xref="GI:1787270"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to 177 residues
SW: P45637"
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/note="0325; This 325 aa ORF is 32 pct identical (2 gaps)
to 177 residues of an approx. 312 aa protein YPRA_CORGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
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2338. .2365
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Pred. No. 1.7e-57;
0; Mismatches 136;
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                                                                                                                                        The Japan E. coli genome database http:bsw3.aist-nara.ac.jp.
                                                                                                                                                                                                                                                                                                                              Headed by:
Name: Takashi Horiuchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Members: (1995.4
Aiba,H., Baba,T.
                                                                                                                                                                                                      Address: NARA Institute of Science Ikoma, 630-01, Japan E-mail: hmori@gtc.aist-nara.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax:81-7437-2-5669)
Collaboration Information:
                                                                                                                                                                                                                                                                                              E-mail: kishori@nibb.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (E-mail:hmori@gtc.aist-nara.ac.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                   Name: Hirotada Mori
                                                                                                                                                                                                                                                                                                                 Address: National Institute
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Escherichia coli K12
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D90741.1 GI:1651509
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                                                   /mol_type="genomic DNA
/strain="K12"
/db_xref="taxon:8333"
 /clone="Kohara clone #231"
/note="Nucleotide position
                                     /map="23.7-24.0 min"
                                                                                                       organism="Escherichia
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Submitted (29-JUL-1996) Hirotada Mori, NARA Institute and Technology, Res. & Edu. Center for Genetic Info., Takayama, Ikoma, Nara 630-01, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alba, H., Baba, T., Fujita, K., Hayashi, K., Honjo, A., Horiuchi, T., Ikemoto, K., Inada, T., Isono, K., Isono, S., Itoh, T., Kanai, K., Kasai, H., Kashimoto, K., Kim, S., Kimura, S., Kitagawa, M., Kitakawa, M., Wakino, K., Masuda, S., Miki, T., Mizobuchi, K., Mori, H., Motomura, K., Nakamura, Y., Nashimoto, H., Nishio, Y., Oshima, T., Saito, N., Sampel, G., Seki, Y., Tagami, H., Takemoto, K., Wada, C., Yamamoto, Y. and Yano, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The systematic sequencing of the Escherichia coli genome in Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Japan E.coli genome DNA sequencing project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Japan E.coli genome DNA sequencing group
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K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Biology,
                                                                                                                                                                                                                                                                                        Technology,
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8916-5
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Sgo

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/db v=-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAA35822.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTMAPLTRDAISAMWDELEEDSEE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similar to SwissProt Accession Number P45637"
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intergenic region."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="unnamed protein product; ORF_ID:o231#4'
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transl_table=
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                                                                        db_xref="GI:4062610"
                                                                                                                                                                                                                                                                                                   ement (4117.
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Best Local Similarity
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SdS

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CDS

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CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC
                                              AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT 240
                                                                                                                                                                                                                                                 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
                                                                                                                                                                                                                                                                                             ATGAAACTTTTAAAAGTAGCÄGCAATTGCÄGCÄÄTCGTATTCTCCGGTÄGCGCTCTGGCA 7772
                                                                                                                                                                                                                                                                                                                               ATGAAACTITTAAAAGTGGCAGCAGTTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
ACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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S"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (5418. .5807)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="csgB"
7217. .7672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (5812. .6462)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="cagD"
/note="ORF_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="csgD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CagF precursor.
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/note="ORF_ID:o231#6
similar to SwissProt Accession
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="Probable csgAB operon transcriptional regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="Curli production
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transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                       52.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 238.4; DB 1;
Pred. No. 1.7e-57;
                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .6462)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           csgA gene; csgB gene; csgD gene; curlin-csgA protein; component of curlin monomers; regulatory protein. Citrobacter freundii
Citrobacter freundii
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AJ515701.1 GI:31790495
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/gene="csgD"
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Karolinska Institute, Box
Location/Qualifiers
/codon_start=1
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1624. .2082
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/db_xref="GI:31790496"
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                                                                                                                                                                                                                                                                                                                                                                      country="Germany"
                                                                                                                                                                                                                                                                                                                                                                                    /isolation_source="faeces"
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(db_xref="taxon:546"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Citrobacter
/mol_type="genomic DNA"
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Sequence
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                                                                                       Escherichia coli
Escherichia coli
Bacteria; Proteobacteria;
Enterobacteriaceae; Escher
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Patent: WO 03064446-A 15 07-AUG-2003; Hansa Medical Research Aktiebolag (SE) Location/Qualifiers

Bjoerck, L.,

Olsen, A.,

Wikstroem, M.

and Herwald,

Escherichia.

Enterobacteriales;

Peptides

AX814811.1

GI:39104001 from Patent

15

456 bp WO03064446.

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On Jun 11, 1993
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                                                                              l (bases 1 to 648)
Olsen, A., Arnqvist, A., Hammar, M., Sukupolvi, S. and Normark, S.
The RpoS sigma factor relieves H-NS-mediated transcriptional repression of csgA, the subunit gene of fibronectin-binding in Escherichia coli in Escherichia coli mol. Microbiol. 7 (4), 523-536 (1993)
                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
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LDQWNGKNSEMTVKQFGGGNGAAVDQTASNSSVNVTQVGFGNNATAHQY"
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this sequence version replaced gi:145630. text: Escherichia coli (sub_strain W3110, Kohara) DNA.
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Pred. No. 4.1e-57;
0; Mismatches 137;
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Matches 319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCGGCAATAGTTCCCGGC
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                            GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
                                                                                                                                  GCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGTGGT
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143. .535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sub_strain="W3110"
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0; Mismatches 137;
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Result
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
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    GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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AAC64629
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Aac64626 AgfA::PT3
Aaq87467 AgfA
Baqual
Aat74142 Salmonell
Aac64617 Salmonell
Aac64625 AgfA::PT3
Aac64625 AgfA::PT3
Aac64628 AgfA::PT3
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Aac64619 EgfA sequ
Aat74141 Salmonell
Aac64619 Escherich
Aaq62646 FNB curli
Aac64619 FNB curli
Acd68807 E. coli C
Aag62646 PNB curli
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Aac63615 E. coli C
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ALIGNMENTS	ABL09481	AAA09500	ACD68809	AAD54217	AAD54223	ABL06749	ABA90521_17	ABL51711	AAD27016	AAD29125	AAL41133	AAA14939	AAD00669	AAX09007	ABQ81847	ADA71938	ACD68808	AAC64616	AAC64605	ACF36148	AAC64606	AAC64621
	Abl09481 Drosophil	Aaa09500 V. furnis	Acd68809 E. coli K	Aad54217 Streptomy		Ab106749 Drosophil	Continuation (18 o	Abl51711 Erwinia a		Aad29125 Erwinia a	Aal41133 Hypersens	Aaa14939 DNA encod	Aad00669 Erwinia a	Aax09007 Hypersens	Abq81847 Bifidobac		Acd68808 E. coli K	Aac64616 S. enteri	Aac64605 SefA (SEF	Acf36148 E. coli C	Aac64606 SefA (SEF	Aac64621 Leishmani

## ALI GIVINEIVI S

RESULT 1 AAC64626

AAC64626 standard; DNA; 456

26-FEB-2001 AAC64626;

(first entry)

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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                                                                                                                                                P-PSDB; AAB36350.
                                                                                                                                                          WPI; 2000-672631/65.
                                                                                                                                                                                                                                        05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                                WO200060102-A2
                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                       Salmonella enteritidis.
                                                                                                                                                                                                                                                                                                                                          Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
vaccine; immune response; immunogen; ds.
                                                                                                                                                                                                                    05-APR-1999;
                                                                                                                                                                                                                                                             12-OCT-2000
                                                                                                                                                                                                                                                                                                                                         vaccine; immune response; immunogen;
                                                                                                                                                                                                                                                                                                                                                                       AgfA::PT3#5 DNA sequence SEQ ID NO:19.
                                                                                                                                                                                                 (UYVI-) UNIV VICTORIA.
                                                                                                                                                                            Doran JL,
                                                                                                                                                                                                                     99US-0127888P
                                                                                                                                                                             Collison SK,
                                                                                                                                                                            Kay WW;
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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the

Disclosure; Page 137; 139pp; English.

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RESULT 2
AAQB7467
ID AAQB
XX AAQB
AC AAQB
AC AAQB
DT 25-M
DT 26-J
XX AgfA
XX AgfA
XX Salm
XX Salm
XX Salm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant AgfA comprising separating an amino acid polymer comprising a recombinant AgfA containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino containing a replacement segment or segments of foreign amino contained the segment of segments of the combinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for containing an immune response in an animal. In a fimbrial presentation continuous antigens are presented in high numbers (up to system the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live contained the inserted epitope, and hybrid fimbria are usually strong contained the inserted epitope, and hybrid fimbriae are easy and contained the exemplification of the present invention
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Best Local S
Matches 456
                     Salmonella
                                                         Salmonella; AgfA;
                                                                                               AgfA sequence.
                                                                                                                                   25-MAR-2003
26-JUN-1995
                                                                                                                                                                                           AAQ87467;
                                                                                                                                                                                                                           AAQ87467 standard; DNA;
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                                                   vaccine; genetic immunization;
                                                                                                                                 entry)
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Matches 429
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 456 BP; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 7B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strains,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1994-358275/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-APR-1993;
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GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
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94.1%;
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Pred. No. 3.6e
0; Mismatches
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3.6e-125;
hes 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Col 19-112; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
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P-PSDB; AAW23570.
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29-SEP-1997
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CC The present invention describes a recombinant agfA gene (I) where a CC seguence of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: CC (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) CC directing recombination of a recombinant gene into the chromosome of the homologous species, replacing the native CC comprising species; (3) directing recombination of a recombinant gene in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC comprising separating an amino acid polymer comprising a recombinant AgfA CC comprising separating an amino acid polymer comprising the native CC acid sequence or sequences grown on a Salmonella, E. coli or C acid sequence or sequences grown on a Salmonella, E. coli or C acid sequence or sequences grown on a Salmonella, E. coli or C sterobacteriaceae host cell, from the host cell and introducing the colitory of the expression of recombinant AgfA protein which is useful for CC useful for the expression of recombinant agfA protein which is useful for CC system the heterologous antigens are presented in high numbers (up to System the heterologous antigens are presented in high numbers (up to immunogenicity and adhesion properties relevant for an efficient live
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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                                                                                                                                          Salmonella enteritidis.
Escherichia coli.
Synthetic.
                                                                                                                                                                            Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope; vaccine; immune response; immunogen; ds.
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                                                                                                                                                                                                                                                                                     AAC64629 standard;
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                                                                                                                                                                                                                                                                                                                                                       GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                             AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420
   Doran JL,
                                                                                                                                                                                                                                                                                                                                                                               AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                          GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTAĞĞCCAĞĞĞTĞCĞĞATAATAĞTACTATTĞAACTĞACTCAĞAATĞĞTTTCAĞAAATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTTACCCCATGAAATGGCACAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCGĂTĠĊĊĊĠŦĂĂĂŦĊŦĠĂAACĠACCAŤŦĂĊĊĆAGAGCĠGŦŦATGGŦĀĀCGGCĠĊCGĀŦ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GÉCGTCÓTTCCÁCAÁTGGGGCGGCGGCGGTAATCATAACGGCGGCGGCÁATAGTTCCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCGTCGTTCCACAATGGGGCGGCGGCGGCATAATCATAACGGCGGCGGCAATAGTTCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGĀĀĀĊŦŦŦŔĀĀĀĠŦĠĠĊĀĠĊĀŦŦĊĠĊĀĠĊĀĀŦĊĠŦĀĠŦŦŦĊŦĠĠĊĀĠŦĠĊŦĊŦĠĠĊŦ
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                                                                                                                                                                                                                                        (first entry)
                                             99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                       DNA; 456
Collison SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.5%;
                                                                                                                                                                                                                                                                                     ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.6e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 412.8;
Pred. No. 3.6
 Kay ww;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; DB 3;
3.6e-125;
                                                                                                                                                                                                                                                                                                                                        456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 456;
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WPI; 2000-672631/65.
P-PSDB; AAB36353.
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 138; 139pp; English

The present invention describes a recombinant agfA gene (I) where a CC sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC AgfA, CsgA and AgfA, homologue fimbria subunits, respectively; (2) CC homologous species; (3) directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing an immune response in an animal, CC protein containing a replacement segment or segments of foreign amino CC Enterobacteriaceae host cell, from the host cell and introducing the combinant AgfA (2) comprising an animal in conjunction with a carrier or diluent. (I) is cliciting an immune response in an animal. In a fimbrial prosentation of system the heterologous antigens are presented in which is useful for system the heterologous antigens are presented in high numbers (up to immunogens, which may be important for directing an efficient live insurance in the inserted epitope, and hybrid fimbriae are easy and conjunction the repensive to purify in large amount. The present sequence is given in

Sequence 456 B₽; 114 A; 108 C; 123 G; 111 T; 0 U; 0 Other;

Ϋ́	) B	8	. 당	δ	В	Ś	皮	γQ	Ъ	Ş	Дb	Ş	뫄	8	. 3	ያመይ
															Marches	Query Match Best Local
421 G	361 7	361 /	301 (	301 (	241	241	181	181	121	121	61	61	ь	<b>_</b>	, 4T7	Match ocal
	ATAAC	ATAAC	CCACC	CACC	TAGG	GCAGG	CTGGT	AGCGA'	CCGGA	CCGGA	GGCGT	GGCGT	ATGAA	ATGAP		≅.
GGCAA	eccec	60060	ATCGA	ATCGA	CAGGG	CAGGG	Accce	I CCCC	CTCAAC	CTCAA	CGTTC	CGTTC	ACTIT	ACTT	Conservative	rity
PAACGO	SCTGGT	GCTGG	CCAGTO	CCAGIO	TGCGG	Teces	TGTTG	TAAAT	GTTGA	CGTTGA	CACAAT	CACAAT	TAAAA	TAAAA	ative	84.6%;
CACGG	TAATC	TAATO	GAACG	GAACG	ATAATA	ATAATA	TTACC	ATGATO	GCATT	GCATT	- GGGGC	, 199995	TGGCA	STGGCA	0;	
CTAACC	AGACC	AGACC	CTAAA	CTAAA	GTACT	GTACT	CATGAA	CAGCTG	TATCAC	TATCAC	99099	eecee	GCATT	GCATT		Score 385. Pred. No.
CACGGCTAACCAGTATTAJ	CATCT	CATCI	PACTCC	AACTC	ATTGAJ	ATTGAJ	ATGGC	GTTAC	TACGG	TACGG	GGTAA	GGTAA	CCAGC	CGCAGC	Mismatches	385.6; No. 3.
GGTTTTGGCAACACGCCACGCTAACCAGTATTAA 456	GATTC	GATTC	GATAT	GATAT	CTGAC	CTGAC	ACATGO	ccerer	TTCCGC	Ticce	TCATA	TCATA	AATCG	AATCG	8 44;	.6; DB 3; 3.1e-116;
6	AGCGT	AGCGT	PACTG	IACTG	TCAGA	TCAGA	AGGTT	TGTTA	TAACG	TAACC	rceece	25957	PAGTT	PAGTT		
	AATGG	PAATGG		CGGCC	ATGGTT	ATGGT	ATGGT/	CCCAT	CTGCG	CTGCG	GCGGC	eceec 3	CTGGC	CTGGC	Indels	Length
	TGCGT	TGCGT	AATAC	AATAC	TCAGA	TO ACA	ACGGC	BAAATG	CTTTAI	CTTGC	AATAG:	AATAG	AGTGC	AGTGC	0;	456;
·	AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT	AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT	GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT	GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT	GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAATAAT	GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTTCAGAGAGAG	CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAGGTTATGGTAACGGCGCCGAT	AGCGATGCCCGTAAATATGATÇAGCTGGTTAÇCÇGTGTTGTTACCCATGAAATGGCACAT	CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTTATGATCAG	CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA	GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC	GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCCC	ATGANACTITTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT	ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT	Gaps	
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421

GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456

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RESULT 6
AAC64625
                                                                                                                         directing recombination of a recombinant gene into the chromosome of the Chomologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene; and (4) eliciting an immune response in an animal, (2) comprising a reparating an amino acid polymer comprising a recombinant AgfA (3) comprising a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for sequences antigens are presented in high numbers (up to 500,000 copiese/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in
Query Match
Best Local Similarity
Matches 398; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                             Sequence 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          White AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AgfA::PT3#4 DNA sequence SEQ ID NO:17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immune response; immunogen; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYVI-) UNIV VICTORIA
                                                                                                               exemplification of the present invention
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 136; 139pp; English.
                                                                             BP;
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                                                                           120 A; 110 C; 122
                 79.6%;
87.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collison
 Score 363.2;
Pred. No. 7.3e
0; Mismatches
   0
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                                                                         G; 104 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kay WW,
               .3e-109;
                                   DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fimbrin; epitope,
                                                                           0 Other;
                                   Length 456;
 Indels
0,
Gaps
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RESULT 7
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                                              Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
                       Disclosure;
                                                                                                 WPI; 2000-672631/65.
P-PSDB; AAB36352.
                                                                                                                                                                                                                                                                                                            Salmonella enteritidis.
Escherichia coli.
                                                                                                                                         White AP,
                                                                                                                                                                                           05-APR-1999;
                                                                                                                                                                                                                     05-APR-2000; 2000WO-CA000356
                                                                                                                                                                                                                                                                       WO200060102-A2
                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                   vaccine; immune response; immunogen;
                                                                                                                                                                                                                                                                                                                                                              Salmonella; agfA; chromosomal gene replacement; fimbrin; epitope;
                                                                                                                                                                                                                                                                                                                                                                                           AgfA::PT3#7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA; 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
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                                                                                                                                       Doran JL,
                       Page 137; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence SEQ ID NO:23.
                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                           99US-0127888P
                                                                                                                                         Collison
                                                                                                                                       SK,
                                                                                                                                       Kay ww
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The present invention describes a recombinant agfA gene (I) where

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comprising separating an amino acid polymer comprising a recombinant AgfA protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant AgfA protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong against the inserted epitope, and hybrid fimbriae are usually strong the capainst the inserted epitope, and hybrid fimbriae are easy and the exemplification of the present invention
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Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

White AP,

Doran JL,

Collison

SK,

Kay WW;

2000-672631/65.

(UYVI-) UNIV VICTORIA

05-APR-2000; 2000WO-CA000356

99US-0127888P

WO200060102-A2.

12-OCT-2000

Escherichia

Salmonella enteritidis

response;

mmunogen;

gb

Salmonella;

agfA; chromosomal gene replacement; fimbrin; epitope;

AgfA::PT3#1 DNA sequence SEQ ID NO:11.

Ş 문 δ В Ś 밁 á 밁 á B Ś 밁 S Query Match Best Local Sequence 456 BP; 119 A; 110 C; 120 G; 107 T; 0 U; 0 Other; Local 421 421 361 361 301 241 301 241 181 181 121 121 61 61 397; AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT CATGAAATGGCACATGCAAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGG Similarity GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA GCCACCATCGACCAGTGGAACGCTAAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT GCCACCATCGACCAGTGGAACGCTAAAAACTATGATCAGCTGGTTACCCGTGTTGTTACC GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT ĠĠĊĠŦĊĠŦŦĊĊĀĊĀĀŦĠĠĠĠĠĠĠĠĠĠĠĠĠĠŦĀĀŦĊĀŦĀĀĊĠĠĊĠĠĊĠĠĊĀĀŦŖĠŦŦĊĊĠĠĊ AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT CCGGACTCAACGTTGAGCATTTATCAGTACGGTTACGCTAACGCTGCGCTTGCTCTGCAA GGCGTCGTTCCACAATGGGGCGGCGGCGGCGATAATCATAACGGCGGCGCGCAATAGTTCCCGGC ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT TTGGCAACAACGCCACGGCTAACCAGTATTAA Conservative 79.3%; 87.1%; 0, Score 361.6; Pred. No. 2.5 Mismatches ; DB 3; 59; Length 456; Indels 0, Gaps 420 420 360 360 180 240 240 180 120 60

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Best Local
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121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCGCTTGCAA
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                                                                                                    GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCGAATAGTTCCGGC
                                                                                                                                                   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                                                                                                                                                                  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                                                GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
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87.1%;
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Pred. No. 2.5e
0; Mismatches
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Indels Length 456;

0,

Gaps

180 120 120 60

RESULT 8
AAC64622
ID AAC6
XX
AC AAC6
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AC AAC6
XX
DT 26-F
XX

AAC64622 standard;

DNA;

ВP

26-FEB-2001 AAC64622;

(first entry)

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The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SER17/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbria mubunits, respectively, (2) directing recombination of a recombinant gene into the chromosome of the homologous species, (3) directing recombination of a recombination of a recombination of the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal, agfA comprising separating an amino acid polymer comprising a recombinant AgfA
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DB; AAB36347.
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                                                                                                                                                                                                                                                                                                                                                               Doran JL,
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XX AAC64
XX Z6-FE
XX AgfA:
XX Salmo
KW Vacci
XX Salmo
OS Eschee
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Escherichia coli.
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                                                                                                                 vaccine;
                                                                                                                                    Salmonella;
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                                                                                                                 immune response;
                                                                                                                                                                                                                                                                    standard; DNA; 456 BP
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                                                                                                                                  agfA;
                                                                                                                                                                 DNA sequence SEQ ID NO:27.
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                                                                                                                                    chromosomal
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                                                                                                                 immunogen;
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Pred. No. 2.5e
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unogen; ds.
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2.5e-108;
ches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 456 BP; 115 A; 116 C; 118
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GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
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                                                                                                         AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
                                                                                                                                  AGCGATGCCCGTAAATATGATCAGCTGGTTACCCCGTGTTGTTACCCCATGAAATGGCACAT
                                                                                                                                                                                CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                         CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                                                                                                       GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
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86.8%;
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The present invention describes a recombinant agfA gene (I) where a CC segment of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: (I) use of thin aggregative fimbriae (SERT/TRAP) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CSGA and AgfA-homologue fimbria bubunits, respectively; (2) directing recombination of a recombinant gene into the chromosome of the homologous species, (3) directing recombination of a recombinant gene CC copy of that gene; and (4) eliciting an immune response in an animal, CC comprising separating an amino acid polymer comprising a recombinant AgfA CC comprising separating a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E coli or Enterobacteriaceae host cell, from the host cell and introducing the CC useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for celiciting an immune response in an animal. In a fimbrial presentation CC immunogenicity and adhesion properties relevant for an efficient live communicating the carrier fimbrial subminit protein sare usually strong communicating the carrier fimbrial subminit proteins are usually strong the miniman communication that the carrier fimbrial subminit proteins are usually strong the immunocane which are being are usually strong the immunocane which are the horizal subminit proteins are usually strong the immunocane which has be immorement.
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
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                                           Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                99US-0127888P
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; chromosomal gene replacement; fimbrin; epitope;
response; immunogen; ds.
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86.8%;
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                                                Collison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
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Pred. No. 8
                                              SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                              Kay WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .3e-108;
les 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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P-PSDB; AAB36351.

Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.

Disclosure; Page 137; 139pp; English.

CC Segument of the gene has been replaced by a segment of a foreign DNA CC segument of the gene has been replaced by a segment of a foreign DNA CC sequence which encodes a foreign epitope or antigen. Also described are: (1) use of thin aggregative fimbriae (SEF17/TAF) nucleation depended CC assembly system of strains of Salmonella, Escherichia coli and CC Enterobacteriaceae for the production of fimbriae comprising recombinant CC AgfA, CsgA and AgfA-homologue fimbria subunits, respectively; (2) CC directing recombination of a recombination of a recombination of the chromosome of the homologous species; (3) directing recombination of a recombination of a recombinant gene into the chromosome of the homologous species, replacing the native CC comprising separating an amino acid polymer comprising a recombinant AgfA (2) eliciting an immune response in an animal. (3) contraining a replacement segment or segments of foreign amino CC acid sequence or sequences grown on a Salmonella, E. coli or CC eliciting an immune response in an animal and introducing the colymer into the animal in conjunction with a carrier or diluent. (1) is CC useful for the expression of recombinant AgfA protein which is useful for the expression of recombinant AgfA protein which is useful for CC useful for the hybrid fimbrin protein possesses both the CC immunogenicity and adhesion properties are presented in high numbers (up to CC against the inserted epitope, and hybrid fimbriae are usually strong CC eagainst the inserted epitope, and hybrid fimbriae are easy and CC inexpensive to purify in large amount. The present sequence is given in tx

Sequence 456 BP; 112 A; 113 C; 125 G; 106 T; 0 U; 0 Other;

Length 456;

S 맑 Ś 망 8 밁 S ğ Ş 밁 S 뭐 Ś 밁 Ś Matches Query Match Best Local 181 181 121 421 421 361 361 301 301 241 241 121 395; 61 61 1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT Similarity GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC 120 GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT GTAGGCCAGGGTGCGGATAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG 300 GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCCAATAGTTCCGGC ATGAPACTTTTAPAPAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGG GCACATGCAGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT Conservative 78.6**%**; 86.6**%**; Score 358.4; DB Pred. No. 2.8e-10; Mismatches 0; 1; DB 3; 2.8e-107; 61; 456 Indels 0; Gaps 420 360 240 180 120 420 240 60

456

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RESULT 13
AAC64631
                                                                                                                                                                                           directing recombination of a recombinant gene into the chromosome of the homologous species; (3) directing recombination of a recombinant gene back into the chromosome of the homologous species, replacing the native copy of that gene, and (4) eliciting an immune response in an animal, comprising separating an amino acid polymer comprising a recombinant Agfa protein containing a replacement segment or segments of foreign amino acid sequence or sequences grown on a Salmonella, E. coli or Enterobacteriaceae host cell, from the host cell and introducing the polymer into the animal in conjunction with a carrier or diluent. (I) is useful for the expression of recombinant Agfa protein which is useful for eliciting an immune response in an animal. In a fimbrial presentation existem the heterologous anticens are avecanted in high machane.
                                                     system the heterologous antigens are presented in high numbers (up to 500,000 copies/cell), the hybrid fimbrin protein possesses both the immunogenicity and adhesion properties relevant for an efficient live vaccine, the carrier fimbrial subunit proteins are usually strong immunogens, which may be important for directing an immune response against the inserted epitope, and hybrid fimbriae are easy and inexpensive to purify in large amount. The present sequence is given in the account if in the community in large amount.
      Sequence 456 BP; 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a recombinant agfA gene (I) where a segment of the gene has been replaced by a segment of a foreign DNA sequence which encodes a foreign epitope or antigen. Also described (1) use of thin aggregative fimbriae (SEFI7/TAF) nucleation depended assembly system of strains of Salmonella, Escherichia coli and
                                                                                                                                                                                                                                                                                                                                                                                                                        assembly system of strains of Salmonella, Escherichia coli and Enterobacteriaceae for the production of fimbriae comprising recombinant AgfA, CsgA and AgfA-homologue fimbrin subunits, respectively; (2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant agfA gene having a segment replaced by a foreign DNA sequence which encodes foreign epitope or antigen, expresses recombinant AgfA protein useful for eliciting immune response in animal.
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P-PSDB; AAB36355.
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                                          exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Doran JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence SEQ ID NO:29
    A; 110 C; 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SK,
G; 109 T; 0 U; 0 Other;
                                            invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kay WW;
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                                                             'n
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1 ATGAAACTTTTAAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT

Best Loca Matches

393;

Conservative

٥,

Score 355.2; DB 3; Pred. No. 3.1e-106; 0; Mismatches 63;

Length 456; Indels

0,

Gaps

60

Local

Similarity

77.9%; 86.2%;

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RESULT 14
AAQ73066
ID AAQ73
AC AAQ73
AC AAQ73
AC 25-MA
DT 25-MA
DT 26-JU
DE AGFA
XX Salmo
XX Salmo
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25-MAR-2003
26-JUN-1995
                       26-APR-1993;
                                                                  26-APR-1994;
                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                   10-NOV-1994.
                                                                                                                                                                    WO9425598-A2
                                                                                                                                                                                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Salmonella; AgfA; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AgfA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ73066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ73066 standard; DNA; 361
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                    93US-00054452
                                                                  94WO-IB000207
                                                                                                                                                                                                                               /note= "TAP6 primer (pair with TAF5)"
complement(292. .402)
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "AgfA"
37. .60
                                                                                                                                                                                                                                                                                                                                    /note= "TAF3 primer (pair complement(103. .129)
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                                                                                                                                                                                                                                                                                                                                                                note= "TAF3
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/note=_"TAF5 primer (pair with TAF6)"
                                                                                                                                                                                                                                                                                                                                                                                       *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                 . 69
                                                                                                                                                                                                           "TAF4 primer (pair with TAF3)
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360 360

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AAT74141
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The DNA encodes the Salmonella enteritis27655-3b TnphoA mutant strain agfA gene cloned into pUC19. The DNA and isolated proteins are used in genetic immunization and vaccine compositions, respectively, to elicit immune response to Salmonella in animals (e.g. food producing animals) and humans. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-MAR-2003) to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KING/)
                     primer_bind
                                                                               Salmonella enteritidis
                                                                                                Enteropathogenic bacteria;
                                                                                                                 Salmonella enteritidis 27655-3b TnphoA mutant agfA gene fragment.
                                                                                                                                     25-MAR-2003
30-SEP-1997
                                                                                                                                                                  AAT74141;
                                                                                                                                                                                    AAT74141 standard; DNA; 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 361 BP; 94 A; 93 C; 94 G; 80 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bliciting
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                                                                                                                                                                                                                                                                                                                                                                                                  124 GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCCTTGCTGCAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                  GATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTA
                                                                                                                                                                                                                                                                                 ACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATACGGCGGTAAT
                                                                                                                                                                                                                                                                                                              GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC
                                                                                                                                                                                                                                                                                                                                GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                             AACGCCGCGCTGGTTAATCAGACCGCATCTGATTC
                                                                                                                                                                                                                                                     AACGCCGCGCTGGTTAATCAGACCGCATCTGATTC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vector constructs,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an immune response to Salmonella - using attenuated Salmonella vector constructs, or compsns. contg. fimbrial type proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                    (revised)
(first en
/*tag= a
//abel= agfA_gene_fragment
16. .60
/*tag= b
/label= Primer_TAF5
                                                           Location/Qualifiers
                                                                                                                                     entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.3%;
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                                                                                                enterobacteria;
                                                                                                                                                                                    ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 288.6; DB 2
Pred. No. 2.3e-84;
0; Mismatches 29
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                                                                                                S.enteritidis; antibody;
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   completed: March 15,
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from Salmonella enteritidis 27655-3b TophoA mutant strain. The nucleic acid can be used to provide diagnostic assays for Salmonella and/or enteropathogenic bacteria of the family Enterobacteria. It can also be used to provide proteins and antibodies which can be used for assays. The nucleic acid sequence can be used to provide probes or primers which can specifically hybridise to nucleic acid molecules from greater than 99 of Salmonella strains that are pathogenic to warm-blooded animals relative to nucleic acid molecules from virtually all other microbial organisms. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 361 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated Salmonella gene agfA - used for diagnosis of Salmonella enteropathogenic bacteria of the Enterobacteria family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUN-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents an isolated agfA gene fragment derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Col 107-110; 85pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCGTACCACAGTGGGGCGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGCCCG
AACGCCGCGCTGGTTAATCAGACCGCATCTGATTC 398
                                                                                                                                                                  GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC
                                                                                                                                                                                                                                                                    GATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTA
                                                                                                                                                                                                                                                                                                                                                                           GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC
                                                                                                            ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAAT
                                                           ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAAT
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/label= Primer_TAF3
complement(103..128)
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/label= Primer_TAF4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 288.6; DB 2;
Pred. No. 2.3e-84;
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2004, 17:52:03

Job time : 246.684 secs

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Minimum
Maximum
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Perfect score:
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-120-927-1
US-09-431-614-5
US-09-431-614-5
US-09-489-039A-2195
US-09-489-039A-2195
US-09-489-039A-2195
US-09-489-039A-2195
US-09-489-039A-2195
US-09-252-991A-14225
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US-09-207-844-1
US-08-94-772-1
US-08-95-5386-2
US-08-96-761B-1
US-08-96-386-1
US-08-916-421B-1
US-09-103-840A-2
US-09-910-1527-201
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Sequence 58, Appl Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2152, Ap Sequence 2195, Ap Sequence 2162, Ap Sequence 2162, Ap Sequence 14225, Ap Sequence 14137, A Sequence 6, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 492, Appli Sequence 492, Appli Sequence 201, Appli Sequence 201, Appli Sequence 201, Appli Sequence 201, Appli Sequence 201, Appli
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US-08-233-788A-58  Sequence 58, Application Patent No. 5635617 GENERAL INFORMATION: APPLICANT: COLUMNISTION: APPLICANT: Seatch CURRENT APPLICATION NUMBER: COMPUTER: Hashington COMPUTER: Hashington COMPUTER: Hashington COMPUTER: TAPPLICATION NUMBER: FILING DATE: 26-APR CLASSIFICATION NUMBER: FILING DATE: 26-APR CLASSIFICATION NUMBER: APPLICATION FOR SEQ ID N SEQUENCE CHARACTERISTI LEERAY: (206) 682- TELEFAX: (206)		C C C C C C C C C C C C C C C C C C C	98
US/08233788  es L. Karen S. Karen S. Sharon C. ETHODS AND F SALMONELL 61  Berry ia Center, c-pos/MS-Do Release #1. TA: US/08/233, -1994  TION: 35,570 35,570 35,570 35,570 35,570 35,570 3688: 2-4900 BER: 92004 RMATION: CS: 6031 ANHBERRY O: 58: CS: CS: CS: CS: CS: CS: CS: CS: CS: CS	ALIC	6.5 1077 4 US-09-2 6.5 11521 4 US-09-2 6.5 51259 3 US-09-6 6.5 51259 4 US-09-6 6.4 912 4 US-09-5 6.4 1252 4 US-09-5 6.4 1252 4 US-09-2 6.4 536165 4 US-09-2 6.4 4403765 3 US-09-5 6.4 4411529 3 US-09-5 6.4 4913769 3 US-09-6 6.4 939 4 US-09-9 6.4 1097 4 US-09-9 6.4 1097 4 US-09-9	.6 65792 4 US-09-
MPOSITIONS FOR  1 Fifth Avenue  Version #1.25  8A  403C2	ALIGNMENTS	252-991A-10818 252-991A-10818 2781-891-209 618-166-209 5328-352-2055 548-352-2050 5561-756-29 227-721-29 224-808-1 543-681A-2551 5103-840A-2 5103-840A-2 5976-594-108 976-594-108	596-002-31 582-991
DETECTION		Sequence 10818, A Sequence 209, App Sequence 209, App Sequence 205, Ap Sequence 2040, App Sequence 2040, Appl Sequence 29, Appl Sequence 29, Appl Sequence 1, Appl Sequence 2, Appl Sequence 2, Appl Sequence 2, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 10, Appl	31, A

Query Match 90.5%; Best Local Similarity 94.1%; Matches 429; Conservative

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Score 412.8; DB 1; Pred. No. 1.7e-137; 0; Mismatches 27;

Indels Length 456;

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Gaps

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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/08/233,788A
FILING DATE: 26-APR-194
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C2
TELECOMMUNICATION INFORMATION:
TELEPIONE: (206) 622-4900
TELEFAX: (206) 622-4900
TELEFAX: (206) 622-601
TELEEX: 372836 SEEDANBERRY
SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
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US-08-233-788A-56
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Patent No.
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CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DOTAIN, James L.

APPLICANT: Kay, William W.

APPLICANT: Collinson, Karen S.

APPLICANT: Clouthier, Sharon C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTION

TITLE OF INVENTION: OF SALMONELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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RESULT 3
US-09-120-927-1/c
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/055,108
APPLICATION UNMBER: US 60/055,108
APPLICATION UNMBER: 06-AUG-1977
ATTORNEY/AGENT INFORMATION:
NAME: GOldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1581
TELECOMMUNICATION INFORMATION:
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Patent No. 6262018
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                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/120,927
                                                                                                                                                                                                                                                                                            STREET: P.C.
STREET: P.C.
CITY: Rochester
STATE: New York
TOWNTRY: U.S.A.
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Best Local Similarity 91.3
Matches 306; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kim, Jihyun Francis
APPLICANT: Beer, Steven V.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR
TITLE OF INVENTION: ERWINIA AMYLOVORA AND ITS USE
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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LOCATION: 1...
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P.O. Box 1051, Clinton Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCGTACCACAGTGGGGGGGGGGGGGGTAATCATAACGGCGGCGGCAATAGTTCCGGGCCCG
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EDNESS: double
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                      19603/1581
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Pred. No. 3.1
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APPLICANT: Wei, Zhong-Min
APPLICANT: Wei, Zhong-Min
APPLICANT: Schadding, Richard L.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE ELICITOR-INDUCED STRESS
TITLE OF INVENTION: RESISTANCE
FILE REFERENCE: 21829/41 (EBC-003)
CURRENT APPLICATION NUMBER: US/09/431,614
CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 60/107,243
EARLIER APPLICATION NUMBER: 60/107,243
EARLIER FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 18
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 1344
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US-09-499-039A-403
US-09-499-039A-403
Application US/09489039A
Patent No. 6610836
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; ORGANISM: Erwinia amylovora
US-09-431-614-5
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GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1344 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                            112 AGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTT
                                                                                                                                                                                                                                                                                209 GCTCCGGTTGCCGCATTACCTGATTGTGGCGATAGCAGTGACTTTAACAGTTCCGCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 AGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTT
                                                                                                                                                     89
                                                                                                                                                                                                                                                                                                               52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 GCTCTGGCTGGCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCAAT 111
                                                                                                                                                                                                                                                                                                                                                 67;
                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                   GC 88
                                                                                                                                                                                   GC 173
                                                                                                                                                                                                                                                                                                       GCTCTGGCTGGCGTCGTTCCACAATGGGGGCGGCGGCGGCGGCAAT 111
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Pred. No. 0.09;
0; Mismatches
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Pred. No. 0
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0.09;
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LENGTH: 1218
; TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patent.pm
SEQ ID NO 8976
LENGTH: 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET:054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: FILE REFERENCE: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Klebsiella pneumoniae
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Local Similarity 58.0%;
es 58; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                  268
                                                                                                                                                                                                                                          220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        614 TCGTCACAGCGCTGATCCTCAATATGTTCAGCACCTTTATCGTGCTGTCGGTAATTAACC 673
                                     388 GCATCTGATTCCAGCGTAATGGTGCGTCAGGTTGGTTTT 426
                                                                                                                 328 AACTCCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGTTAATCAGACC 387
                                                                                                                                                                                                                                                                                                                        280 STGRWSYRRAMWRGSKSWGGGSYYRMAGYRSSRWRSWYSAMWRKKKMTCWKGRSSWGSRS 221
                                                                                                                                                                                                                                                                                                                                                                                                     340 GWKYWYYWMTSRGSYRRYKTSAMMGRAKMKKRKKTKKMYWMKGGGKKGGSTYMAMRSRRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 TCTGCAAAGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAAT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               674 CGACGCGGCCGGGCAGCGAGCAGGAAATAAAACTCGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 GECACATECAGECCAEGETECEGATAATAETACTATTEAA 273
40
                                                                                                                                                                                                                                                                                                                                                                                                                                           88 GGTAATCATAACGGCGGCGAATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity.
                                                                                                                                                                                                ATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAA 327
                                                                                                                                                                                                                                                                              GTTACCCGTGTTGTTACCCATGAAATGGCACATGCAGGCCAGGGTGCGGATAATAGTACT 267
                                                                                                                                                                                                                                                                                                                                                             TACGGTTCCGCTAACGCTGCGCTTGCCAAAGCGATGCCCGTAAATATGATCAGCTG 207
  WSKMTYWSMMSCYARKCWRTYAKTYTWMTCMTWGKRTYK 2
                                                                                                                                                                                                                                        TGYYAWMYKKSWCTSRKWMYYKKRRKKWRRKCTSTKRTCYRGSTYKCWKAYYTKKRRKWT
                                                                             YWYYAKRAKWSKRCTWSTTCYCMKYMAKKCWSYWWSMSMMKWGKSMWWKWTYYYYYYMMK 41
                                                                                                                                                           RWTYYYYKSYMSMKKTWRMKTAYYWTKRWKWTRTKWTWCTMCWKCTTYWMAGTMMYRYRR
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Pred. No. 0.23;
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PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
INUMBER OF SEQ ID NOS: 14342
FEQ ID NO 2195
LENGTH: 534
ORGANISM: Klebsiella pneumoniae
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US-09-489-039A-2195/c
; Sequence 2195, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                               US-09-489-039A-2195
                                                                                                                                                                            Overy Match 6.9%; Score 31.4; DB 4; Length 534; Best Local Similarity 52.7%; Pred. No. 0.44; Matches 68; Conservative 0; Mismatches 61; Indels
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TITLE OP INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.200401
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR ADDITION DATE: 2000-01-27
PRIOR ADDITION DATE: 2000-01-27
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CURRENT FILING DATE: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 2755
SEQ ID NO 2755
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Best Local (
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Klebsiella pneumoniae
381 TATATCCTC 373
                                        441 GÉCTTCTTTÁGCCGCTGGCTTCAGGCGCTGTGGACGCTGTTCTGGAACACGATCCCCGGTT 382
                                                                     194 AATATGATC 202
                                                                                                      501 ĀĀĀGĀGGGGGGAGCAGCCGGTĀGGGGTGCCTGCTGCACCGTCGGĀAGCGĀCTCĀGGGC 442
                                                                                                                                                                   74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 GTGTTGTTACCCATGAAATGGCACATGCAGGCCAGGGTGCGGAT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                656 CCACGGCCTCGGTGCTGGCTCAAGCGGCTGCGTGATGAGTACCAGCTGGCGATCG 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 CCGCTAACGCTGCGCTTGCTCTGCAAAGCCATGCCCGTAAATATGATCAGCTGGTTACCC 214
                                                                                                                                      Similarity
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RESULT 9

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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14225
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                                                                                                                                                                       Query Match
Best Local :
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LENGTH: 549
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT ELIVENTION: 107195.136
CURRENT ELIVING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER: OF SEQ ID NOS: 33142
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Best Local Similarity
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SEQ ID NO 2162

LENGTH, 1818

TYPE: DNA
ORGANISM: Klebsiella pneumoniae
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APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
ETLE REFERENCE: 2709.2004001
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Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF 675 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2000-01-27
222 GTGCCGÁCGGTCTGCGCGTCGACCACGTTGGTAAGGTCGGAÁTGGCTGCCGAÁGTCCAGG
                   191 GTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAGGCCAGG 250
                                                                                        282
                                                                                           131 CGTTGAGCATŢTĄTCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCC 190
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                                                                                                                                                       66;
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                                                                                                                                                                   Similarity
                                                               CGTTGCACCGTCAGGCTCGGGGTCAGGCCGGTGCTGCACTGGATCTGGATATTGCCCGCTG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 ААТӨӨӨӨСӨӨСӨӨТААТСАТААСӨӨСӨӨСӨӨСААТАӨТТССӨӨСССӨӨАСТСААСӨТ 133
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                                                                                                                                                 Conservative
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                                                                                                                                                              6.8%;
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                                                                                                                                          0; Mismatches
                                                                                                                                                          Score 31.2;
Pred. No. 0.
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Pred. No. 0.92;
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                                                                                                                                     Indels
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CLASSIFICATION:

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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14137
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US-09-252-991A-14137/c
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                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5691162
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PRIOR FILING DATE: 1998-(
NUMBER OF SEQ ID NOS: 331
SEQ ID NO 14137
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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TITLE OF INVENTION:
TITLE OF INVENTION:
            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,104
                                                                                                              ZIP: 10174-6401
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 696
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                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                 APPLICANT: Fuglsang, Claus
APPLICANT: Branner, Sven
TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING INCREASED
TITLE OF INVENTION: ACTIVITY
                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                            MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                              MEDIUM TYPE:
                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                     New York
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                                                                                                                                                                                               405 Lexington Avenue,
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Moyer, Donna L.
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ilarity 53.2%;
Conservative
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                                                                                                                                                                                                   No. 56911620 No. 5691162disk of No. 5691162th America, 5 Lexington Avenue, 64th Floor
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7-MAY-1995
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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1998-07-27
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          US/08/443,104
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Pred. No. 0.61;
0; Mismatches 58; Indels
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                Sequence 6, Application US/08238130 Patent No. 5702934
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                        CORRESPONDENCE ADDRESS:
CORRESPONDENCE No. 57029340 No. 5702934disk of No. 5702934th America,
                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                             TITLE OF INVENTION: PROCESSES FOR PRODUCING AN
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APPLICATION NUMBER: US 0
FILING DATE: 03=MAR-1995
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            APPLICATION NUMBER: FILING DATE: 04-MAN
                                                                                                                                                                     STREET: 405 Le
CITY: New York
                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 41
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 6.8%; Local Similarity 45.6%;
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
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Christensen, Birgitte B.
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Moyer, Donna L.
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Pred. No. 1.4;
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                                                      Version #1.25
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US-08-442-859-5/c; Sequence 5, App
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Best Local Similarity
Matches 109; Conserv
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                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                            ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
                                                                                                                                                                                          APPLICANT: Fuglsang, Claus
APPLICANT: Branner, Sven
TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING INCREASED
TITLE OF INVENTION: ACTIVITY
NUMBER OF SEQUENCES: 10
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APPLICANT:
APPLICANT:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
         MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
URRENT APPLICATION DATA:
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LENGTH: 2052 base pairs
TYPE: nucleic acid
    APPLICATION NUMBER:
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STREET: 4(
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REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 390
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                                                                                                                                                             405 Lexington Avenue,
                                                                                                                                                                                                                                                                   Shuster, Jeffrey
Madden, Mark
Moyer, Donna L.
Fuglsang, Claus
                                                                                                                          USA
                                                                                                                                                       No. 5807729o No. 5807729disk of No. 5807729th America,
US Lexington Avenue, 64th Floor
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join(1..363, 416..802, 856..1821,
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join(1..363,
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US/08/442,859
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Pred. No. 1.4;
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                            Version
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US-08-398-489-5/c
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Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 2052 base pairs TYPE: nucleic acid
                                                                      COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Batentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
TO TO THE TOTAL TO TOO TOO TOO
                ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL METALLOPROTEASE HAVING INCREASED TITLE OF INVENTION: ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                              APPLICATION NUMBER: US/0
FILING DATE: 03-MAR-1995
CLASSIFICATION: 435
     NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Agris Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                       STREET: 405 Lexington Avenue, CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 01
FILING DATE: 03=MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-MAY-CLASSIFICATION: 252
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648 GTGAGCTTAGCCTCGGGCTTGCTGACGGTACCCTTGGTACCAGTGAAGGTGTAGTGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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Agris Dr., Cheryl H
                                                                                                                                                                                                                     New York
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Moyer, Donna L.
Fuglsang, Claus
Branner, Sven
Branner, Svouer, M
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                                                                                                                                                                                                                                             No. 58437530 No. 5843753disk of No. 5843753th America, Inc. 5 Lexington Avenue, 64th Floor
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45.6%;
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                                                             US/08/398,489
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ER: 4180.010-US
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REGISTRATION NUMBER: 34,086
REPERENCE/DOCKET NUMBER: 4180.010-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-879-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2052 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-398-489-5
Search completed: March 16, 2004, 04:37:54 Job time: 58.6647 secs
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Best Local Similarity 45.6%;
Matches 109; Conservative
                                                                                                                   395 ATTCCAGCGTAATGGTGCGTCAGGTTTGGTTTTGGCAACAACGCCACGGCTAACCAGTAT 453
                                                                                                                                                                                                               335 ATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGTTAATCAGACCGCATCTG 394
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                                                                                   468 TTGCCCTCGTAGAAGCTGTTTCCGTAGGAGAAGACCTCGCCGTCAGCGCCAATCTGTAT 410
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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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nucleic search, using sw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
2_6/ptodata/2/pubpna/USO9A_PUBCOMB.seq:*
             15 US-10-441-736-5

14 US-10-184-644-418

15 14 US-10-184-634-418

16 US-10-156-761-7222

17 US-10-156-761-1

18 US-10-132-134-1

19 US-10-132-134-1

10 US-10-1369-493-33133
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US-09-880-371-6
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US-10-010-390-6
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Sequence 6, Appli
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Sequence 418, App
Sequence 722, Ap
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	US-10-355-956-3	-10-425-114	US-10-282-122A-13500	US-09-873-367C-255	-10-424-	-10-029-386	-10-369	-10-140-864-3	-10-140-805-	-10-141-	-756-		-10-137-871-3	-10-158-79	-10-142-889	-10-141-761-	-10-140-	-731	-10-	-108-	-10-156-761	-10-205-	-09-764-	US-10-260-238-787	-901-	US-10-369-493-24265	US-10-369-493-24480	US-10-282-122A-20335
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## ALIGNMENTS

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APPLICANT: ONDAY, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HARTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FULRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 3483
LENGTH: 1662
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                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (1).
US-10-156-761-3483
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                                                                                           Matches
                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3483, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Streptomyces avermitilis FEATURE:
590 GCGCGCGGGTCGACGTCGATACAGATCGCGACGCCGTCGTTCATCGTCACGGCGAGCGGC 531
                                           50 GTGCTCTGGCTGGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCA 109
                                                                                           88;
                                                                                           Conservative
                                                                                                                                                                                                              .. (1662)
                                                                                                                7.6%;
49.7%;
                                                                                         Score 34.6; DB 14;
Pred. No. 0.78;
0; Mismatches 89;
                                                                                                                                       Length 1662;
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RESULT 2 US-10-156-761-1

APPLICANT: OMURA
APPLICANT: IKED

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RESULT 3
US-09-835-684-6/c
/ Sequence 6, Application US/09835684
Parent No. US20020019337A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:

NAME/KEY: misc_feature

LOCATION: (4187715)

OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
                                                         GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wei, Zhong-Min

APPLICANT: Qiu, Dewen

APPLICANT: Qiu, Dewen

APPLICANT: Qiu, Dewen

APPLICANT: Qiu, Dewen

APPLICANT: Remick, Dean

TITLE OF INVENTION: TREATMENT OF FRUITS OR VEGETABLES WITH HYPERSENSITIVE

TITLE OF INVENTION: RESPONSE ELICITOR TO CONTROL POSTHARVEST DISEASE OR

FILE REFERENCE: 21829/71

CURRENT APPLICATION NUMBER: US/09/835,684

CURRENT FILING DATE: 2001-04-16

PRIOR APPLICATION NUMBER: 60/198,359

PRIOR FILING DATE: 2000-04-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 49.7%;
Marches 88; Conservative
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/156,761 CURRENT FILING DATE: 2002-05-29 PRIOR APPLICATION NUMBER: JF 2001-204089 PRIOR FILING DATE: 2001-05-30
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Streptomyces avermitilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGCTCTGCAAAGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCC 226
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Pred. No. 77;
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US-09-879-248-5/c
; Sequence 5, Application US/09879248
; Patent No. US20020062500A1
; GEMERAL INFORMATION:
; GEMERAL INFORMATION:
; APPLICANT: Wei, Zhong-Min
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: THEREOF
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; TYPE: DNA
; ORGANIEM: Erwinia amylovora
US-09-880-371-6
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US-09-880-371-6/c
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CURRENT APPLICATION NUMBER: US/09/880,371
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: 60/211,585
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 6
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Best Local
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PATENT NO. US20020059658A1
GENERAL INFORMATION:
APPLICANT: Wei, Zhong-Min
APPLICANT: DeRocher, Jay
TITLE OF INVENTION: METHODS OF IMPROVING THE EFFECTIVENESS OF TRANSGENIC
TITLE OF INVENTION: PLANTS
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; ORGANISM: Erwinia amylovora
US-09-835-684-6
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Best Local Similarity 54.9%;
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
SEQ ID NO 6
LENGTH: 1344
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67; Conservation
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Pred. No. 1.1;
0; Mismatches 55; Indels
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SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 5 LENGTH: 1344

FILE REFERENCE: 21829/81
CURRENT APPLICATION NUMBER: US/09/879,248
CURRENT FILING DATE: 2001-06-12
PRIOR APPLICATION NUMBER: 60/212,211
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 18

TYPE: DNA ORGANISM: Erwinia amylovora -09-879-248-5

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RESULT 7
US-10-441-736-5/c
; Sequence 5, Application US/10441736
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; ORGANISM: Erwinia amylovora
US-10-010-390-6
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                                                                                                                                                                                                                                                                                                                                                    Query Match 7.5%;
Best Local Similarity 54.9%;
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SEQ ID NO 6
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CURRENT FILING DATE: 2001-11-05
PRIOR APPLICATION NUMBER: 60/248,169
PRIOR FILING DATE: 2000-11-13
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wei, Zhong-Min
APPLICANT: Leon, Ernesto
APPLICANT: Oviedo, Agustin
TITLE OF INVENTION: METHODS OF INHIBITING DESICCATION OF CUTTINGS REMOVED
TITLE OF INVENTION: FROM ORNAMENTAL PLANTS
FILE REFERENCE: 21829/111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1344
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                                                                                                                                                                                                                                                                                                                                      67;
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                                                                                                                                                                                                                                                      GCTCCGGTTGCCGCATTACCTGATTGTGGCGATAGCAGTGACTTTAACAGTTCCGCCAAT 150
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18 GGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCCTGGCGTTCCACAATG 77 ::: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : :: | : : | : :: | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : : | : : | : : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | :

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RESULT 8
US-10-184-644-418/c
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                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrap:
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 418
   Matches
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Best Local Similarity 54.9%;
Matches 67; Conservative
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 418, Application US/10184644
Publication No. US20030044930A1
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CURRENT APPLICATION NUMBER: US/10/441,736

CURRENT FILING DATE: 2003-05-20

PRIOR APPLICATION NUMBER: 60/107,243

PRIOR FILING DATE: 1998-11-05

PRIOR APPLICATION NUMBER: 09/431,614

PRIOR FILING DATE: 1999-11-02
                                                                                                                                                                                                                            TITLE OF INVENTION: ACIDS ENCODING FILE REFERENCE: P3430R1C227
                                                                                                                                                                                                                                           APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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                                                                                                       LENGTH: 65
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wei, Zhong-Min
APPLICANT: Schading, Richard L.
TITLE OF INVENTION: HYPERSENSITIVE RESPONSE
TITLE OF INVENTION: RESISTANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 GC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 AATTGAGCCATTTGCTCAATGGTTTGCCGATCGATGGGTTGTTGCCCCCAACGCAGAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209 GCTCCGGTTGCCGCATTACCTGATTGTGGCGATAGCAGTGACTTTAACAGTTCCGCCAAT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 GC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
   39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCTGGCTGGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCAAT 111
                                                                                                                                                                                                                                                                                                    Smith, Victoria Watanabe, Colin K. Wood, William I.
                                                                                                                                                                                                                                                                                                                                                            Pan, James
                                                                                                                                                                                                                                                                                                                                                                           Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                             Goddard, Audrey
Godowski, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                 Desnoyers, Luc
   Conservative
                                                                                       Sapien
                7.3%;
                                                                                                                                                                            See File Wrapper or
76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 1
Pred. No. 1.1;
0; Mismatches
Score 33.4; DB 14;
Pred. No. 1.2;
6; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 15; Length 1344;
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   Indels
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                                   Length
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149 AATTGAGCCATTTGCTCAATGGTTTGCCGATCGATGGGTTGTTGCCCCAACGCAGAATTT

90

52 GCTCTGGCTGGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCAAT 111

Mismatches

55; Indels

0

Gaps

Score 34; DB 9; Length 1344; Pred. No. 1.1;

Matches Query Match

Local

ch 7.5%; l Similarity 54.9%; 67; Conservative

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ORGANISM: Homo Sapien
US-10-184-634-418
                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 7.3%; Score 33.4; DB 14; Best Local Similarity 14.9%; Pred. No. 1.2; Matches 39; Conservative 76; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney Austin L
APPLICANT: Pan, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 655
TYPE: PRT
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
CURRENT FILING DATE: 2002-06-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                    258 TAATAGTACTATTGAACTGACT 279
                                                                                        145
                                                                                            198 ȚGĂȚCAGCTGGTTĂCCCGTGȚȚGTTACCCATGAAATGGCACATGCAGGGCCĂGGGTGCGGA 257
85 .SANAGD.SBRACT.GMHGA.B 64
                                                                                                                                   205 MAC.M.BB.N.S.GHARTMGMKBSS.BHS.ACYTG.MGYBH.A.ACMMYBCWCB.GBAD.
                                                                                                                                                                   138 сатттатсавтасветтесветалеветвеветрестетвелальвератверевальна 197
                                                                                                                                                                                                        265 M.YBSTSSNS.ASNKCM.BRASS.B.DA.KD..Y...TAC.S.SASSS.S..ACGBNHA. 206
                                                                                                                                                                                                                                                                                  325 SSM.CCAT.KS...M..DYDD.C..DNBB..N..AMNBH.MCYTSSANH.BAC...SS.B 266
                                                                                                                                                                                                                                             78 GGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCCGGACTCAACGTTGAG 137
                                                                                                                                                                                                                                                                                                                     18 GGCAGÇAȚTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGÇTGGCGTCGTTÇCACAATG 77
                                                       TGATNS..KC..GAG.YHA:TTG..M..K.W.G..SGHDGM..CN.DYA.ACB.GSSGBY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 TAATAGTACTATTGAACTGACT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 TGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAGGCCAGGGTGCGGA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 MÁC.M.BB.N.S.GHARTMÓMKBSS.BHS.ACYTÓ MGYBH.Á.ACMMYBCWCB.GBÁD. 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 CATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265 M.YBSTSSNS.ASNKCM.BRASS.B.DA.KD..Y...TAC.S.SASSS.S..ACGENHA.
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Godowski, Paul J.
Gurney, Austin L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .SANAGD.SBRACT.GMHGA.B 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGATNS...KC..GAG.YHA.TTG..M..K.W.G..SGHDGM..CN.DYA.ACB.GSSGBY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSM.CCAT.KS...M..DYDD.C..DNBB..N..AMNBH.MCYTSSANH.BAC...SS.B 266
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                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Length 655;
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APPLICANT: IKEDA, HARUO

APPLICANT: IKEDA, HARUO

APPLICANT: ISHIKAWA, JUN

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: SHIBA, TADAYOSHI

APPLICANT: NATORI, MOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29

PRIOR APPLICATION NUMBER: JP 2001-204089

PRIOR TELLING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 7222

LENGTH: 1848

TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                Query Match 7.3%;
Best Local Similarity 47.6%;
Matches 98; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: CDS
LOCATION: (1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7222, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Streptomyces avermitilis
654 GCCGAAGCGGCGCAGCAGGTCCTCGG
                                 226 CATGAAATGGCAÇATGCAGGCCAGGG 251
                                                               714 dedegritácechachaedredreteccecchahraheadecedretecteccecedecead
                                                                                                                                                                             774
                                                                                                                                                                                106 GGCAATAGTTCCGGGCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGGTAACGCT 165
                                                                                                                                                                                                                               834 GÓCGGCGTACACCGCCGCAGCAGCGAGGCCGGGTCCGGAGCCGACGATGAGGACGTCGCC
                                                                                                                                                                                                                                                                   46 GGCAGTGCTCTGGCTGGCTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGC 105
                                                                                                   GCGCTTGCTCTGCAAAGCGATGCCCGTAAATATGATCAGCTGGTTACCCGGTGTTGTTACC 225
                                                                                                                                           GTGACGGTTTCCGGGGGGGGGGGCAGGCAGGCCGATGAGCCGGGGCCAGTTCCGCGTTGCT 715
                                                                                                                                                                                                                                                                                                                Score 33.2; DB 14; Length 1
Pred. No. 2.5;
0; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                           Length 1848;
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APPLICANT: SHIBA, TRADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAITRA
TITIE OF INVENTION: NOVEL POLYMUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR PELLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: OMURA, SA
APPLICANT: IKEDA, H
APPLICANT: ISHIKAWA
APPLICANT: HOALKAWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-156-761-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                           IKEDA, HARUO
ISHIKAWA, JUN
HORIKAWA, HIROSHI
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RESULT 13
US-10-132-134-1
US-10-132-134-1
; Sequence 1, Application US/10132134
; Publication No. US20030171562A1
; GENERAL INFORMATION:
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US-10-132-134-13
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; TYPE: DNA
; ORGANIEM: Streptomyces platensis subsp. rosaceus
US-10-132-134-13
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CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/10132134 Publication No. US20030171562A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Farnet, Chris
APPLICANT: Yang, Xianshu
APPLICANT: Staffa, Alfredo
APPLICANT: Staffa, Alfredo
TITLE OF INVENTION: POLYKETIDE SYNTHASE
FILE REFERENCE: 3012-2US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptomyces avermitilis FEATURE:
NAME/KEY: misc feature
LOCATION: (4187715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: a, t,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8638105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8638165 GTGACGGTTTCCGGCGGGGAGTGACGGCAGGCCGATGAGCCGGGCCAGTTCCGCGTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8638225 GGCGGCGTACACCGCGGCAGCGAGGCCGGCCGGGTCCGGAGCCGATGAGGACGTCGCC
                                                                                                                                                                                                                                                                                                                                                                       / Match 7.2%;
Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                               20347
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                                                                                                                                                                                                                                                                                                                 46 GGCAGTGCTCTGGCTGGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGC 105
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                                                                                                                                                                                                                                                                                                                                                        82;
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Similarity 47.6%;
                                                                                                                                                                                                                                        GGCAATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCT 165
                                                                                                                                                                                                     GCCACCGAACGCCGCACGACACGCCGCCGCCATGCTGCCGATCCGCGCCCCGCACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGTTGCGCAACAGGGTGGTGTCCCGCCAGATGACGAGCGGTGTCTCCTCCGGGCCGAC 8638046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GECAATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCT
                                                                                                                               GTGGAGGCGCTACGCGCTACGGCACCGGCACCCGCACGT 20390
                                                                                                                                                                                                                                                                              GGCCGCACACTGGTGGCTCGGCTGGCCCCTGTGGGCCGACGGCGCATGACGGTGGACGCC
                                                                                                                                                                GCGCTTGCTCTGCAAAGCGATGCCCGTAAATATGATCAGCTGGT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATGAAATGGCACATGCAGGCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gcgcTTgcTCTgcAAAgcgATgcccGTAAATATGATCAGCTGGTTACCCGTGTTGTTACC
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                                                                                                                                                                                                                                                                                                                                                    Score 32.8; DB 14;
Pred. No. 14;
0; Mismatches 82;
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Pred. No. 1.9e+02;
0; Mismatches 108;
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US-10-169-493-3313/c

Sequence 33133, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Farnet, Chris
APPLICANT: Yang, Xianshu
APPLICANT: Yang, Xianshu
APPLICANT: Staffa, Alfredo
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES
FILE REFERENCE: 3012-2US
CURRENT APPLICATION NUMBER: US/10/132,134
CURRENT FILLING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: XYlella fastidiosa
US-10-369-493-33133
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                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 33133
LENGTH: 1083
                                                                                                                                                                                    Query Match 7.1%;
Best Local Similarity 59.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 52101
TYPE: DNA
ORGANISM: Streptomyces platensis subsp.
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428
                                       422 GTTTTGGCAACAACGCCACGGCTAACCAGTATT 454
                                                                                  488 ATCTCACCGAGCTGGGATAAAAAACCGCGCACAATCACACCATAACGCTGCTTCAGCCAC 429
                                                                                                                         362 ATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTTG 421
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TTTTTAGCAACCACCCCAGCAGTCACACGCATT 396
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Pred. No. 21;
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RESULT 15 US-09-815-242-6028 Commence 6028, Ap

Application US/09815242

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APPLICANT: WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, WASH, W
Search completed: March 17, 2004, 08:16:43 Job time: 424.736 secs
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Travick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Xu, H. Howard
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                                                                                                                                                                                                                                                                 353 GCAAGTTCATG 363
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BZ569281 pacs2-164
BG71547 DRNBUB05
BZ565783 pacs2-164
BB581987 BB581987
CA711477 wdk2c.pk0
AZ180696 SP 0181 A

BI959328 HVSMEn001 AV058630 AV058630

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seg length: 2000000000
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237.4
37.4
35.4
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Match
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CA141136
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BJ618688 BJ618688
AV430994 AV430994
CA141136 SCJFRT205
BX251172 BX251172
                                         Description
                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                          RESULT 1
BJ618688/c
LOCUS
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ORGANISM
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KEYWORDS
                                                                   COMMENT
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                                                                            TITLE
JOURNAL
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      Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available the
                                                                                                  Xenopus laevis (African clawed frog)
Xenopus laevis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 680)
1 (bases 1 to 680)
1 (bases 1, Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
                                                                                                                                                                                 680 bp mRNA linear EST 01-OCT.
BJ618688 NIBB Mochii normalized Xenopus early gastrula library
Xenopus laevis cDNA clone XL186b22 5', mRNA sequence.
BJ618688
                                                                           Expressed genes in X. laevis embryo Unpublished (2001)
                                                                                                                                                                 BJ618688.1 GI:37256713
EST.
                                                                                              Kohara,Y
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AL809250
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AV058630
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        available through the following
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AA785291 g6c08a1.r AL231386 Tetraodon B2204853 CH230-390 CK246169 EST729806 CK247920 EST731557

EST 01-OCT-2003

AY414592 Pan trogl AZ577991 17d03 Sho AA784257 d3g05al.f AA785291 g6c08al.f

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BZ462870 BONBW34TR
CA703231 wdk1c.pk0
BIC26794 RH67848.5
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CB935126 ru03d09.y
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BJ334624 BJ334624 BU444683 603765715 BQ939900 AGENCOURT BM333324 MEST189-B BF501499 AT16857.5

Triticum

CD374421 TNWbmfC2H
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BZ569250 Pacs2-164
CG178280 PUJDF79TD
AL196666 Tetraodon
BF668888 602123291
BQ718166 AGENCOURT

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Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                           173
                                                                                                                                                                                                                                                                                                                                                                                      421
                                                                                                                                                                                                                                                                                                                                                                                                            361 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                               Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
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                                                                                                                        Tabata, S
                                                                                                                                     Nikaido,
                                                                                                                                                         Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
                                                                                                                                                                                     Porphyra yezoensis
Porphyra yezoensis
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AV430994 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                          GGCÁACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGAAACTTTTAÁAÁGTAGCAGCÁATTGCÁGCÁÁTCGTÁTTCTCCGGTÁGCGCTCTGGCA 534
                                                                                                                               I., Asamizu, E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Xenopus laevis"
/mol_type="mRNA"
/db xref="taxon:8355"
/clone="XL186b22"
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70.0%;
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_stage="stage 10.5"
ne_lib="NIBB Mochii normalized Xenopus early gastrula.
                                                                                                                   Nakajima,M., Nakamura,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 237.4; DB 12; Length
Pred. No. 6.4e-57;
0; Mismatches 137; Indels
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                                                                                                                   Saga, N.
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Best Local S
Matches 68
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                                                                                                                                                                                                                                                                                       Email: parruda@unicamp.br clone distribution information can be through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br plate: 058 row: D column: 10 Seq primer: T7 Promoter Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA141136
SCJERT2058D10.g RT2
5', mRNA sequence.
CA141136
CA141136.1 GI:3503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 TCAGACCGCATCTGATTCCAGGGTAATGGTCGCGTCAGGTTTGGGTATTTGGCAACGACGCA 439
                                                                                                                                                                                                                                                                                                                                                                                                                           Centro de Biologia Molecular e Engenharia (
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     381 GÓCGÁAAGCTGGTGTATÓCÁAAGTÁCTGGTGCAGGAGGGGGGAAAGGGCGTCGCCCGGCÁ 323
                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 55 19 3788 1137 Fax: 55 19 3788 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vettore, A.L., da Silva, F.R., The libraries that made SUCE Genet. Mol. Biol. 24 (1-4),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharum officinarum
Bukaryota, Viridiplantae, Streptophyta, Embryo
Spermarophyta, Magnoliophyta, Liliopsida, Poa.
Clade, Panicoideae, Andropogoneae, Saccharum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 664)
/clone_lib="RT2"
//clone_lib="RT2"
//ncle="Organ: Root tips(0.3cm-long) from adult plants;
//octor: pSport1; Site_1: Sali; Site_2: Not1; An unidirectional cDNA library generated from [Root tips(0.3cm-long) from adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                  /Clone="SCJFRT2058D10"
/lab_host="DH10B"
/clone_lib="RT2"
                                                                                                                                                                                                          /organism="Saccharum officinarum"
/mol type="mRNA"
/db_xref="taxon:4547"
                                                                                                                                                                                                                                                                                     Location/Qualifiers
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/clone="pL027e10 r"
/clone_lib="Porphyra yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:35034821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Porphyra yezoensis"
/mol_type="mRNA"
/strain="TU-1"
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Pred. No. 10;
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marum officinarum
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a; Poales; Poaceae; PACCAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 CTTGTTGTTGCAC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401 CTGCACGACGGCTCCGGTGGCCGTGCTGGCGTGCCGTGGCCGGCGTCATCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 TATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATATGAT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 GCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCGTCGTTCCACAATGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases I to 675)
Canton, F.R., Le Provost, G., Garcia, V., Barre, A., Frigerio Canton, F.R., Fevereiro, P., Avila, C., Mouret, J.-F., Brach, J., Daruvar, A., Canovas, F.M. and Plomion, C.
Transcriptome analysis of wood formation in maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BX251172 675 bp mRNA lin BX251172 Pinus pinaster differenciating xylem cDNA clone PP046C03, mRNA sequence.
BX251172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2003)
Contact: Frigerio JM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pinus pinaster
                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Frigerio@pierroton.inra.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          route d'Arcachon 33612 Cestas CEDEX France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetique et Amelioration 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pinus pinaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BX251172.1 GI:28513831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCCGGACTCAACGTTGAGCATT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAGGCCAGGGTGCGGATAAT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGCGCGCGGGGCGCCATCCCGGCGGCGACCCCCACGGCCTGGCCAAGAACCTGAGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTACTATTGAAC 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Frigerio@pierroton.inra.fr
/clone lib="Pinus pinaster differenciating xylem adult"
/note="Vector: Uni-Zap XR lambda (Stratagene); Site 1: Eco
RI; Site 2: Xho I; A composite CDNA library was made with
mRNA isoTated from normal, compression, opposite, early
and late wood of Maritime pine uni-directionally cloned
into Uni-Zap XR using the ZaP-CDNA Synthesis kit
(Stratagene). pBluescript SK(-) plasmids were obtained by
in vivo mass excision. The nucleotide sequence of the
5'end was obtained by automated sequencing with the T3
primer by GENOME EXPRESS, Meylan, France"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                 /tissue_type="differenciating xylem"
/dev_stage="adult"
                                                                                                                                                                                                                                                                            /strain="ecotype: Corsican"
/db_xref="taxon:71647"
/clone="PP046C03"
                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                               organism="Pinus pinaster"
mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.2%;
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Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brach, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frigerio, J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pinus pinaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 24-FEB-2003
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BI959328/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity 57.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 TGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 526 TAAAATTCCTCAGATAGATGCTATTATTTTGACACATGAACATGCAGATGCATTGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 TAAATATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAGGCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 699)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T.,
Simmons,J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex rachis cDNA library
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 452.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI959328 699 bp mRNA linear EST 22-OCT-200 HVSMEn0019E09f Hordeum vulgare rachis EST library HVCDNA0015 (normal) Hordeum vulgare subsp. vulgare cDNA clone HVSMEn0019E09f,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: rwing@clemson.edu
Total hq bases = 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI959328.1 GI:16310583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGGATGATGTTAGGAGTGTACAACCATATAACCCGTACAATGATATTG
/notes "Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: /notes "Vector: plants were grown at Washington State University, Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmonns, Rambo, Main). The sequence has been triamed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="HVSMEn0019E09f"
tissue_type="Rachis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lab host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sub_species="vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Hordeum vulgare subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xref="taxon:112509"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lib="Hordeum vulgare rachis EST library HVcDNA0015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No. 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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В

202

37 GTAGTTTCTGGCAGTGCTCGGCTGGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCAT 96

sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

97

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Matches Query Match

85, Similarity

Conservative

7.6%; 50.3%;

Score 34.6; DI Pred. No. 76; 0; Mismatches

DB 12; 84;

Length 699; Indels

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Gaps

Local

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FEATURES
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AZ959284/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0226 row: G column: 20
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       371 CGCTGGTTAATCAGA 385
                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Miederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse whole genome plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 TCCAGTGAAGCACAAAAATGAAGAAGAAAATGATTACCCAAAAGTTGGAATTAAGGTAG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     669 bp DNA linear GSS 27
2M022GG20R Mouse 10kb plasmid UUGC2M library Mus musculus
clone UUGC2M0226G20 R, genomic survey seguence
AZ9592R4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
1 (bases 1 to 669)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ959284.1 GI:13830511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                        ass: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCG
//Ab_host="E_coli strain XL10-Gold, T1-resistant, F-"
//Ab_host="E_coli strain XL10-Gold, T1-resistant, F-"
//Clone lib="Mouse 10kb plasmid UUGC2M library"
//note="Wector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
0.005 inch orifice at constant velocity. The sheared DNA
0.005 inch orifice at constant velocity. The sheared DNA
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGAGÁCCÁCÁGTTTTTTCTÁGGTCÁCCAÁGGCTGGGTAAÁGÁÁÁAGÁAGCATCAÁCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="UUGC2M0226G20"
/
                                                                                                                                                                                                                                                                                         organism="Mus musculus"
|mol_type="genomic DNA"
|strain="C57BL/6J"
                                                                                                                                                                                                                                        sex="Female"
                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No. 68;
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FEATURES

Thermostabilization and thermoactivation of thermolabile enzymes k trehalose and its application for the synthesis of full length cDN (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (http://genome.rtc.riken.go.jp) for

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: 81-298-36-9145

Fax: 81-298-36-9098

genome-res@rtc.riken.go.jp

Genome Science Laboratory

Chie Owa

RIKEN

RIKEN Mouse ESTs Unpublished (1999)

source

organism="Mus musculus" |mol\_type="mRNA" db\_xref="taxon:10090" strain="C57BL/6J"

ocation/Qualifiers

tissue\_type="pancreas' dev\_stage="adult"

sex="male" clone="1810054H02" COMMENT

Contact:

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 296)

AUTHORS

Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T. Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogal Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muzamatsu, M., Okazaki, Y., and Hayashizaki, Y.

Inaya,...,
, Izawa,M.,
, Oda,H.,

Aizawa, K.,

SOURCE ORGANISM

Mus musculus (house

mouse)

KEYWORDS

AV058630 AV058630.1 GI:5158377

AV058630 296 bp mRNA linear EST 23-AV058630 Mus musculus pancreas C57BL/6J adult Mus musculus clone 1810054H02, mRNA sequence.

EST 23-JUN-1999

RESULT 6 AV058630

DEFINITION

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82

142

157 есталося теретелестве в предоставляющей предоставления предоставления предоставления предоставляющей предо

AAGGTCCACGGCGCCGACGGCCAGGAAGCAGAAAGCGCCGCGAGCACGCGAGGGA AACGGCGGCGGCAATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCC 156 GTACTTGGTGGCGTCGCTTCGAGGTCGACGTCGAAGGGGGAGGCGTCGGTGGCGTT 143

GGGGÁGGGAGCCCATGCCGCGCGCTGTGTGTGTGTGTGTGTGTGCGGC 34

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KEYWORDS
SOURCE
ORGANISM
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BZ569281
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                                                                                  Query Match 7.5%;
Best Local Similarity 53.3%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTACCCCATGAAATGGCACAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          978 bp DNA linear GSS 17-DEC-20 pacs2-164_8328.y2 pacs2-164_Pseudomonas aeruginosa genomic clone pacs2-164_8328, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library J. Bacteriol. (2002) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.Burns,J.L., Kaul,R. and Olsen,M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chris K. Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BZ569281.1 GI:27203648
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CGGTATCGATACCCATTCGATTGAAAATGATGGCGAGTTCGTTGATCAGAGCAATATTGA
                                      CCGTGTTGTTACCCATGAAATGGCACATGCAGGCCAGGGTGCGGATAATAGTACTATTGA 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGCTTCAGGTCAATATGAGCTCTCAGCTGTCCCTGCCATGCCATGCCTTTACTGGCCCAT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGAGGCATGCTTAAGGTTTCAGAAGCAATGTAACGTTCCCATTGTGCTTTCTCTGCTT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 978)
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                                                                                                                                                                                                                                                                                                                                                                                                                      shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                    craymond@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy_number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XIJO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                               /clone="pacs2-164_8328"
/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole
                                                                                                                                                                                                                                                                                                      /organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="2-164"
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                 db_xref="taxon:287"
                                                                                                                                                                                             ibrary."
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                                                                               Score 34.2; DB 28;
Pred. No. 1.1e+02;
0; Mismatches 63;
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Pred. No. 97;
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                                                                                                                                                 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Zhang Xu
Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-647148700-121
Fax: 86-21-647148700-121
Fax: 86-21-647148146
Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xiao, H.S., Huang, Q.H., Zhang, F.X., Bao, L., Lu, Y.J., Guo, C., Yang, L., Huang, W.J., Fu, G., Xu, S.H., Cheng, X.P., Yan, Q., Zhu, Z.D., Zhang, X., Chen, Z., Han, Z.G. and Zhang, X.

Identification of gene expression profile of dorsal root ganglion in the rat peripheral axotomy model of neuropathic pain Proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: T3 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRNBUB05 Rat DRG Library
                                                                                                                                                                Similarity
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                                                                                              CACAATGGGGCGGCGGTAATCATAACGGCGGCGAATAGTTCCGGCCCGGACTCAA 130
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CTGTAGGAGTCCTCGCTGGTAACGATGCCGAGAGTGCACATCGATATCGGTGGGCCGGTTA
                                                                      TGAAAGATACATGAGTGACAGTGTCCGTGATTGCAGACATTGCTGTATGATGCGTCCTGT 227
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                                                                                                                                                 Conservative
                                                                                                                                                                                                                                     /tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="DRNBUB05"
                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                  sex="male"
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Pred. No. 1.2e+02;
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ACCESSION
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Best Local Similarity
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cDNA clone 9030005005 5', mRNA sequence.
                                                           Mus musculus (house mouse)
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Box 352145, Seattle, WA 98105-2145, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whole-Genome-Sequence variation among multiple isolates of Psedomonas aeruginosa library
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/clone_lib="pacs2-164"
/note="clinical isolate 2-164 Whole genomic shotgun
library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Pseudomonas aeruginosa"
/mol_type="genomic_DNA"
/strain="2-164"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: genome-resegsc.riken.go.jp,
    URL:http://genome.gsc.riken.go.jp/
    Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S.,
    Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
    Thermostabilization and thermoactivation of thermolabile enzymes by
    trehalose and its application for the synthesis of full length
    Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
    Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
    Natomated filtration-based high-throughput plasmid preparation
    system. Genome Res. 9 (5), 463-470 (1999)
    Carninci, P. and Hayashizaki, Y.
    High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S Aizawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T., Carninci, P., Hanagaki, T., Hayatsu, N., Hiraoka, T., Hirozane, T., Hodoyama, Y., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kawai, J., Kojima, Y., Komo, H., Kusakabe, M., Matsuyama, T., Miyazaki, A., Okido, T., Owa, C., Sakai, C., Sakai, K., Sasaki, D., Sato, K., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Shibata, K., Yamamura, T., Yasuni, T., Tanaka, T., Toya, T., Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A., RIKEN Mouse ESTs (Aizawa, K. et al. 2000)

Contact: Yoshihde Hayashizaki

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Please visit our web site (http://genome.rtc.riken.go.jp) for
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Fax: 81-45-503-9216
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 234)
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                                                                              //lone lib="RIKEN full-length enriched, adult male colon"
//clone lib="RIKEN full-length enriched, adult male colon"
//note="Site_1: Sal1; Site_2: BamHI; cDNA library was
propered and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
GAGAGAGAGAGCATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], CDNA was
GAGAGAGAGAGCATCCAAGAGCTCTTTTTTTTTTTTVN 3'], CDNA was
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mol_type="mRNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
             Score
             34;
     DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
Length 234;
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RESULT 13
AZ180696
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AUTHORS
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ORGANISM
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CA711477/c
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                   DEFINITION
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AZ180696 500 bp DNA linear of SP_0181_A1_C06_SP6E Strongylocentrotus purpuratus, purchin, sperm genomic BAC library Strongylocentrotus
                                                                                                                                                                                                                  61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tingey, S.V., Powell, W., Wolters, P., Miao, G., Caraher, N. and Hanafey, M.K. DuPont Wheat cDNA Sequence Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    500 l wdk2c pk014.o3 wdk2c Triticum end, mRNA sequence. CA711477
                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark,
Tel: 302-631-2607
Fax: 302-631-2607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crop Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Scott V. Tingey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pooideae; Triticeae; Triticum.
1 (bases 1 to 500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA711477.1 GI:25433270
                                                                                                                                                                                                              h 7.5%;
Similarity 54.5%;
61; Conservative
                                                                                                                                                         AGNTGNTGCAGTCGCAGCCNCCGGTCTCCCCGGCCGTNTCGAACCCGCCGGAGCTCCCCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGCTAACGCTGCGCTTGCTGCAAAGCGATGC 188
                                                                                                    TGTGGGAGGCGGTGGGCATGACCATGGCGGCGGCGGCGGCGGCGGTGGCCNCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGAACGCCGGGTGCTTTATAGCCTTGTTCAAAATATGGTAGCGCATTTACCACCACCTTT
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                                                                                                                             ATGGGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGCCCGGAC 126
                                                                                                                                                                                     CCGGTTACCAAGCCCGTGCCCGCCATTGCGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGTAGTTTCTGGCAGTGCTCTGGCTGGCGTCGTTCCACAATGGGGCGGCGGCGGTAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                             primer: M13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scott.V.Tingey@USA.dupont.com
                                                                                                                                                                                                                                                                                /note="Vector: pBluescript SK+; Site 1: EcoRI; XhoI; Wheat (Triticum aestivum L.) developing days after anthesis."
                                                                                                                                                                                                                                                                                                                                                                       organism="Triticum aestivum"
|mol_type="mRNA"
|db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                             /clone="wdk2c.pk014.o3"
/tissue_type="kernel"
/clone_lib="wdk2c"
                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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n aestivum cDNA clone wdk2c.pk014.o3 5'
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purple sea
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                 193
                                                                     mRNA sequence.
AA746477
AA746477.1 GI
                                                                                                                                                                                                                                                                                                                                                                                                   82;
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  Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS.
                                                           EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: acameron@caltech.edu
Plate: 181 row: E column:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: (626) 395-8421 Fax: (626) 793-3047
                                            Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Cameron,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10920195
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                                                                      GI:2786463
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50.3%;
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Pred. No.
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128 GATGATGATAATAATAATGAATTAATAATGATGATTACAGAA 170
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                                                                                                                                                                                                     AA746477

AA746477

AA746477

mK02e02.81 NCI CGAP GCB1 Homo sapiens cDNA clone IMAGE:1251194 3' similar to TR:000555 NEURONAL CALCIUM CHANNEL ALPHA 1A SUBUNIT ISOFORM A-1. ;contains element TAR1 repetitive element ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACGATGATGATGATGATGATGATGATGATGATACGATGATGATGATGATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:7668"
/clone="plate=181 Col=11 Row=E"
/clone_lb="Strongylocentrotus purpuratus,
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Strongylocentrotus
/mol_type="genomic DNA"
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Craniata; Vertebrata;
Catarrhini; Hominidae;
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                          Euteleostomi;
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                           Wuchereria bancrofti

Bukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Wuchereria.

1 (bases 1 to 558)

Ndi, J.S., Ribeiro, J.M., and Nutman, T.B.
Toward the characterization of the Wuchereria bancrofti
microfilarial transcriptome with comparisons to those of Brugia
malayi and Onchocerca volvulus
                                                                                                                                                                                                                                                                                                                                                     75
                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                                             CD374421
TNWbmfC2H3T3 Wuchereria bancrofti microfilaria cDNA Wuchereria bancrofti cDNA clone TNWbmfC2H3 5', mRNA CD374421
CD374421.1 GI:31229939
                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                        Wuchereria bancrofti
                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 56.9
62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 661 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert Length: 661 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Louis M. Staudt, M.D., Ph.D., I
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 365)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                        ATGGGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCG 123
                                                                                                                                                                                                                                                                                                              AGCGGCCCTCGGAGGTACCCAGGCCCGCACGGCCGACGCTACTGGCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="IMAGE:1251194"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33.8; DB 9; Length 3
Pred. No. 97;
0; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing Center information can be
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                                                                                                                                                                                                             EST 19-AUG-2003
(SAW95SjL-WbMf)
                                                                                                                                                                                             sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. Fatima
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Search completed: March 16, 2004, 04:29:16 Job time: 2234.91 secs

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                                                                                                                                                                       Matches
                                                                                                                                                                                            Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                     Local Similarity
101 GACATTTANCCAAGANCGGTGGCGGNANCTCTGCNCTTGCTCTGNAA 55
                               136 AGCATTTATC--AGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                       161
                                                                                                              76 TGGGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCGGACTCAACGTTG 135
                                                                                                                                                                     65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2003)
Contact: Thomas B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Building 4 Room 126, Bethesda, Email: tnutman@niaid.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Thomas B. Nutman
Laboratory of Parasitic Diseases
                                                                           TGGCGCGGTGGCGGTAACCNCGGTGGTGGCGGTAATAATAAGCGGCCCAAATTCTANGCT 102
                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                      /note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Lymphatic filarial nematode parasite of humans. mRNA was prepared from approximately 85,000 microfilariae isolated from the blood of an infected individual from Guyana, South America and converted to double-stranded CDNA using reverse transcriptase and oligo (dT) followed by RNase H and DNA pol I. The library has 2.9 x 10E5 independent recombinants and the average insert size is library is available from Dr.S.A.Williams, email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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/clone="TNWbmfC2H3"
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/lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             r: pBluescript T3.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SAW95SjL-WbMf)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism≈"Wuchereria
                                                                                                                                                                               7 4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _lib="Wuchereria bancrofti microfilaria cDNA
                                                                                                                                                              0;
                                                                                                                                                            Score 33.8; DB 14;
Pred. No. 1.2e+02;
0; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bancrofti"
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                                                                                                                                                      Gaps
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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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5491.177 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 1
US-08-233-642A-56
; Sequence 56, Application US/08233642A
; GENERAL INFORMATION:
WEST William W.
                                                                                                                                                   NUMBER OF SEQUENCES: 5
NUMBER OF SEQUENCES: -
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                            APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
NUMBER OF INVENTION: BASED VACCINES
                            STREET: 6300 Columi
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
                                                                                                         ADDRESSEE: Seed and Berry STREET: 6300 Columbia Center,
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52 3US-09-543-407-1
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                                                                                                         701 Fifth Avenue
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.2
PAPLICATION NATA:
APPLICATION DATA:
VILING DATE: 26-APR-194
CLASSIFICATION: 424
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION UNUMBER: 920043.403C3
TELEPHONE: (206) 622-4900
TELEPAX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
TYPE: nucleic acid
STANUBENESS: single
TOPOLOGY: linear
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Sequence 1, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
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Length 456;

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Sequence 19, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Asron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 19
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US-09-543-407-19
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; TYPE: DNA
; ORGANISM: Salmonella
US-09-543-407-1
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Best Local !
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
 OTHER INFORMATION:
OTHER INFORMATION:
                                                             TYPE: DNA
ORGANISM: Artificial
                                                       FEATURE:
                                                                                                           LENGTH: 456
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Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
                                                                    Sequence
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US-09-543-407-17

(Sequence 17, Application US/09543407

(GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTE

TITLE OF INVENTION: PRESENTATION OF HETEROL

(CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17

LENGTH: 456

Type: Non
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                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA;
; OTHER INFORMATION: sequence containing the replacement fragmen
; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-17
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                                                                                                  Query Match
Best Local Similarity
Matches 425; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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                                                ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
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 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC 120
                                  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCCT
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                                                                                                Score 406.4; DB 23;
Pred. No. 2.5e-119;
0; Mismatches 31;
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Pred. No. 2.2e-121;
0; Mismatches 27;
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Sequence 11, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
ITITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
ITITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/09/543,407

ITITLE OF INVENTION UNMEER: US/09/543,407

CURRENT FPLICATION NUMBER: US/09/543,407

INUMBER OF SEQ ID NOS: 59
SOFTWARE: FRASTSEQ FOR WINDOWS Version 4.0

LENGTH: 456
ITYE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
US-09-543-407-11
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US-09-543-407-11
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                                                               CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
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93.0%;
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                                                                                                                                                                                                                 Score 404.8; DB 23;
Pred. No. 8.3e-119;
0; Mismatches 32;
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043,406
CURRENT FILING DATE: 20043,407
CURRENT FILING DATE: 2000-04-05
SOPTWARE: FASC ID NOS: 59
SOPTWARE: FASC FOR Windows Version 4.0
LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: THORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
US-09-543-407-13
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Matches 424;
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US-09-543-407-13
; Sequence 13, Application US/09543407
; GENERAL INFORMATION:
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                            AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420
                                                                                                                                  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
                                                                                                ĠĊĊĀĊĠĀĊĠĀĊĊĀĠŸĠĠĀĀĠĠĊŦĀĀĀĀĀĊŢĊĊĠĀŦĀŤŢĀĊŢĠŢĊĠĠĊĊĀĀŢĀŢĠATCAG 360
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Pred. No. 8.3e-119;
0; Mismatches 32;
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APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
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APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
APPLICANT: COLORDER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
INUMBER OF SEQ ID NOS: 59
SOFTWARE: FABCISEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-23
                                                      RESULT 8
US-09-543-407-25
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US-09-543-407-23
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Best Local S
Matches 424
                  Sequence 25, Application US/09543407 GENERAL INFORMATION:
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APPLICANT: White,
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93.0%;
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Pred. No. 8.3e-119;
0; Mismatches 32;
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
WIMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 456
TYPE: DNA
OPCRNISM: Artificial Sequence
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
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US-09-543-407-15
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Best Local Similarity
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93.0%;
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Pred. No. 8.3e-119;
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
TITLE OF INVENTION: UNMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
NUMBER OF SEQ ID NOS: 59
NUMBER: FASESSQ for Windows Version 4.0
                                                                                                      US-09-543-407-21
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US-09-543-407-21
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                                                                                                   SEQ ID NO 21

LENGTH: 456

TYPE: DNA

ORGANIAM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragmer
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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                                          Query Match
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      Best Local Similarity
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ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 2.7e-118;
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401.6; DB 23;
No. 8.8e-118;
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                       Length 456;
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APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITILE OF INVENTION: BRESENTATION OF HETEROLOGOUS PER
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
ISEQ ID NO 27
LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-643-407-27

; SEQUENCE 27, Application US/09543407

; GENERAL INFORMATION:
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                                                                                                                                                                 Matches
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                                          ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
                                                                                                              ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAGTCGTAGTTTCTGGCAGTGCTCTGGCT
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                                                                                                                                                               Conservative
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92.5%;
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Pred. No. 8.8e-118;
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; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA;
OTHER INFORMATION: sequence containing the replacement fragmer
; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-29
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Best Local S
Matches 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: White, Aaron P.
APPLICANT: Coran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29, Application US/09543407 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 45
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GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
                                                              AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
                                                                                                                              CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
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                                                                                                             CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
                                                                                                                                                                           GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
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92.1%;
                                                                                                                                                                                                                                                                                                            Score 398.4; DB 23;
Pred. No. 9.4e-117;
O; Mismatches 36;
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US-08-233-642A-54
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GENERAL INFORMATION:
CAPPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
                                                                                                                                           Query Match
Best Local Similarity
Matches 333; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
DECISIONATION: MINERER 26-670
                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 54:
                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..357
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REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
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                      124 GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC 183
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GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC 120
                                                                      GTCGTACCACAGTGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCG
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E: DNA (genomic)
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                                                                                                                                           Score 331.8; DB 6
Pred. No. 2.2e-95;
0; Mismatches 2
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; 'ORGANISM: E.
US-09-543-407-3
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US-09-543-407-3
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 330;
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Best Local Similarity
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
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                                                                      GGCAACGGTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT
                       GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA
                                                                                                     AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                                                                                                                              GCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGTGGT
                                                                                                                                                                                 GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 254.4; DB 23; Pred. No. 1.8e-70; 0; Mismatches 126;
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US-09-252-691-172
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GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 107196.135
CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
SEQ ID NO 172
LENGTH: 477
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Best Local :
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ORGANISM: Enterobacter cloacae
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                               GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
                                                                    GGCAACGGCGCGGCGGTAGACCAGACAGCGTCCGGCTCAACGGTGACTGTGCACCAGGTT
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Search completed: March 18, 2004, 02:46:32 Job time : 2926.24 secs

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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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(cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*
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Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence
5057, Ap	<ol><li>Appli</li></ol>	1446, Ap	1515, Ap	1, Appli	1287, Ap	10679, A	1187, Ap	1173, Ap	1185, Ap	279, App	12607, A	6292, Ap	2020, Ap	28293, A	3735, Ap	12516, A	154, App	153, App

## ALIGNMENTS

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PRIOR FILING DATE: 1994-01-20
PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 675
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                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (83)..(538)
US-09-741-873C-3
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CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR PLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 07/970,846
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Matches 330; Conserv
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TITLE OF INVENTION: Fibronectin Binding Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1992-11-03
APPLICATION NUMBER: US 08/187,865
121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
                                                                         143
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                                                                                                     GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
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                                                                         GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC 202
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Pred. No. 2.5e-77;
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US-09-741-873C-1
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NUMBER OF SEQ ID NOS: 11
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CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
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PRIOR FILING DATE: 1997-11-26
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APPLICANT: Olsen, Arne
                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 396
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OR FILING DATE: 1991-11-06
OR PPLICATION NUMBER: US 07/970,846
OR FILING DATE: 1992-11-03
OR APPLICATION NUMBER: US 08/187,865
OR FILING DATE: 1994-01-28
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OR FILING DATE: 1994-01-28
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APPLICATION NUMBER: US 07/347,189
FILING DATE: 1989-05-04
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                                                       ACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGCAGAT
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                                                                                                                                                                                                                                                                                                   46.1%;
70.7%;
                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                            Score 210.4; DB 5;
Pred. No. 2.2e-62;
0; Mismatches 116;
                                                                                                                                                                                                                                                                                                              Length 396;
                                                                                                                                                                                                                                                                              Indels
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PRIOR APPLICATION NUMBER: PCT/US98/12718
PRIOR APPLICATION UNMBER: 60/057,483
PRIOR FILING DATE: 1997-09-03
PRIOR APPLICATION NUMBER: 60/053,344
PRIOR FILING DATE: 1997-07-22
PRIOR APPLICATION NUMBER: 60/053,377
PRIOR APPLICATION NUMBER: 60/053,377
PRIOR APPLICATION NUMBER: 60/053,377
PRIOR APPLICATION NUMBER: 60/050,359
PRIOR FILING DATE: 1997-07-22
PRIOR PRIOR PRIOR OF SEQ ID NOS: 756
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 756
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SEQ ID NO 629
                                                                                                                                                                                                                                                                             Sequence 629, Application US/09830230A
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Lyme Disease Vaccines
NAME/KEY: misc feature
LOCATION: (1251)
OTHER INFORMATION: n equals
                                                                LOCATION: (1250)
OTHER INFORMATION: n equals
                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (1247)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1139)
OTHER INFORMATION: n equals a,t,9,
                                                                                        NAME/KEY: misc feature LOCATION: (1250)
                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (1148)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: PB481US
CURRENT APPLICATION NUMBER: US/09/830,230A
CURRENT FILING DATE: 2001-09-27
                                                                                                                                                                                                       OTHER INFORMATION: n equals
                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: (1244)
                                                                                                                                                                                                                                                             LOCATION: (1210)
OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: n equals
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (1143)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AATAACGCCGCGCTCGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 396
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; DATABASE ACCESSION NUMBER: NC 001491, ; DATABASE ENTRY DATE: 2000-08-01 US-10-624-149A-1
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CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: 60/403,282
PRIOR FILING DATE: 2002-08-14
PRIOR PPLICATION NUMBER: DE 10233064
PRIOR FILING DATE: 2002-07-19
PRIOR FILING DATE: 2003-04-11
PRIOR FILING DATE: 2003-04-11
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US-10-624-149A-1
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                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Equine herpesvirus 1
PUBLICATION INFORMATION:
AUTHORS: Telford,E.A.
AUTHORS: Watson, M.S.
AUTHORS: MCBride, K.
AUTHORS: Davison, A.J.
TITLE: The DNA sequence of equine herpesvirus-1
JOURNAL: Virology
VOLUME: 189
                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Version 3.0 SEQ ID NO 1
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Best Local Similarity 47.4%;
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TITLE OF INVENTION: gM-Negative EHV-Mutants without Heterologous Elements
FILE REFERENCE: 1/1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Neubauer, Antonie APPLICANT: Ziegler, Christi
                                                                                                                                                                                                                                                                                                                                                  ISSUE: 1
PAGES: 304-316
DATE: JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                 Local Similarity
les 75; Conserv
                                                          95602 TCAAGCCCATGAGCCACGGACCGGATATGGTTTCTGTATACCAGTCTCTGGGGCGCGTCA
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293 GAMATMATGCCACCATCGACCAGTGG 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150223
                                                                                                                                     CTGTGGTAACGGTGGGCCTTAGTTTTGATACGGCTCATTTCCACAGCATGTTTGCCTACG
                                                                                                                                                                          CTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACG
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                                                                                               GCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCA 292
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                                                                                                                                                                                                               7.1%;
ilarity 51.4%;
Conservative
                                                                                                                                                                                                               Score 32.4; Di
Pred. No. 2.8;
0; Mismatches
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                                                                                                                                                                                                                                                   DB 6;
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                                                                                                                                                                                                                                                     Length 150223;
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RESULT 6
US-10-788-792-27/c
; Sequence 27, Application US/10788792
; GENERAL INFORMATION:
                                                                                            ; ORGANISM: Homo sapiens US-10-788-792-27
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)
CURRENT APPLICATION NUMBER: US/B
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 14522
LENGTH: 1588
                                                                                                                                                                                      SOFTWARE: Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14522, Appl GENERAL INFORMATION:
Query Match 6.8%;
Best Local Similarity 55.7%;
Matches 59; Conservative
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                                                                                                                                                                                                                                APPLICANT: Eveleigh, Deepa
APPLICANT: Bigwood, Douglas
TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
FILE REFERENCE: 5152
CURRENT APPLICATION NUMBER: US/10/788,792
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US 60/450,655
PRIOR FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 254
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bayer Pharmaceuticals Corporation APPLICANT: Eveleigh, Deepa APPLICANT: Bigwood, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kovalic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Sorghum
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                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 GGCGGCGGCAATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 GGTGGTGGCGGCTTCGGTGGTGGTGGCTATGGCGGTGGCGGCGGTGGCTATGGTGGTGGC 514
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125; Conserv
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                                                                                                                                                                   1575
                                                                                                                                                                                                               PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTGGTGGTGTTGGTGATTATGGAGCTGCAGGTGGAGCTGGAGGCAACTTTGCTGCTGGA 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCGGTGGCTATGGTGGCTATGGTGGCAACTACGGCAACAGGGGTGGCGGTGGCTAT 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTGGTAGCTTTGGCGGTGGTTCCACTGGCGCCGAGAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.9%;
  Score 30.8; DE Pred. No. 1.2; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 31.4; DB 6; Length 1588; Pred. No. 0.76; 0; Mismatches 156; Indels 0
                                              DB 6;
                                              Length 1575;
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47;

Indels

0,

Gaps

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> GGÁTTTÓCATACAGTÓTGACCGTGCAGTTÓCTCAGTTÓGGTCAAAAGAACGTCGCGCTGG GGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCGCTGG

422

629 376 317

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, OTHER INFORMATION: Clone ID: US-10-767-701-28437
                                                                                                                         ; NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 28437
LENGTH: 300
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-10-767-701-28437
                Query Match 6.4
Best Local Similarity 54.1
Matches 60; Conservative
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US-10-767-471-10736/C
i Sequence 10736, Applic
i GENERAL INFORMATION:
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                                                                                                                                                                                APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KRY: misc_feature; LOCATION: (1)...(24900); LOCATION: (1)...(24900); OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables US-10-767-471-10736
                                                                                                                                                                                                                                                                                                                                                  Sequence 28437, Application US/10767701
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.5%;
Best Local Similarity 52.4%;
Matches 65; Conservative
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETI
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT PILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
LERGTH: 24900
TYPE: TAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10048 CÁGCÁTCCTGÁCTGCTTTTAGTGTCTCAAAAGTCCTGGGTCÁAGTGGTGCÁTÁÁTTGGTG 9989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9988 TCCTGAACCCAAACTGTATGGTACTAAAAATAGTGCAATCCTGGTTTGTTGTATATTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 CATTACCCAGAGCGGTTATGGTTAACGGCGCCGATGTAGGCCCAGGGTGCGGATAATAGTAC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATC 9925
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                               6.4%;
         Score 29.4; DB
Pred. No. 1.7;
0; Mismatches
                  0
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                                             DB
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                                          6;
           51;
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                                    Length 300;
       Indels
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Gaps
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RESULT 10
US-60-545-213-2134/c
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CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR FILING DATE: 2001-04-17
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SQCTWARE: Patentin Ver. 2.1
FENOM: 1504
Sequence 2134, Application US/60545213
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROKEY, KRISTIN L.
APPLICANT: HOET, REME
                                                                                                                                                                                                                                                                                    Matches
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NAME/KEY: CDS
LOCATION: (1)
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TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMI
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
FILE REFERENCE: DYAX/002 CIP2
                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1355
TYPE: DNA
                                                                                                                                                                                                                                                                                              Local
                                                                                  888 YAARGGSGCYATGACYGAXAAYGCYGAYGARAAYG 922
                                                                                                                               198
                                                                                                                                    828 YGGYMSYGGRGGYGGYMSYGGYMSYGGYGAYTTYGAYTAYGARAARATGGCMAAYGCYAA 887
                                                                                                                                                              138 CATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATC 197
                                                                                                                                                                                                                       768
                                                                                                                                                                                                                           78 GGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCGGACTCAACGTTGAG 137
                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                        Similarity 25.2
39; Conservative
                                                                                                              TGAAACGACCATTACCCAGAGCGGTTATGGTAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 GTAAGGGCGGCGGCTTATGGCGGCGGCGGCGGCTTACGGTGGCAACCGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 AAGAAGGCGGTTACGAAGCCGGTGGTTACGGTGGCGGCGGCGGCGGTTACGGCGGTCCCC
                                                                                                                                                                                                74 ANTGGGGCGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGGCCCGG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .. (1305)
                                                                                                                                                                                                                                                                                                                                                                                      Description of Artificial Sequence: M13-III nucleotide sequence
                                                                                                                                                                                                                                                                                       6.4%;
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                                                                                                                                                                                                                                                                 Score 29.4; DB Pred. No. 3.4; 50; Mismatches
                                                                                                                                                                                                                                                                                          DB 6; Length 1355;
                                                                                                                                                                                                                                                                     66;
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Myeth
APPLICANT: Mounts, william Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AMIO1083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18

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RESULT 12
US-60-545-213-6406/c
; Sequence 6406, Application US/60545213
; GENERAL INFORMATION:
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US-60-545-213-2135/c
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-545-213-2134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wyeth
APPLICANT: Weth
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
TILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 2135
LENGTH: 1400
TYPE: DNA
ORGANISM: Homo sapiens
US-60-545-213-2135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2135, Application US/60545213 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3
SEQ ID NO 2134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.4%;
Best Local Similarity 45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 6.4%;
Local Similarity 45.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  212 CCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCCAGGGTGCGGATAATAGTACTATTG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                108;
                                                                                                                                                                  CTGATTCCAGCGTAATGGTGCGTCAGGTTTGGGTTTTGGCAACAACGCCACGGCTAACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                 CCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGTTGGAGCAGGCGGTGCTGATGGCATTAACCTCGCTGTACTGGTCCATCAGGTTTTCT
                                                                                                                                                                                                                                                 CCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGTTAATCAGACCGCAT 391
                                                                                                                                                                                                                                                                                            TTGGGGTTCTCCATCCACTGCTTGAAAAGGCCAGAGACCATCTCCTCACACTCTGGAACT
                                                                                                                                                                                                                                                                                                                                    AACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACT 331
                                                                                                                                                                                                                                                                                                                                                                             CCCTGGGCGATAGCGTTGCAGTAGACGGTGGACCGCAGGTTGGGGGTGGATCGGGTTATTA 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGGGTTCTCCATCCACTGCTTGAAAAGGCCAGAGACCATCTCCTCACACTCTGGAACT
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                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 29.4; DB 7;
Pred. No. 3.5;
0; Mismatches 131;
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Pred. No. 3.5;
0; Mismatches 131; Indels
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APPLICANT: Mounte, William Martin
ITITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
ITITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILLING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 6407
LENGTH: 1447
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; ORGANISM: Homo sapiens
US-60-545-213-6406
                                                                                                                                                                                                                                                                                                                             Query Match 6.4%;
Best Local Similarity 45.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn
SEQ ID NO 6406
                                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AN101083 (031896-042099)
CURRENT FILLING IN NUMBER: US/60/545,213
CURRENT FILLING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1400
TYPE: DNA
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CTGATTCCAGCGTAATGGTGCGTCAGGTTTGGTTTTGGCAACGACGCCACGGCTAACCAG 450
                                                                                                                                                                                                                                                                 CCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACT 331
                                                                                              CCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCGCTGGTTAATCAGACCGCAT
                                                                                                                                           TTGGGGTTCTCCATCCACTGCTTGAAAAGGCCAGAGACCATCTCCTCACACTCTGGAACT 318
                                                                                                                                                                                 AACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACT 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGATTCCAGCGTAATGGTGCGTCAGGTTGGTTTTGGCAACAACGCCACGGCTAACCAG 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTG 271
                                                              CCGTTGGAGCAGGCGGTGCTGATGGCATTAACCTCGCTGTACTGGTCCATCAGGTTTTCT
                                                                                                                                                                                                                            CCCTGGGCGATAGCGTTGCAGTAGACGGTGGACCGCAGGTTGGGGGTGGATCGGGTTATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTGGGCGATAGCGTTGCAGTAGACGGTGGACCGCAGGTTGGGGTGGATCGGGTTATTA 378
                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No. 3.5;
0; Mismatches 131;
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                                                              258
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APPLICANT: Zyskind, Judith
APPLICANT: Zyskind, Judith
APPLICANY: FORSyth, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA,001C1
CURRENT APPLICATION NUMBER: US/10/771,241
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2004-01-27
PRIOR FILING DATE: 2000-01-27
PRIOR FILING DATE: 2000-01-27
NUMBER: OF SEQ ID NOS: 485
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 117
LENGTH: 249
TYPE: DNA
                                                                                              CURRENT FILING DATE: 2004-02-03

PRIOR APPLICATION NUMBER: 09/492,709

PRIOR FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: 60/117,405

PRIOR FILING DATE: 1999-01-27

INUMBER OF SEQ ID NOS: 485

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 29

LENGTH: 757

TYPE: DNA

ORGANISM: E. Coli

FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(757)
                                                                    ; OTHER INFORMATION: n = A,T,C \cdot or G US-10-771-241-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-10-771-241-29
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; ORGANISM: E. Coli
US-10-771-241-117
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US-10-771-241-117/c
                    Query Match
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      Matches
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Best Local Similarity
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CURRENT FILING DATE: 2004-02-03
                    Local Similarity
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52.5%;
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; Pred. No. 3.1;
0; Mismatches
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Pred. No. 1.8;
0; Mismatches 58; Indels
                              DB 6;
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384 GA 385
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                                            GGCACCGACTATCCCCAGCAGATAGTCATAAAGAATCCACCTCCATCTTTACCTGGCAT 383
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Search completed: March 17, 2004, 08:25:30 Job time: 71.6301 secs

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Title:
Perfect score:
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Maximum Match 100%
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Maximum DB
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEF
FILE REFERENCE: 920043,406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 456
TYPE: DNA
ORGANISM: Salmonella enteritidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
No.
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US-09-543-407-2
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31 US-10-360-457-3
40 US-10-33-860-1574
40 US-10-723-860-1574
10 US-10-231-416-3
31 US-10-231-426-3
32 US-09-949-016-12887
33 US-09-949-016-17052
39 US-09-947-911-51
30 US-09-947-911-51
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US-09-252-691C-171
US-10-417-886-171
US-10-146-492B-80
US-10-146-492B-81
US-09-139-449-3383
US-09-803-110-3383
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Sequence 171, App
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Sequence 80, Appl
Sequence 81, Appl
Sequence 3383, Ap
Sequence 342, App
Sequence 208, App
Sequence 13, Appl
Sequence 14, Appl
Sequence 154, Appl
Sequence 574, App
Sequence 174, Appl
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043,406
FILE REFERENCE: 920043,406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 4
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                                                                                                                                                                                                                                     LENGTH: 456
; TYPE: DNA
; ORGANISM: E. Coli
US-09-543-407-4
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                                                                                                                                                                 Query Match
Best Local Sim
Matches 379;
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                   Similarity
                                                       GCGACAAATTATGATCTGGCTCGTTCAGAATATAATTTTTGCGGTAAATGAATTAAGCAAG
                                                                                                 ATGAAAAACAAATTGTTATTTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCC
                                                                                                                   ATGAAAAACAAATTGTTATTTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACC
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                               GCAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAG
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                                                                                                                                                                 Score 332.8; DB 23;
Pred. No. 7.2e-92;
0; Mismatches 77;
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Pred. No. 4.9e-130;
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CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
SEQ ID NO 171
LENGTH: 561
TYPE: DNA
ORGANISM: Enterobacter cloacae
US-09-252-691-171
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US-09-252-691-171
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GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
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                                         GGAAATAAGGCCAATATTACCCAGTACGGTACGCAGAAAACAGCAGTTGTAGTGCAGAAA
                                                                                                                    GATGCCAGTATATCGCAAAGCGCTTACCGGTAATAGTGCAGCTATTATCCAGAAAGGTTCT
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Pred. No. 3.9e-80;
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GENERAL INFORMATION:

APPLICANT: Keith G. Weinstock et al.

APPLICANT: Keith G. Weinstock et al.

FITLE OF INVENTION: UCCLEIC ACID AND AMINO ACID SECTION:

FILL REFERENCE: 107196.135

CURRENT APPLICATION UNMBER: US/09/252,691C

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,145

PRIOR APPLICATION NUMBER: US 60/074,787

PRIOR APPLICATION NUMBER: US 60/074,787

PRIOR APPLICATION NUMBER: US 60/074,787

PRIOR APPLICATION NUMBER: US 60/074,787

PRIOR PILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 11326

SEQ ID NO 171

LENGTH: 561
RESULT 5
US-10-417-886-171
Sequence 171, Application US/10417886
GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER;
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
CURRENT APPLICATION MYMBER: US/10/417,886
; CURRENT FILING DATE: 2003-04-17
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; ORGANISM: Enterobacter cloacae
US-09-252-691C-171
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78.0%;
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Pred. No. 3.9e-80;
); Mismatches 100;
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Sequence 80, Application US/10146492B
GENERAL INFORMATION:
APPLICANT: MWG Biotech AG
ITITLE OF INVENTION: Biochip
FILE REFERENCE: REN-14043
CURRENT FILLING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: US/10/146,492B
PRIOR APPLICATION NUMBER: EP 0111279.5
PRIOR APPLICATION NUMBER: EP 0111279.5
PRIOR FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 12816
SEQ ID NO 80
PRIOR FILING BATE: 2001-05-17
LENGTH: 100
                                         US-10-146-492B-80
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US-10-146-492B-80
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PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,145
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 11326
SEQ ID NO 171
LENGTH: 561
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                                               OTHER INFORMATION: csgb bl042 U00096 1103174..1103629 PUBLICATION INFORMATION: RELEVANT RESIDUES: 39-58
                                                                                                    TYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655
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Best Local Similarity
Matches 355; Conserv
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78.0%;
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Pred. No. 3.9e-80;
0; Mismatches 100;
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US-10-146-492B-81
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US-10-146-492B-81
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US-10-146-492B-82
; Sequence 82, Appli
; GENERAL INFORMATIO
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                                                                                                                                                                                                                                                                                                                   Sequence 81, Application US/10146492B
GENERAL INFORMATION:
APPLICANT: MWG Biotech AG
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TITLE OF INVENTION: Biochip
FILE REFERENCE: REN-14043
CURRENT APPLICATION NUMBER: US/10/146,492B
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: EP 0111279.5
PRIOR FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 12816
           Best Local Similarity
Matches 78; Conserv
                                             Query Match
                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 12816
SEQ ID NO 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                            OTHER INFORMATION: csgb b1042 U00096 1103174..1103629
FUBLICATION INFORMATION:
RELEVANT RESIDUES: 38-57
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                                                                                                                                                                                                                       TITLE OF INVENTION: BIOCHIP
FILE REFERENCE: REN-14043
CURRENT APPLICATION NUMBER: US/10/146,492B
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: EP 0111279.5
PRIOR FILING DATE: 2001-05-17
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 82
LENGTH: 100
                                                                                                                                    LENGTH: 100
TYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: csgb b1042 U00096 1103174..1103629
PUBLICATION INFORMATION:
RELEVANT RESIDUES: 57-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 CCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGAA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 TTCATTTAATCAGGCGGCCATTATTGGTCAAGTCGGCACGGATAATAGTGCCAGAGTACG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ATGGTĀĀTĀCTGCGATGĀTTĀTCCĀGĀĀĀĀGGTTCTGGTĀĀ 100
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          Conservative
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                     14.2%;
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79.0%;
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      Score 64.8; D
Pred. No. 4.4e
0; Mismatches
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Pred. No. 1.4e-09;
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0; Mismatches 16;
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.4e-09;
22;
                               DB 45;
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                               Length 100;
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Gaps

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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
FILE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT APPLICATION NUMBER: US/09/514,000
PRIOR APPLICATION NUMBER: US/09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 3383
LENGTH: 438
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
US-09-739-449-3383
                                                          APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Ge:
FILE REFERENCE: 38-10(15490) B
CURRENT APPLICATION NUMBER: US/09/803,110
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION UNMBER: US 09/739,449
PRIOR FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: US 60/168,139
PRIOR FILING DATE: 1999-12-01
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US-09-739-449-3383
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                 NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 3383
LENGTH: 438
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Best Local Similarity
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Pred. No. 0.017;
0; Mismatches 143;
                                                                                                                                                                                                      Genome Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 438;
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RESULT 12
US-09-739-449-208
; Sequence 208, A
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                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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   Application US/09739449
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RESULT 11
US-09-514-000-342/c
; Sequence 342, Application US/09514000
; GENERAL INFORMATION:
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FILE REFERENCE: 38-10(15.490) B
CURRENT PEPPLICATION UNMERR: US/09/514,000
CURRENT FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 15034
SEQ ID NO 342
LENGTH: 29058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hinkle, Gregory J. APPLICANT: Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                18622 ATCCGCACCTACCAGAACGGCGGTTACAACCGGATCGTCGGCCACCAGTATGGTCGTCAC 1856
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                                         TACGGTACGCAGAAAACAGCAGTTGTAGTGCAG 417
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                                                                                          AACCGCAACGTGGCCGGCATCGGCCAGTTCGGCTCCAACCACCACCCATCCTGACCCAG 18443
                                                                                                                                     TACGGTAATAGTGCAGCTATTATCCAGAAAGGTTCTGGAAATAAGGCCAATATTACCCAG 384
                                                                                                                                                                                    AACCTTTCGGCTGTCGGTCAGGAAGGGGCATGACAATTACGGTTCCACCACCCAGAACGGC 18503
                                                                                                                                                                                                                             AACTTTGCGTATATTGAGCAAACGGGCAATGCCAACGATGCCAGTATATCGCAAAGCGCT 324
                                                                                                                                                                                                                                                                                                                          GACGGCAATGGCAACATTGCTGCAGGCGTTCAG
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Pred. No. 0.073;
0; Mismatches 143;
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Pred. No. 0.017;
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PRIOR APPLICATION NUMBER: US 09/739,449
PRIOR FILING DATE: 2000-12-19
PRIOR PRIOR PAPPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: US 60/168,139
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 208
LENGTH: 187892
                                            ; NAME/KEY: unsure
; CATTION: (1)..(187892)
; OTHER INFORMATION: unsure
US-09-803-110-208
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        Query Match
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GENERAL INFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/514,000
PRIOR FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 13351
SEQ ID NO 208
LENGTH: 187892
TYPE: DNA
ORGANISM: Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/803,110
CURRENT FILING DATE: 2001-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490) D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 130;
                                                                                                                               ORGANISM: Agrobacterium tumefaciens
                                                                                                                             FEATURE:
                                                                                                                                                               TYPE: DNA
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APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)C
CURRENT APPLICATION NUMBER: US/09/739,449
CURRENT FILING DATE: 2000-12-19
CURRENT FILING DATE: 2000-12-19
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LOCATION: (1)...(187892)
OTHER INFORMATION: unsure at all n locations
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Pred. No. 0.14;
0; Mismatches 143; Indels 0;
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Score 44.2;

DB 33;

Length 187892;

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RESULT 14
US-08-466-194-14/c
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                                                                                                               INFORMATION FOR SEQ ID NO:
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IMMEDIATE SOURCE:
    CLONE: pTZgpt-
                                                                                                                                                               REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/935,313
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/466,194
FILING DATE: 06-JUN:1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,463
FILING DATE: 22-ARR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SCHEIFLINGER, F. APPLICANT: FALKNER, F. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                              STRANDEDNESS:
                                                                                                                                                                                                              NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                            TOPOLOGY:
                                                                              LENGTH:
                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: DC
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                                                                                                                                                 (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Foley & Lardner 3000 K Street, NW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FALKNER, F. G.
VVENTION: RECOMBINANT FOWLPOX VIRUS
                          linear
                                         single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
US-09-543-407-13
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                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
                                                                                                                                                                                                                Query Match 8.2%;
Best Local Similarity 51.2%;
                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DORAN, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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392 CGCAGAAAACAGCAGTTGTAGTGCAGAAACAGTCGCATATGGCTATTCGCGT 443
                                     263 GTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACG 322
                                                                            332 ATAGTGCAGCTATTATCCAGAAAGGTTCTGGAAATAAGGCCAATATTACCCAGTACGGTA 391
                                                                                                                                        272 CGTATATTGAGCAAACGGCCAATGCCAACGATGCCAGTATATCGCAAAGCGCTTACGGTA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        423 G 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 TGCCAGTATATCGCAAAGCGCTTACGGTAATAGTGCAGCTATTATCCAGAAAGGTTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 CCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGAAGGAGGAAATAATCGGGCGAA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 TTCATTTAATCAGGCGGCCATTATTGGTCAAGTCGGCACGGATAATAGTGCCAGAGTACG
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                                                                                                                                                                                                   88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                     CGACCATTACCCAGAGCGGTTATGGTAACGCCGCTCGATGTAGGCCAGGGTGCGGATAATA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTCGACCAGGCAGGAATTATAACTTTGCGTATATTGAGCAAACGGGCAATGCCAACGA 302
                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                           Score 37.6; DB 23; Length Pred. No. 2; 0; Mismatches 84; Indels
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                                                                                                                                                                                                                                    Length 456;
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323 CTAAAAACTCCGATATTACTGTCGGCCAATATGATCAGCTGGTTACCCGTGT 374

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Search completed: March 18, 2004, 02:46:45 Job time: 2935.24 secs

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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
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US-10-767-471-18837
US-10-767-471-8837
US-10-767-471-8439
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                    Sequence 554, App
Sequence 3321, App
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Sequence 2887, App
Sequence 8837, App
Sequence 342, App)
Sequence 44, Appl
Sequence 45, Appl
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6.2	6.2	6.2	6.3	6.3	6.3	6.3	6.3	6.3	6.3	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.5
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US-60-548-091-8	US-60-548-091-9	US-10-771-241-139	US-10-417-375A-63	US-10-486-977-58	US-10-417-884A-2080	US-09-741-873C-3	US-10-779-543-12419	US-10-767-471-10892	US-10-767-471-10755	US-10-765-790-48	US-10-417-375A-18	US-10-100-683-2753	US-10-100-683-1253	US-10-765-790-70	US-10-779-271-1	US-10-417-375A-125	US-10-767-701-3762	US-10-487-578-44
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
8, Appli	9, Appli	139, App	63, Appl	58, Appl	2080, Ap	<ol> <li>Appli</li> </ol>	12419, A	10892, A	10755, A	48, Appl	18, Appl	2753, Ap	1253, Ap	70, Appl	<ol> <li>Appli</li> </ol>	125, App	3762, Ap	44, Appl

## ALIGNMENTS

Sequence 554, Application PC/TUS0402000

[GENERAL INFORMATION:

[APPLICANT: Science Applications International Corporation

[FITLE OF INVENTION: Method and System for Identifying Biological and Environmental Samples

[FILE REFERENCE: 36609-183264 (SAIC0087-PCT)

[CURRENT APPLICATION NUMBER: PCT/US04/02000

[CURRENT APPLICATION NUMBER: PCT/US04/02000

[CURRENT FILING DATE: 2004-01-23

[PRIOR APPLICATION NUMBER: US 60/441,745

[PRIOR APPLICATION NUMBER: US 60/441,806

[PRIOR APPLICATION NUMBER: US 60/441,806

[PRIOR FILING DATE: 2003-01-23

[PRIOR FILING DATE: 2003-01-23

[PRIOR FILING DATE: 2003-01-23

[PRIOR FILING DATE: 2003-01-23

[PRIOR FILING DATE: 2003-01-23 ; TYPE: DNA; Clostridium perfringens PCT-US04-02000-554 SOFTWARE: PatentIn version 3.2 SEQ ID NO 554 LENGTH: 500 Query Match Best Local Similarity Matches 147; Conserv 57 AACCGCGACAAATTATGATCTGGCTCGTTCAGAATATAATTTTGCGGTAAATGAATTAAG 116 AGTACGCCAGGAAGGATCAAAACTATTGTCCGTTATTTCACAAGAAGGAGGAAATAATCG 236 CTCTGTTGAAAATGATTTAAATAGCGAGTAC GGCGAAAGTCGACCAGGCAGGGAATTATAACTTTGCGTATATTGAGCAAACGGGCAATGC 296 TATAGTTCCTGATATTACAAATCCATTCTTTGGATCAATAATAAAAAGGAATAAGTGATGT 247 CTATACTCCTAGTGCTATTGCTAGAAGTCTTTCAAAAAGTATTACTAATACTATTGGAGT 187 AATAAAGGCTATTAAAAACATTAAAAGAACAAAGAATTAGGGGGAATTATAAATTTGTCCAAC 367 CAACGATGCCAGTATATCGCAAAGCGCTTACGGTAATAGTGCAGCTATTATCCAGAAAGG 356 CAAGTCTTCATTTAATCAGGCGGCCATTATTGGTCAAGTCGGCACGGATAATAGTGCCAG 176 TGCAGAAGTGCATAATCTTAATTTGATTCTTTGTGACTCTAACGAGAGTATCGATAGGGA TTCTGGAAATAAGGCCAATATTACCCAGTAC 387 8.0%; ilarity 44.4%; Conservative 0 Score 36.6; DB 1; Pred. No. 0.051; Mismatches 184; ying Biological Entities Samples Length 500; Indels 0; Gaps 307

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CURRENT FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: 10/076,555
PRIOR FILING DATE: 2002-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Williams et al
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS
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APPLICANT: Gannon, Allison
APPLICANT: Harvey, Jeanne
APPLICANT: Harvey, Jeanne
APPLICANT: Lechner, John F.
APPLICANT: Lechner, John F.
APPLICANT: Lichner, John F.
APPLICANT: Lichner, John F.
APPLICANT: Lichner, John F.
APPLICATION: Identification and Verification of Methylation Marker Sequences
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: US/10/765,790
PRIOR APPLICATION NUMBER: US/10/737,082
NUMBER OF SEQ ID NOS: 300
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ORGANISM: Homo sapiens
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                                                                                                                                                          APPLICATION NUMBER: 607105,234
FILING DATE: 1998-10-21
APPLICATION NUMBER: 09/297,648
FILING DATE: 2000-04-10
APPLICATION NUMBER: PCT/US99/01619
FILING DATE: 1999-01-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270593 ACTAAGAACAGGAAACCAGATGAGAGTATGTGGAAACATAGAATA 270549
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/217,471
FILING DATE: 1998-12-21
APPLICATION NUMBER: 60/068,755
FILING DATE: 1997-12-23
APPLICATION NUMBER: 60/080,664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270713 ÁGÁÁATÁTÍTÍTÍTÍTÍTÍTTTGÍAGÍATGTTÍÁĆTÍGAAAAĆTAĆTGGGÁACAAÁÁĆATGGT 270654
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                                                          FILING DATE: 1998-01-28 APPLICATION NUMBER: 60/075,954
                                                                                                      APPLICATION NUMBER: 60/072,910 FILING DATE: 1998-01-28
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60/080,114
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CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8836
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-10-767-471-8836
                                                                                                                                                             US-10-767-471-34493/c
; Sequence 34493, Application US/10767471
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; PRIOR FILING DATE: 1998-03-31
; Remaining Prior Application data removed - Se
; NUMBER OF SEQ ID NOS: 23767
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9321
; LENGTH: 418
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-779-543-9321
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34493
LENGTH: 201
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US-10-767-471-8836, Application US/10767471
                                 APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETE
FILE REFERENCE: CLOO1505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
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Best Local
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THERBOF
FILE REFERENCE: CL001505
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70; Conserv
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55.6%;
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53.0%;
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Pred. No. 0.78;
1; Mismatches 47;
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Pred. No. 0.72;
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                                                                                                     DETECTION AND USES THEREOF
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US-10-767-471-10718/c
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; LENGTH: 1227
; TYPE: DNA
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-501
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US-10-767-471-501/c
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Best Local S
Matches 60
                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 10718
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                                         Query Match
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Best Local
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NAME/KEY: misc feature

LOCATION: (1) ... (76573)

OTHER INFORMATION: n = A,T,C or G,

-10-767-471-10718
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TITLE OF INVENTION: GENETIC POLYMORPHISMS
TITLE OF INVENTION: REUMATION ARTHRITIS,
FILE REFERENCE: CLOO1505
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: HERDMATOID ARTHRITIS, METHODS OF DETE
FILE REFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50331
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                            LENGTH: 76573
TYPE: DNA
ORGANISM: Homo mapiens
                      Local
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Local Similarity 55.6%;
Les 60; Conservative
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cn 7.1%;
l Similarity 55.6%;
60; Conservative
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55.6%;
  Score 32.4; DB 6; Length 76573; Pred. No. 4.3; 1; Mismatches 47; Indels 0;
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                                                                                                 or insertion/deletion polymorphism (see Tables 1-
                                                                                                                                                                                                                                                                                                                                                        ASSOCIATED WITH , METHODS OF DETECTION AND USES THEREOF
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US-10-775-169-342/c
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                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.2 SEQ ID NO 342
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GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihua
                                                                                                                          Matches
                                                                                                                                           Query Match
Best Local Similarity
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LENGTH: 1310
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APPLICANT: Dorner, Andrew
APPLICANT: Trepicchio, William
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In
FILE REFERENCE: AM101080 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5278
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CURRENT FILING DATE: 2004-01-30.
NUMBER OF SEQ ID NOS: 117596
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 38-21(53534)B
                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C71322_1
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                                                                                                                                                                                                                                                                    LENGTH:
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  CGACAAATTATGATCTGGCTCGTTCAGAATATAATTTTGCGGTAAATGAATTAAGCAAGT 121
                                        TGAAAAACAAATTGTTATTTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACCG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATGCATCCATTGTTCCCAATGAGGATGGGAACATTGCCTGAAAATGGCTATGAATGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burczynski, Michael
                                                                                                                          Conservative
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                                                                                                                                           7.0%;
51.0%;
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55.4%;
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                                                                                                                                         Score 31.8; DI
Pred. No. 3.1;
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Pred. No. 1.8;
                                                                                                                        Mismatches
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                                                                                                                                                             Length 5495;
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RESULT 12
US-60-548-091-5725
, Sequence 5725, Application US/60548091
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; ORGANISM: Homo sapiens
US-10-767-471-34439
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US-10-767-471-34439/c
Sequence 34439, Application US/10767471
GENERAL INFORMATION:
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CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTMARE: FASTSEQ for Windows Version 4.0
FENOMERY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PROPERTY OF TAXABLE PR
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-8837
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US-10-767-471-8837/c
; Sequence 8837, Application US/10767471
; GENERAL INFORMATION:
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001505
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Best Local !
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SEQ ID NO 8837
LENGTH: 201
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CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 55.6%; hes 60; Conservative
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                                                                                                                                       123 AGGATTATCATGTACATGATGASGCAGAGCAGGAACAGAAAAAGCTGG
                                                                                                                                                                                       386 ACGGTACGCAGAAAACAGCAGTTGTAGTGGAGAAACAGTCGCATATGG 433
                                                                                                                                                                                                                                                 183 ATGGGAGTATGGAGGCGAGAATCCAAGATGGTGATGATAATGAGGAGGCTATTTCCCAGG
                                                                                                                                                                                                                                                                                                    326 ACGGTAATAGTGCAGGTATTATCCAGAAAGGTTCTGGAAATAAGGCCAATATTACCCAGT 385
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                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/257,047
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: PCT/GB01/01599
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: GB 0008582.9
PRIOR FILING DATE: 2000-04-08
PRIOR FILING DATE: 2000-04-08
PRIOR FILING DATE: 2000-04-08
SOFTWARE: Patentin Ver. 2.1
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Best Local S
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                                                                                                                                                                                               Matches
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LENGTH: 309
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GENERAL INFORMATION:
APPLICANT: STEWARD, MICHAEL
APPLICANT: COX, VIVIENNE FRANCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-60-548-091-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA INMUNIZATION VECTORS FILE REFERENCE: 37945-0041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SEQ ID NO 5725
SEQ ID NO 5725
LENGTH: 394468
                                                                                                                                                                                                                                                                                                 TYPE: DNA
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LOCATION: (1)...(394468)
COTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-;
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                                            192 CACCGAÁGAAGACTCTÓGTTCTAACGGAÁAGATTACTTGCGAÁTGTÁCTAÁGCCAGA
252 ČT 253
                              122 CT 123
                                                                                                                                 132
                                                                       62 CGACAAATTATGATCTGGCTCGTTCAGAATATAATTTTGCGGTAAATGAATTAAGCAAGT 121
                                                                                                                                     2 TGAAAAAACAAATTGTTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACCG
                                                                                                                                                                                               65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 ATCGGGCGAAAGTCGACCAGGCAGGGAATTATAACTTTGCGTATATTGAGCAAACGGGCA 292
                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                        6.8%;
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57.9%;
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                                                                                                                                                                                                     Score 30.8;
Pred. No. 2.
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Pred. No. 18;
0; Mismatches
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RESULT 14 US-10-257-047-46

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CURRENT APPLICATION NUMBER: US/10/257,047
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: PCT/GB01/01599
PRIOR FILING DATE: 2001-04-09
PRIOR PILING DATE: 2000-04-08
PRIOR FILING DATE: 2000-04-08
PRIOR FILING DATE: 2000-04-08
NUMBER OF SEO ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 46
LENGTH: 309
TYPE: DNA
ORGANISM: Plasmodium falciparum
US-10-257-047-46
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SEQ ID NO 44

LENGTH: 3147

TYPE: DNA

ORGANISM: Artificial Sequence

PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Vector
OTHER INFORMATION: pVK104-01

US-10-257-047-44
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US-10-257-047-44
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GENERAL INFORMATION:
APPLICANT: STEWARD, MICHAEL
APPLICANT: COX, VIVIENNE FRANCES
TITLE OF INVENTION: DNA IMMUNIZATION VECTORS
FILE REFERENCE: 37945-0041
                                                                                                                                                                                    Query Match 6.8%; Score 30.8; DB 6; Length 3147; Best Local Similarity 53.3%; Pred. No. 5.3; Matches 65; Conservative 0; Mismatches 57; Indels 0
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Best Local Similarity 53.3%;
Matches 65; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/257,047
CURRENT FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: PCT/GB01/01599
PRIOR FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: GB 0008582.9
PRIOR FILING DATE: 2000-04-08
NUMBER OF SEQ ID NOS: 66
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TITLE OF INVENTION: DNA IMMUNIZATION VECTORS
FILE REFERENCE: 37945-0041
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                                                                                       198 TGAGAACCCAAACCCTACCTGTAACGAGAACAACGGTGGATGCGACGCTGACGCTAAGTG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 CT 123
258 CACCGAAGAAGACTCTGGTTCTAACGGAAAGAAGATTACTTGCGAATGTACTAAGCCAGA 317
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                              62 CGACAAATTATGATCTGGCTCGGTCAGAATAATAATTTTGCGGTAAATGAATTAAGCAAGT 121
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                                                                                                                                  2 TGAAAAACAAATTGTTATTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACCG 61
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Search completed: March 17, 2004, 08:25:32 Job time: 71.6301 secs OLISH WWW TH FOWER SIHL

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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2: /cgn2_6/ptodata/2/pna/US08_C

3: /cgn2_6/ptodata/2/pna/US080_C

4: /cgn2_6/ptodata/2/pna/US081_C

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69. / cgp2_6/prodates/2/pna/USI013C
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 1

US-09-543-407-3

Sequence 3, Application US/09543407

ERNERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

FILE REFERENCE: 920043-406

CURRENT FILING DATE: 2000-04-05

CURRENT FILING DATE: 2000-04-05

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 456

TYPE: DNA

ORGANISM: E. Coli
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13 US-09-741-873B-3
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GENERAL INFORMATION:
APPLICANT: Hultgren, Scott
APPLICANT: Matt, Chapman
ITITE OF INVENTION: BACTERIAL MODEL SYSTEM FOR AMYLOID FORMATION
FILE REFERENCE: WSHU 2059
CURRENT APPLICATION NUMBER: US/60/352,946
CURRENT FILING DATE: 2002-01-30
CURRENT FILING DATE: 2002-01-30
SOFTWARE: Patentin version 3.0
LENGTH: 453
TYPE: DNA
ORGANISM: Escherichia coli
US-60-352-946-1
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US-60-352-946-1
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Pred. No. 8.9e-130;
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US-60-444-371-1
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GENERAL INFORMATION:
APPLICANT: Hultgren, Scott J
APPLICANT: Matt, Chapman R
TITLE OF INVENTION: BACTERIAL MODEL SYSTEM FOR AMYLOID FORMATION
FILE REFERENCE: WSHU 2059.1
CURRENT APPLICATION NUMBER: US/60/444,371
CURRENT FILING DATE: 2003-01-31
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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Best Local Similarity
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TYPE: DNA
ORGANISM: Escherichia
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APPLICANT: OLSEN, Arne
APPLICANT: OLSEN, Arne
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WEL
FILE REFERENCE: 012889-081
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: US 0801723-1
EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER APPLICATION NUMBER: US 07/347,189
EARLIER FILING DATE: 1988-05-04
EARLIER FILING DATE: 1989-05-04
EARLIER FILING DATE: 1991-11-05
EARLIER APPLICATION NUMBER: US 07/789,437
EARLIER APPLICATION NUMBER: US 07/970,846
EARLIER APPLICATION NUMBER: US 08/87,865
EARLIER APPLICATION NUMBER: US 08/87,865
EARLIER FILING DATE: 1992-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER APPLICATION NUMBER: US 08/87,865
EARLIER APPLICATION NUMBER: US 08/87,865
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EARLIER APPLICATION NUMBER: US 08/87,865
EARLIER APPLICATION NUMBER: US 08/87,865
EARLIER FILING DATE: 1994-01-0-5
EARLIER APPLICATION NUMBER: US 08/495,959
EARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
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; LOCATION: (83)..(538)
US-08-978-878-3
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SEQ ID NO 3
LENGTH: 675
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Best Local Similarity
Matches 454; Conserv
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                                                                   GGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT 420
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     GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA
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Pred. No. 9.9e-129;
0; Mismatches 2;
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442

382

240 262

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Sequence 3, Application US/09741873B

Sequence 3, Application US/09741873B

GENERAL INFORMATION:

APPLICANT: Normark, Staffan

APPLICANT: Olsen, Arne

FIILE OF INVENTION: Fibronectin Binding Protein As Well As Its Prep

FILE REFERENCE: 012889-084

CURRENT FILING DATE: 1030-04-04

PRIOR APPLICATION NUMBER: US/09/741,873B

PRIOR FILING DATE: 1998-05-06

PRIOR FILING DATE: 1998-05-06

PRIOR PILING DATE: 1997-11-26

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR FILING DATE: 1999-05-04

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR APPLICATION NUMBER: US 07/347,189

PRIOR FILING DATE: 1991-11-06

PRIOR APPLICATION NUMBER: US 07/789,437

PRIOR FILING DATE: 1991-11-05

PRIOR APPLICATION NUMBER: US 07/789,437

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/187,865

PRIOR APPLICATION NUMBER: US 08/318,519

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin version 1 0
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CORGANISM: Escherichia c
FEATURE:
NAME/KEY: CDS
LOCATION: (83) ..(538)
US-09-741-873B-3
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US-09-741-873B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 675
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503
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         GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 456
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                                                                   GGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT
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ilarity 99.6%; Pred. No. 9.9e-129;
Conservative 0; Mismatches 2;
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Its Preparation

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RESULT 7
US-09-741.873B-1
; Sequence 1, Application US/09741873B
; GENERAL INFORMATION:
; APPLICANT: Normark, Staffan
; APPLICANT: Olsen, Arne
; TITLE OF INVENTION: Fibronectin Bindi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS :
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
EARLIER FILING DATE: 1988-05-06
EARLIER FILING DATE: 1988-05-06
EARLIER FILING DATE: 1989-05-04
EARLIER FILING DATE: 1991-01-04
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1991-11-06
EARLIER FILING DATE: 1992-11-03
EARLIER FILING DATE: 1992-11-03
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-10-05
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1994-01-28
EARLIER FILING DATE: 1995-06-28
UNDMER OF SEQ ID NOS: 10
SOFTWARE: PATENTION OWNER: US 08/495,959
UNDMER OF SEQ ID NOS: 10
SOFTWARE: PATENTION DATE: 1995-06-28
TYPE: DNA
ORGANITSM. FECHACTION OF COLUMBER: US 08/495,959

NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTION OF COLUMBER: US 08/495,959

NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTION OF COLUMBER: US 08/495,959
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; ORGANISM: Escherichia coli
US-08-978-878-1
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Best Local S
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96; Conservative
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100.0%; Prr
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; Pred. No. 3e-111;
0; Mismatches 0;
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Sequence 172, Application US/09252691B

GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ITTLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NO 172
LENGTH: 477
TYPE: DNA
ORGANISM: Enterobacter cloacae
US-09-252-691-172
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US-09-252-691-172
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CURRENT APPLICATION NUMBER: US/09/741,873B
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR PRILING DATE: 1989-05-04
Query Match
Best Local Similarity
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Best Local Similarity
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TYPE: DNA
ORGANISM: Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR FILING DATE: 1991-11-06
OR APPLICATION NUMBER: US 07/970,846
OR FILING DATE: 1992-11-03
OR APPLICATION NUMBER: US 08/187,865
OR FILING DATE: 1994-01-28
OR APPLICATION NUMBER: US 08/318,519
OR FILING DATE: 1994-10-05
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larity 100.0%; Pred. No. 4e-100;
Conservative 0; Mismatches 0
60.7%;
75.4%;
Score 276.8; DB 17; Pred. No. 2.4e-74;
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RESULT 9
US-09-252-691C-172
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                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SEQ ID NO 172
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                                                                                                                                                                                                                                              Matches 344;
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND
FILE REFERENCE: 107196.135
                                                                                                                                                                                                                                                                                                                                              LENGTH: 477
TYPE: DNA
ORGANISM: Enterobacter cloacae
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                       CCAAATTCTGAGCTGAACATTTACCAGTACGGCGGTGACCTCTGCACTTGCACTTGCAA 180
                                                                               GETETTETTECTEAGTACGECGECGECGGTAACCACGGTGGTGGCGGTAATAATAGCGGC
GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 456
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; ORGANISM: Enterobacter cloacae
US-10-417-886-172
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US-10-417-886-172
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Best Local Similarity 75.4%;
Matches 344; Conservative
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LENGTH: 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/094,145
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 11326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: US/09/252,691C
PRIOR FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/417,886
CURRENT FILING DATE: 2003-04-17
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
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Pred. No. 2.4e-74;
0; Mismatches 112;
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Best Local S
Matches 330
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GENERAL INFORMATION;
APPLICANT: Kay, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/233
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 3723836 SEEDANBERRY INFORMATION FOR SEQ ID NO: 56:
                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
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STRANDEDNESS: sing
TOPOLOGY: linear
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STATE: Washington
COUNTRY: U.S.A.
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                                                                                   -CCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAA 180
                                                                                                                           GGCGTCGTTCCACAATGGGGCGGCGGCGGCAATAGTTCCGGC
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AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
                                                           CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
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6300 Columbia Center, 701 Fifth Avenue
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Collinson, S. Karen
Clouthier, Sharon C.
Doran, James L.
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                                                                                                                                                                                                                                                         Score 254.4; DB 6;
Pred. No. 2e-67;
0; Mismatches 126;
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; TYPE: DNA
; ORGANISM: Salmonella
US-09-543-407-1
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GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
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APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM
TITLE OF INVENTION: PRESENTATION OF HETEROLOG-
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
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NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Ve-
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RESULT 14 US-09-543-407-19

Sequence 19, Application GENERAL INFORMATION:

US/09543407

APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. K
APPLICANT: Kay, William W.

. Karen

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; FEATURE:
; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA;
; OTHER INFORMATION: sequence containing the replacement fragmer;
; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 23
LENGTH: 456
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Best Local Similarity
Matches 320; Conser
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
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                     GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 456
                                                                    CATGAAATGGCACATGCAAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
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GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION PRESENTATION OF HETEROLOGOUS PEI FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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US-09-543-407-17
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                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09543407 GENERAL INFORMATION:
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Best Local S
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LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
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Pred. No. 5.4e-62;
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                             GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 456
                                                                                              GGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT
                                                                                                                                                                                               GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
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GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
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Pred. No. 5.2e-60;
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Search completed: March 18, 2004, 02:46:48 Job time : 2925.24 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
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Gapop 10.0 , Gapext 1.0
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456
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 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
             US-09-741-873C-3
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US-10-021-69BA-715
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US-10-021-69BA-1006
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                                      Sequence 3, Appli
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Sequence 715, App
Sequence 1006, Ap
Sequence 593, Ap
Sequence 5635, Ap
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Sequence 31342, A
Sequence 13342, A
Sequence 13343, A
Sequence 1398, Ap
Sequence 61343, Appl
Sequence 614, Appl
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	portugation
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ALIGNMENTS

## RESULT 1 US-09-741-873C-3 ¡ Sequence 3, Application US/09741873C ¡ GENERAL INFORMATION: APPLICANT: Normark, Staffan APPLICANT: Olsen, Arne TITLE OF INFORMATION: ¡ PRIOR REFERENCE: 01289-084 [ CURRENT FILLING DATE: 0200-12-22 ¡ PRIOR APPLICATION NUMBER: US/09/741,873C [ CURRENT FILLING DATE: 1998-05-06 ] PRIOR APPLICATION NUMBER: US 08/978,878 PRIOR FILLING DATE: 1997-11-66 PRIOR APPLICATION NUMBER: US 07/347,189 PRIOR APPLICATION NUMBER: US 07/970,846 PRIOR APPLICATION NUMBER: US 07/970,846 PRIOR APPLICATION NUMBER: US 07/970,846 PRIOR APPLICATION NUMBER: US 07/970,846 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR PILING DATE: 1992-11-03 ¡ PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR PILING DATE: 1994-01-28 ¡ PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR PILING DATE: 1994-01-28 ¡ PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR PILING DATE: 1994-01-28 ¡ PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR PILING DATE: 1994-01-28 ¡ PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR PILING DATE: 1994-01-28 ¡ PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR PILING DATE: 1994-01-28 ¡ PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR PILING DATE: 1994-01-28 ¡ PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR PILING DATE: 1994-01-28 ¡ PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,878 PRIOR APPLICATION NUMBER: US 08/187,878 PRIOR APPLICATION NUMBER: US 08/187,878 PRIOR A

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143 121

CCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAC

120

180

Matches

454; Conservative

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ATGAAACTTTTAAAAGTAGCAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCTGTGGCA 142

Query Match Best Local Similarity

99.3%;

Score 452.8; DB 5; Pred. No. 2.3e-145; 0; Mismatches 2;

Length Indels

675;

Gaps

60

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Sequence 1, Application US/09741873C

GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As
FILE REFERENCE: 012889-084
CURRENT APPLICATION UNMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR APPLICATION NUMBER: US 07/790,846
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
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Best Local
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396; Conserv
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                                                                                       ACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGGGGGTAATGGTGCAGAT
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RESULT 4 US-10-021-698A-715

Sequence 715, Application US/10021698A GENERAL INFORMATION:

KEITH,

TIM E, RANDALL

LITTLE,

APPLICANT: APPLICANT: APPLICANT:

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

VAN EERDEWEGH, PAUL DUPUIS, JOSEE DEL MASTRO, RICHARD SIMON, JASON ALLEN, KRISTINA PANDIT, SUNIL

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US-10-765-790-58/c
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APPLICANT: Li, Zheng
TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
FILE REFERENCE: 1657/2015
CURRENT APPLICATION NUMBER: US/10/765,790
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION UNUMBER: US 10/737,082
PRIOR APPLICATION UNMBER: US 10/737,082
PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 300
SOFTWARE: Patentin version 3.2
SEQ ID NO 58
LENGTH: 79977
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Best Local Similarity 48.2%;
Matches 96; Conservative
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APPLICANT:
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GGTGGTGATGGTGAAGATG 14949
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Gannon, Allison
Harvey, Jeanne
Lechner, John F.
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Pred. No. 0.59;
0; Mismatches 103;
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TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY FILE REFERENCE: 2976-4044USI CURRENT APPLICATION NUMBER: US/10/021,698A CURRENT FILING DATE: 2001-10-22 PRIOR APPLICATION NUMBER: 60/211,749 PRIOR APPLICATION NUMBER: 60/211,749 PRIOR PILING DATE: 2000-06-14 NUMBER OF SEQ ID NOS: 6160 SOPTWARE: Patentin 2.1 SEQ ID NO 7.15
                                                                                                                 NAME/KEY: modified base LOCATION: (90344)..(90443) OTHER INFORMATION: a, t, c
                 NAME/KEY: modified_base
LOCATION: (111786)..(111885)
                                                           OTHER INFORMATION: a, t,
                                                                                                                                                                                OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
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LOCATION: (41057). (41156)
OTHER INFORMATION: a, t, c
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ORGANISM: Homo sapiens
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LOCATION: (40991)
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LOCATION: (90306)
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NAME/KEY: modified_base
LOCATION: (41047)
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, NAME/KEY: modified base
, LOCATION: (183290)...(183389)
; OTHER INFORMATION: a, t, c or
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US-10-021-698A-1006/c
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OTHER INFORMATION: a, t, c or
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NAME/KEY: modified_base
LOCATION: (129353)...(129452
OTHER INFORMATION: a, t, c
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LOCATION: (178024)..(178123)
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OTHER INFORMATION: a, t, c o
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OTHER INFORMATION: a, t, c o
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Local Similarity 43.9%;
hes 147; Conservative
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148844

Sequence 1006, Application US/10021698A GENERAL INFORMATION:

MIL

LITTLE, RANDALL VAN EERDEWEGH, PAUL DUPUIS, JOSEE

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PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
PRIOR PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: Patentin Ver. 2.1
LENGTH: 1355
TYPE: NAT
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APPLICANT: DEL MASTRO, RICHARD

APPLICANT: SIMON, JASON

APPLICANT: SIMON, JASON

APPLICANT: SIMON, JASON

APPLICANT: PANDIT, SUNIL

TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY

CURRENT APPLICATION NUMBER: US/10/021,698A

PRIOR APPLICATION NUMBER: 06/211,749

PRIOR FILING DATE: 2000-06-14

NUMBERD OF SEC ID NOS. 5160
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APPLICANT: LADNER, ROBERT
APPLICANT: COHEN, EDWARD
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-021-698A-1006
                                                                                                                                                                                                      APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAM.
TITLE OF INVENTION: OF EMPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION UNMBER: US/10/045,674A
DEFICE APPLICATION UNMBER: 2001-10-25
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LAUNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HORE
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SOFTWARE: Patentin 2.1
SEQ ID NO 1006
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SEQ ID NO 10809
LENGTH: 290892
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(290892)
OTHER INFORMATION: n = A,T,C or G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOISOS
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Best Local
234005 TGATGATGGTAATGTTGGTGATGATCGTGGCTGTGATG 233968
                                                       234065 TGATAGTGGTGGTGACGACGGTGATGCTAATGATTATGATGATGATGGTGGTGGTAATGG 234006
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                                                                                                                                                                                 234185 CTACATTÁGTGATGTTGGTAATGGTGGTGGTGÁTGATGATGGTGATGCCAÁTGÁTTATGA 234126
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LOCATION: (1)
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                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                              162
                                                                                                                                                  102 Тевсевтанталтавсевсскалаттствавствалсатттассавтасевтевсевтал
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 AATCGATCTGACCCAACGTGGCTTCGGTAACAGCGCTACTCTTGATCAGTGG 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 GTACGGTGGCGGTAACTCTGCACTTGCTCTGCAAACTGATGCCCCGTAACTCTGACTTGAC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        663 YĞĞYAARTTYMGWGAYTĞYĞCYTTYCAYWSYĞĞYTTYAAYGARGAYCCWTTYGTYTGYGA 722
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                           CGGCGGTAATGGTGCAGATGTTGGTCAGGGCTCAGATG
                                                                                                                     TGATGATGÁTGGTÁATGGTGATGÁTGGTGÁTGGTGÁTÁGTTÁCAGTAGTGATGTTÁGTÁÁ 234066
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Similarity 25.4%; Pred. No. 0.49;
59; Conservative 64; Mismatches
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                                                                                                                                                                                                                                                               Conservative
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0; Mismatches
                                                                                                                                                                                                                                                                           Score 30.8;
Pred. No. 16
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US-10-767-701-7789/c

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; TYPE: DNA
; ORGANISM: Sorghum bicolor
; PEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS14531_1
US-10-767-701-7789
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Best Local :
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 63693
TYPE: DNA
ORGANISM: Homo sapiens
-60-548-091-5635
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILLING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED
TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND
FILE REFERENCE: CL001506
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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Local Similarity 53.3%;
les 64; Conservative
 53410
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                                                                                                                                                                                                                                                      61 GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC 120
                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                               CCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAA 180
                                                                                                                                                                                                                      AACTCTGACTTGACTATTACCCAGCATGGCGGCGCGGTAATGGTGCAGATGTTGGTCAGGGC
GGTGGTGGTGGTGATGATAG 53388
                                    GTTGGTCAGGGCTCAGATGACAG 263
                                                                      AATGATGGTGATGGTGATGATGGTGATGTTGATGGCAGTAATGATGGGGGGT
                                                                                                         ACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGCAGAT
                                                                                                                                             ATCTATGGAGGCACGTGCACCATCCACGGTTGTGATAATTGGAACCTTGTAGGCGAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGGAAGTAATCTTGCAAGGCGAGGGTCTCAATGGACTTGTTCTTCAAGCTCTTGATGGC
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                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 13
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RESULT 10

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RESULT 11
US-10-021-698A-1217/c
; Sequence 1217, Application US/10021698A
GENERAL INFORMATION:
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, NAME/KEY: misc feature
; LOCATION: (1)...(290892)
; OTHER INFORMATION: n = A,T,C or G,
US-10-767-471-10809
                                                                                                                                    US-10-021-698A-1217
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                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/211,749
PRIOR FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 6160
SOFTWARE: Patentin 2.1
SEQ ID NO 1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10809, Application US/10767471
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
                                                                  Matches
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Best Local :
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LENGTH: 290892
                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                    APPLICANT: SIMON, JASON
APPLICANT: ALLEN, KRISTINA
APPLICANT: PANDIT, SUNIL
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: 2976-4044US1
CURRENT APPLICATION NUMBER: US/10/021,698A
CURRENT FILLING DATE: 2001-10-22
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CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
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                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                      LENGTH: 372
                                                                                   Local Similarity
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340
                                                                  144;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
77; Conserv
                              GTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGCC 121
 CATGGCGGCGGTAATGGTGCAGATGTTGGTCAGGG
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DEL MASTRO, RI
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                                                                  Conservative
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GENETIC POLYMORPHISMS ASSOCIATED WITH
RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
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49.7%;
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43.1%;
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Pred. No. 25;
0; Mismatches
                                                                                Score 30; DB Pred. No. 1.3;
                                                                  Mismatches
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                                                                                                DB 6;
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                                                                190;
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                                                                                                  Length 372;
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NAME/KEY: misc feature; LOCATION: (987)...(987); OTHER INFORMATION: n is PCT-US04-05654-1019
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        Best Loc
Matches
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 1019
LENGTH: 992
TYPE: Dark
                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES
FILE REFERENCE: MBI-0047 PCT
CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
PRIOR FILING DATE: 2003-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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PRIOR FILING DATE: 2003-09-30
                                                                                                                                           OTHER INFORMATION: n is
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                                                                                                                                                         NAME/KEY: misc feature
LOCATION: (978)..(984)
                                                                                                                                                                                                  OTHER INFORMATION: Predicted polypeptide sequence is orthologous to G652
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                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                         ORGANISM: Glycine max
                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                            FEATURE:
      Local Similarity
les 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 GCAACGGTGCTGCAGTTGACCAGACTGCATCTAA 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 CAPATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGTGGTAATACTGATGATGGTGCTGGTGATGATGGTGATAGTGATGGTGATGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu, Guo-Liang
Broun, Pierre E
Kumimoto, Roderick W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repetti, Peter
Century, Karen
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Haake, Volker
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Jiang, Cai-Zhong
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Dubell III, Arnold N
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      Conservative

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 Score 30; DB 1; Length 992; Pred. No. 2.1; 0; Mismatches 30; Indels
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RESULT 14
PCT-US04-02242-43
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; ORGANISM: Homo sapiens
US-10-021-698A-796
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US-10-021-698A-796/c
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Best Local
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APPLICANT: ALLEN, KRISTINA
APPLICANT: PANDIT, SUNIL
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: 2976-4044US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/211,749
PRIOR FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 6160
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                                                                      179
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                                                                                                                                                                                                                                       106 GGTAATAATAGCGGCCCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCT 165
                                                                                                                                                                                                                                                                       359 GGTGGTGATGATGATGATGATGGTGACGGTGATGGTGATGGTGATGGTGATGGTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  324 CTATGGCGGGGACGAGGAGGTGGAGGTGGATATGGCGGTGGCGGCGGCTACGGTGG
                                                                                                                                                                                                                                                                                                        46 GGTAGCGCTCTGGCAGGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42
                                                                                                                                                                                                                                                                                                                                                99;
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                   GATGATGATGCTGACGGTGATGATGGTGATGGTGATGCTGATGCTGGTGGTGGT
                                                                                                                                                                    GCACTTGCTCTGCAAACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGC 225
                                                                    GGTGATGATGGTGGTGATGATGATGATG
                                                                                                   GGTAATGGTGCAGATGTTGGTCAGGGCTCAGATG 259
                                                                                                                                                                                                      GATGGTGACGGTGGTGATGGTGATGATGGTGATGCTGATGGTGATGGTGACGGT
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DUPUIS, JOSEE
DEL MASTRO, RIC
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Pred. No. 5.9;
0; Mismatches 115; Indels
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APPLICANT: Diversa Corporation
APPLICANT: Darton, Nelson; Robertson, Dan; E
APPLICANT: Barton, Nelson; Robertson, Dan; E
ITITLE OF INVENTION: EXYMES AND NUCLEIC ACIDS
TITLE OF INVENTION: THEM
FILE DEFERENCE: 56446-20118.40
CURRENT APPLICATION NUMBER: PCT/US04/02242
CURRENT APPLICATION NUMBER: 607/442,794
PRIOR APPLICATION NUMBER: 607/442,794
PRIOR FILING DATE: 2003-01-24
NUMBER OF SEQ ID NOS: 224

Dan; Elkins, James; Chang, Kristine C ACIDS ENCODING THEM AND METHODS FOR MAKING

ANI

SOFTWARE:

PatentIn version 3.1

Sequence 43, Application PC/TUS0402242 GENERAL INFORMATION:

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; Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 13468
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13342
LENGTH: 306
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-100-663-13342
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US-10-100-683-13342
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; OTHER INFORMATION: Obtained from an environmental sample
PCT-US04-02242-43
                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 64; Conserv
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LENGTH: 1203
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Best Local Similarity 56.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/047,601 FILING DATE: 1997-05-23 APPLICATION NUMBER: US 60/056,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/056,892 FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/043,314
FILING DATE: 1997-04-11
APPLICATION NUMBER: US 60/047,632
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/047,599
FILING DATE: 1997-05-23
APPLICATION NUMBER: US 60/056,664
FILING DATE: 1997-08-22
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APPLICATION NUMBER: US 60/043,580
FILING DATE: 1997-04-11
248 AG 249
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                                                            184 TCTTTTGTTCTGGATTGAAAGTCCGCAAACATAGCGTTTATGCTGTTGAAGCTGTGAATC
                                                                                    188 CCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGCAGATGTTGGTC 247
                                                                                                                                          124 CTCAGGTGAGTTCCTCTCACCACCCTGGGCAGCAGTGTGCAGTTGGTTACAAAGCTCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 CGGTGGTGGCGGTAATAATAGCGGCCCAAATTCTGAGCTG 135
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                                                                                                                                                                                    CTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAAACTGATG
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                                                                                                                                                                                                                         6.4%; Score 29.2; DB 6; Length 306; ilarity 52.5%; Pred. No. 2.2; Conservative 0; Mismatches 58; Indels
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Db 244 AG 245

Search completed: March 17, 2004, 08:25:34 Job time: 71.6301 secs

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Database
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Maximum DB seq
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 summaries
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/ cgm2_6/ptodata/2/pna/USO87_COMB.seq: *
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/ cgm2_6/ptodata/2/pna/USO83_COMB.seq: *
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/ cgm2_6/ptodata/2/pna/USO95_COMB.seq: *
/ cgm2_6/ptodata/2/pna/USO98_COMB.seq:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /pna/PCTUS
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

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Sequence 4, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Asron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Callinson, S. Karen
APPLICANT: Kay, William W.
ITITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                    RESULT 1
US-09-543-407-4
  LENGTH: 456
TYPE: DNA
ORGANISM: E.
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                                                                                                                                                 Sequence 2, Application US/09543407 GENERAL INFORMATION:
                                                                                                              APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 456
TYPE: DNA
ORGANISM: Salmonella enteritidis
US-09-543-407-2 GCAGCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAG GCGACAAATTATGATCTGGCTCGTTCAGAATATAATTTTGCGGTAAATGAATTAAGCAAG ATGAAAAACAAATTGTTATTTATGATGTTGACAATACTGGGTGCGCCTGGGATTGCAACC ATGAAAAACAAATTGTTATTTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCC Score 332.8; DB 23 Pred. No. 4.7e-88; 0; Mismatches 77; DB 23; Indels Length 0, 120 120 60

PEPTIDE SEQUENCES

TOTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTA 180

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Sequence 171, Application US/09252691B
GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SECURITIES OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THE FILE REFERENCE: 107196.135
CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
SEQ ID NO 171
LENGTH: 561
TYPE: DNA
OTARANISM: Enterobacter cloacae
US-09-252-691-171
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                                                     GGTAATAAAGCAAATATTACACAGTATGGTACTCAAAAAACGGCAATTGTAGTGCAGAGA 420
                                                                                                     GATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCT
                                                                                                                                                                              AAGATTGACCAGACAGGAGATTATAACCTTGCATATATTTGATCAGGCGGGCAGTGCCAAC
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Pred. No. 2.5e-75;
0; Mismatches 103
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RESULT 5
US-10-417-886-171
Sequence 171, Application US/10417886
GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND
FILE REFERENCE: 107196.135
CURRENT APPLICATION NUMBER: US/10/417,886
CURRENT FILING DATE: 2003-04-17
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEC
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THE
FILE REFERENCE: 107196.135
CURRENT PILICATION NUMBER: US/09/252,691C
CURRENT FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,145
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR FILING DATE: 1998-07-24
PRIOR FILING DATE: 1998-07-24
PRIOR FILING DATE: 1998-07-24
PRIOR FILING DATE: 1998-07-18
NUMBER OF SEQ ID NOS: 11326
SEQ ID NO 171
LENGTH: 561
TYPE: DNA
ROANISM: Enterobacter cloacae
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Best Local
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Pred. No. 2.5e-75;
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AND AMINO ACID SEQUENCES RELATING

DIAGNOSTICS AND THERAPEUTICS
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CURRENT APPLICATION NUMBER: US/10/146,492B
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: EP 0111279.5
PRIOR FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 12816
SEQ ID NO 80
LENGTH: 100
ORGANISM: Escherichia coli K-12 MG1655
                                         OTHER INFORMATION: csgb b1042 U00096 1103174..1103629; PUBLICATION INFORMATION: RELEVANT RESIDUES: 39-58
US-10-146-492B-80
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US-10-146-492B-80
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; ORGANISM: Enterobacter cloacae
US-10-417-886-171
          Query Match
                                                                                                                                                                                                                                                                                                                           Sequence 80, Application US/10146492B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           APPLICANT: MWG Biotech AG
TITLE OF INVENTION: Biochip
FILE REFERENCE: REN-14043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US/09/252,691C
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,145
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 11326
SEQ ID NO 171
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Best Local
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       21.9%;
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     Score 100;
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   DB
   45;
Length 100;
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US-10-146-492B-82
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                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SEQ ID NO 82
LENGTH: 100
                                                                                                                                                                                                                                                                                             Sequence 82, Application US/10146492B
GENERAL INFORMATION:
APPLICANT: WWG Biotech AG
TITLE OF INVENTION: Biochip
FILE REFERENCE: REN-14043
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      Matches
                   Best Local Similarity
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                                    Query Match
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SEQ ID NO 81
LENGTH: 100
Type: Fxx
                                                                       OTHER INFORMATION: csgb b1042 U00096 1103174..1103629
PUBLICATION INFORMATION:
RELEVANT RESIDUES: 57-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/146,492B
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: EP 0111279.5
PRIOR FILING DATE: 2001-05-17
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FILE REFERENCE: REN-14043
CURRENT APPLICATION NUMBER: US/10/146,492B
CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: EP 0111279.5
PRIOR FILING DATE: 2001-05-17
                                                                                                                                  LENGTH: 100
TYPE: DNA
ORGANISM: Escherichia coli K-12 MG1655
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ilarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.9%; 5c.
100.0%; Pr
21.9%; Score 100; DB 45;
100.0%; Pred. No. 6.7e-19;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 100; DB 45; Pred. No. 6.7e-19;
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; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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ches 0;
                          Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307
                                                                                                                                                                                                                                                                                                                                                                                                                                           100
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                                                                                                                                                    Matches
                                                                                                                                                                                  Query Match
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-AUG-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 26-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/466,194 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 22-APR-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
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                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT: SCHEIFLINGER, F.
PPLICANT: FALKNER, F. G.
TILE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                        124 TCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTACGG 183
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                                                                                                                   64 GCAGGTTATGATTTAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAGTCT 123
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CAGGGAGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCAAAG 243
                            GCAGGGAGGCTCAAAACTTTTTGGCGGTTGTTGCGCAAGAA 222
                                                                                      GCAGGGAGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                    eic acid
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2.8;
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                                                                                                                                                 Mismatches 165; Indels
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APPLICANT: Arterburn, Matthew APPLICANT: Asghari, Vida APPLICANT: Blun, Linda APPLICANT: Cheung, Patrick

Patrick

Simin

APPLICANT: APPLICANT:

: Damavandi, Sim : Dickson, Mark : Drake, Jim

Drmanac, Radoje

Carrie

APPLICANT:

Fox, Melvin Garcia, Vero Engleman, Carrie Faulkner, Brandy

Giedt, Jomek,

Gretchen Leni Veronica

Jones, Lee Kita, David

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US-09-332-782-15700
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                               US-09-515-694-15700
                                                   RESULT 11
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Sequence 15700, Appl GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-754CON1
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/332,782
                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1998-10-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EARLIER APPLICATION NUMBER: US 09/181,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hyseq,
                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                 Local Similarity
nes 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1223
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                                                                                                                                        369 AGCAAATATTACACAGTATGGTACTCAAAAAACGGCAATTGTAGTGCAGAGACAG 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 ATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAACGAT 303
                                                                                                                                                                                                                                                                                                                                                                         391
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                                                                                                                                                                           TTTCGCGCAACAAGCTGGTCATGCTGAACTGGATATTCCGCAATAATCTGGAAATGT 336
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              Application US/09515694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inc.
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Pred. No. 2.7;
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                                                                                                                                                                                                                                                                                  DB 18;
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                                                                                                                                                                                                                                                                                  Length
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Kofler, Janette

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US-09-515-694-15700
                                                             NUMBER OF SEQ ID NOS:
SEQ ID NO 3221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 15700
LENGTH: 391
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              Sequence 3221,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                     CURRENT APPLICATION NUMBER: US/10/431,652
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: US 09/328,352
PRIOR FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: US 60/088,701
PRIOR FILING DATE: 1998-06-09
                                                                                                                                                                                                                                APPLICANT: Breton, Gary L.
APPLICANT: Bush, David
APPLICANT: Bush, David
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: PATH03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 09/332,782
EARLIER FILING DATE: 1999-06-14
EARLIER APPLICATION NUMBER: 09/181,430
EARLIER FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 21027
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yim, Kenneth
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 754CIP
CURRENT APPLICATION NUMBER: US/09/515,694
CURRENT FILING DATE: 2000-02-29
ORGANISM: Acinetobacter baumannii
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                                       ENGTH: 4860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 8.4%;
Local Similarity 58.3%;
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Verna, Ron
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Smythe, Ashleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Randhwa, Gurpreet
Sahourieh, Hannah
Sidhu, Navjiwan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nogra, Margie
Ojeda, Jesse
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Nguyen, Phuong
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                                                                                 1998-06-09
DS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Matches Query Match

36;

Conservative

8.3%; Score 37.8; DB 36; 13.1%; Pred. No. 6.2; ative 121; Mismatches 118;

Length 2000;

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Gaps

0

Best Local Similarity

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; ORGANISM: Oryza
US-09-887-272A-5263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-887-272A-5263/c
; Sequence 5263, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                               SEQ ID NO 5263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Hou, Yu-Ming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                              PRIOR FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 09/887,271
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 1360.003US2
CURRENT APPLICATION NUMBER: US/09/887,272A
CURRENT FILING DATE: 2001-06-23
                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                      NUMBER OF SEQ ID NOS: 6813
                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/213,634 PRIOR FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/214,926 PRIOR FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: PATHOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: COOPER, BREE
TITLE OF INVENTION: PLANT GENES INVOLVED IN DEFENSE AGAINST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                            LENGTH: 2000
                                                                                                                                                                                                        APPLICATION NUMBER: 60/264,353 FILING DATE: 2001-01-26 APPLICATION NUMBER: 60/273,879
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/261,320 FILING DATE: 2001-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3685 TTACAAGGTCAAGCTGGGAATGACACTTATATATAGATAAAG 3727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3625 TATGGTGGTGCAGGTAATGACACATTGATTTATGGCGGTAATTCCAATGTGTATACGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3565 TATCTGTATGGTGATGGAGGAGACGATACATTAGTTTCTAATACAGGCTCTGATTATTTG 3624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3445 AATACTATTGGTAAATTATTAGGTACTGATGCAGCAGATAATCTTCAAGCAGATGCTGAG 3504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 ATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166 AATAGTGCTCAGTTACGGCAGGGAGGCTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 AATGAATTGAGTAAGTCTTCATTTAATCAGGCAGCCATAATTGGTCAAGCTGGGACTAAT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 AGTAGCAACCGGGCAAAGATTGACCAGACAGGAGATTATAACCTTGCATATATTGATCAG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATACTGCGATGATT 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTCAACTATTTATGGTTTGGGAGGCAATGATACGATTCAAGGTGGTGTACAGAATGAT 3564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen, Wenquiong
Kataqiri, Fumiaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goff, Steve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glazebrook, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Whitham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chang, Hur-Song
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quan, Sheng
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Tong Steve
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Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4860;
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Sequence 13, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                       RESULT 15
US-09-949-016-17017/c
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US-09-543-407-13
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
Sequence 17017, Application US/09949016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocal Similarity
                                                                                                                                                                                                                                                                328
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                                                                                                                                                                                                                                                                                                      397 AMAACGGCAATTGTAGTGCAGAGACAGTCGCAAATGGCTATTCGCGT 443
                                                                                                                                                                                                                                                                                                                                                                                      337 GCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTATGGTACTCAA 396
                                                                                                                                                                                                                                                                                                                                              268 ATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAA 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201 TTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCAAAGATTGACCAGACAGGAGA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 CATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTACGGCAGGGAGGCTCAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             890 YKWSWRRMYWTMTKWAWTWMTCMCMAKWYMATGWATWMWWRYTMYTYCYAMTCAKCKYKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           277 ATTGATCAGGCGGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTGCTTATGGTAATACT 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 TTATAACCTTGCATATATTGATCAGGCGGGCAGTG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               950 WAAGRWRWRMAWCWYCCMWKWWKMTSCMWWKYWRTWSCWYTMWWGAMRYAYYAMRRRRWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                ATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMTKWWTTWACAWRATSWRWRAMAGMRWKRYKMKRAYWWRWWRCWKAGWARWMKSRYRWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAGTCTTCATTTAATCAGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCCGCAGCAGGTTATGATTTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WKKYATRYYWKMWAMTWWWSWRRWKSYRMWSGMGRMRWSAWRYCSRMKCAKTKYASSARW 711
                                                                                                                                                                                                                                                                AACTCCGATATTACTGTCGGCCAATATGATCAGCTGGTTACCCGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKRAKRSYRYRRRWYWKRKGWTYRYRYWRSCRMTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.2%;
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Pred. No. 5;
0; Mismatches
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                                                                ASSOCIATED OF DETECTION
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                                                                  AND USES
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; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2070-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 17017
; LENGTH: 68667
                                                                                                                        Query Match
Best Local Similarity
Thes 65; Conserve
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                                                                                                                                                                                                              NAME/KEY: misc feature; LOCATION: (1)...(68667); OTHER INFORMATION: n = US-09-949-016-17017
                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                                                                                                         TYPE: DNA
 17437
                                   387
                                                                                                       327
TGATATGAGAATAGCAGCATGTGTGCTGTGATGTTACTTCCAAATTACTTT 17387
                                                                                                    TGGTAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTA 386
                                 TGGTACTCAAAAAACGGCAATTGTAGTGCAGAGACAGTCGCAAATGGCTAT
                                                                    8.2%;
llarity 58.6%;
Conservative
                                                                                                                                                                                                                                A, T, C or
                                                                                                                                         0;
                                                                                                                                                          Score 37.4;
Pred. No. 2
                                                                                                                                           Mismatches
                                                                                                                                                           27;
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                                                                                                                                           Indels
                                                                                                                                                                            Length 68667;
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Gaps

Search completed: March 18, 2004, 02:46:53 Job time: 2927.24 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
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    Score
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/USO9_NEW_COMB.seq:*
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                                                         US-10-767-701-9911
US-10-767-701-9911
US-10-765-790-43
US-10-767-471-10653
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US-09-741-873C-3
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Sequence 103, Appli Sequence 73, Appli Sequence 139, Appli Sequence 139, Appli Sequence 10653, A Sequence 2325, Appli Sequence 36, Appli Sequence 36, Appli Sequence 3787, Appli Sequence 10718, Appli Sequence 10718, Appli Sequence 10718, Appli Sequence 10718, Appli Sequence 10718, Appli Sequence 10718, Appli Sequence 10718, Appli Sequence 10718, Appli Sequence 10718, Appli Sequence 3515, Appli Sequence 3515, Appli Sequence 3787, Appli Sequence 3443, Appli Sequence 3443, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 2111, Appli Sequence 211
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	18788, A	10675, A	5675, Ap	<ol><li>Appli</li></ol>	449, App	285, App	793, App	12012, A	13618, A	326, App	5603, Ap	10705, A	10858, A	17618, A	18004, A	10809, A	697, App	10743, A	4.4.

## ALIGNMENTS

RESULT 1 US-10-765-790-103/c

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Sequence 103, Application US/10765790
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bayer Healthcare LLC
APPLICANT: Beard, Chris
APPLICANT: Burgess, Chris
APPLICANT: Gannon, Allison
APPLICANT: Harvey, Jeanne
APPLICANT: Lechner, John F.
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US-09-741-873C-3
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-765-790-103
Sequence 3, Application US/09741873C
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.2 SEQ ID NO 103
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PRIOR APPLICATION NUMBER: US 10/737,082
PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Li, Zheng
TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
FILE REFERENCE: 1657/2035
CURRENT APPLICATION NUMBER: US/10/765,790
CURRENT FILING DATE: 2004-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 8.2%;
Local Similarity 58.6%;
nes 65; Conservative
                                                                                                                                                                                                                                                                                                16443
                                                                                                                                                                                                                                                                                                                                                                                    387 TGGTACTCAAAAAACGGCAATTGTAGTGCAGAGACAGTCGCAAATGGCTAT 437
                                                                                                                                                                                                                                                                                                                                                                                                                             327 TGGTAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGTA 386
                                                                                                                                                                                                                                                                                              TGATATGAGAATAGCAGCATGTGTGCTGTGATGTTACTTCCAAATTACTTT 16393
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Pred. No. 0.2;
0; Mismatches
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FILING DATE: 1998-05-06
APPLICATION NUMBER: US 08/978,878
FILING DATE: 1997-11-26

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-765-790-73
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CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: US 10/737,082
PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 300
SOFTWARE: Patentin version 3.2
SEQ ID NO 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Li, Zheng
TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
FILE REFERENCE: 1657/2035
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PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
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PRIOR FILING DATE: 1992 11-03
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LOCATION: (83)..(538)
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                                                                                                                                              y Match 7.5%;
Local Similarity 60.9%;
hes 56; Conservative
                                                                 332273 ATAAAATTGAATTTTGTGATCAGTAGCCATGGGCTATCTCTGACAGCATTTGGAAAAAGAG
         332213
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FILING DATE: 1989-05-04
APPLICATION NUMBER: US 07/789,437
FILING DATE: 1991-11-06
                                                                                                 263 ATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAACGATGCCAGTATTTCGCAAGGTG 322
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1 Similarity 100.0%;
35; Conservative (
CTATAGTTGATACAGAAAATATAACCCAAAAA 332182
                                 CTTATGGTAATACTGCGATGATTATCCAGAAA 354
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Lechner, John F.
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                                                                                                                                         Score 34.4; DE Pred. No. 3.3; 0; Mismatches
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Pred. No. 0.24;
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US-10-767-701-9911

RESULT 6

RESULT 4

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; TYPE: DNA
; ORGANISM: E. Coli
US-10-771-241-139
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US-10-771-241-139
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SEQ ID NO 139
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GENERAL INFORMATION:
APPLICANT: Zyskind, Judith
APPLICANT: Forsyth, R. Allyn
                                                                                                                                                                                                             Query Match
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PRIOR FILLING DATE: 200-01-27
PRIOR FILLING DATE: 200-01-27
PRIOR FILLING DATE: 200-01-27
PRIOR FILLING DATE: 200-01-27
PRIOR FILLING DATE: 200-01-27
PRIOR FILLING DATE: 200-01-27
PRIOR FILLING DATE: 200-01-27
PRIOR FILLING DATE: 1999-01-27
PRIOR FILLING DATE: 1999-01-27
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 9911

LENGTH: 887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS40598_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Sorghum bicolor FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                          Local
                                      319 GGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATA 367
                                                                            442 GATRATRACCTGRATTATAGCGTTCAGGTCGGTAACACCCCACGGAGGTAATACATCGTCT 501
                                                                                                                259 GATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAACGATGCCCAGTATTTCGCAA 318
                                                                                                                                                                   al Similarity
62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 CTTATGGTAATACTG 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 TGTCAATGATTCCTAAAGGTGGTGATACAATTTGGGGAAATCTGGATTGGTCTCCAGAAG 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     553 GCAATGGGGAAAATG 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 TGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCAAAGATTGACCAGACAGGAGATT 262
                                                                                                                                                                                                                                                                                                                                                 FastSEQ for Windows Version 3.0
GGCACCAGTGGTTÁCAGTTCTCTTÁATTATCGTGGÁGCTTATGGTÁÁTÁ 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGGCCTTGAATGTAAAGCTAAGAAGCACAAAACCAATGATACCGAGGTTTCTAAGGATA 552
                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                    7.4%;
56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.5%; Score 34.2; DB 6;
53.3%; Pred. No. 0.45;
ative 0; Mismatches 63;
                                                                                                                                                                 <u>,</u>
                                                                                                                                                               Score 33.8; DB 6;
Pred. No. 0.65;
0; Mismatches 47;
                                                                                                                                                               47;
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                                                                                                                                                                                                   Length 1149;
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                                                                                                                                                          Gaps
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; FEATURE:
; NAMB/KEY: misc_feature
; LOCATION: (1)...(261922)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
; OTHER 1NFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-765-790-43
                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10653
LENGTH: 261922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10653, Application US/10767471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43, Application US/10765790 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences FILE REFERENCE: 1657/2035
CURRENT APPLICATION NUMBER: US/10/765,790
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: US 10/737,082
PRIOR FILING DATE: 2003-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bayer Healthcare LLC APPLICANT: Beard, Chris
                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH: 38719
                                                                  72532 AAACAGAGCCTAAAAAACATTGGAAAGAATGAATAAGCCATCTTTTAAAAAATTAACAATT 72473
                                                                                                                                                                           ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10974 GATCCAGCAATTACAATCCTAGTGATA 10948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11034 TAGCTACTTTAGAAAATAAGTTAGCAGTTCCACAAATGATTAAATATAGAGTTACCCTAT 10975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11094 TGTTGATGATATGGAGAAATCTGAACCCTCATACACTGCTAGTGGAAATGTAAAATGGTG
311 TTTCGCAAGGTGCTTATGGTAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATAAAG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 CAGCCATAATTGGTCAAGCTGGGACTA 163
                                                                                                        251 AGACAGGAGATTATAACCTTGCATATATTGATCAGGCGGGCAGTGCCAACGATGCCAGTA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAGCTAATTCAGAATATAACTTCGCGGTAAATGAATTGAGTAAGTCTTCATTTAATCAGG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burgess, Chris
Gannon, Allison
Harvey, Jeanne
Lechner, John F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTTATGATGTTAACAATACTGGGTGCGCCTGGGATTGCAGCCGCAGCAGCTTATGATT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li, Zheng
                                                                                                                                                     Conservative
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51.7%;
                                                                                                                                                                         7.1%;
51.0%;
                                                                                                                                                   Score 32.2; D
Pred. No. 12;
0; Mismatches
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Pred. No. 2.8;
0; Mismatches
                                                                                                                                                                                             DB 6;
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                                                                                                                                                   73;
                                                                                                                                                                                             Length 261922;
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                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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US-10-417-884A-2325
US-10-417-884A-2325
; Sequence 2325, Application US/10417884A
; Sequence 2325, Application US/10417884A
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; APPLICANT: LYNN A DOUCETT ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Clone ID: 18065357 US-10-767-701-31198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-10-767-701-31198
US-10-767-701-31198
; Sequence 31198, Application US/10767701
; GENERAL INFORMATION:
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LENGTH: 512
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Best Local Similarity
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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5355)B
CURRENT FILLING DATE: 2004-01-29
TUMBER: US/10/767,701
CURRENT FILLING DATE: 2004-01-29
TUMBER OF SEQ ID NOS: 63128
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APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1)..(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Sorghum bicolor
COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM IS09660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/417,884A

FILING DATE: 17-Apr-2003

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72412 GAAACAATTCATAATAGTGGATTTAAACA 72384
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                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 TGCACATATGATTGAACATGTCGCGTTTCTTGGCAGTAAAAAACGTGAAAAGCTTTTTGGG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 CTCAAAACTTTTGGCGGTTGTTGCGCAAGAAGGTAGTAGCAACCGGGCAAAGATTGACCA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 TGAGGCTCACATGGAAGTTCATGTTGGATCAATTGATGAGGAGGAGGAGGAGCAGGGAAT 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 252 GACAGGAGATTATAACCTTGCATATATTGA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 TCAGGCAGCCATAATTGGTCAAGCTGGGACTAATAATAGTGCTCAGTTACGGCAGGGAGG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACCGGTGCGAGGTCTAATGCATATACAGA 259
                                                                                                                                                                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                                 CITY: Waltham
                                                                                                                                                                                                                                                                                                                           STREET: 100 Beaver Street
                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                                                                                                                                                                              02354
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50.7%;
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Pred. No. 2.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74;
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; NAME/KEY: CDS
; LOCATION: (1)...(1245)
; OTHER INFORMATION: pepT amino tripeptidase T (EC 3.411.-) ORF# 1190
US-60-546-745-36
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US-60-546-745-36
; Sequence 36, Application US/60546745
; GENERAL INFORMATION:
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Query Match
Best Local Similarity 49.,
Thes 80; Conservative
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SEQ ID NO 36
LENGTH: 1245
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                                                                                                                                                                                                                                                                       APPLICANT: Hamrick, Alice
TITLE OF INVENTION: LACTOBACILLUS ACIDOPHILUS NUCLEIC ACID SEQUENCES ENCODING
TITLE OF INVENTION: PROTEASE HOMOLOGUES AND USES THEREOF
FILE REFERENCE: 5051.604PR2
CURRENT APPLICATION NUMBER: US/60/546,745
CURRENT FILING DATE: 2004-02-23
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Klaenhammer, Todd R. APPLICANT: Russell, William M. APPLICANT: Alternan, Eric
                                                                                                                                                                              ORGANISM: Lactobacillus acidophilus
                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (781)893-500
TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2325:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...525
SEQUENCE DESCRIPTION: SEQ ID NO: 2325:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/107,532
FILING DATE: 30-Jun-198
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: JULY 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 CTATATTGATATGAGTGGTGAAATCAATTATGGCGATAAAGACAAAATTGTAC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 таатастесеатеаттатесаевааевттетеетаатаааесааататтасае 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 TGCAȚATATȚGAȚCAGGCGGCAGTGCCAACGATGCCAGTATȚTCGCAAGGTGCȚTAȚGG 329
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                                                                                                                                                                                                                                                                                                                                                                                             Cano, Raul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 525 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                          version 3.2
                                        6.9%;
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                                      Score 31.4;
Pred. No. 3.
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Pred. No. 2
                         Mismatches
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                      81;
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                                                       Length 1245;
                      Indels
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                                                                                                                                                                                                                                                               FILE REFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-786-065-3
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US-10-786-065-3
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Best Local (
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Best Local &
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LENGTH: 53332
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/10786065
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, FILE REFERENCE: CL001098DIV II CURRENT APPLICATION NUMBER: US/10/786,065 CURRENT FILING DATE: 2004-02-26 NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                   LENGTH: 201
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
386 ATGGTACTCAAAAAACGGCAATTGTAGTGCAGAGACAGTCGCAAATGG 433
                                                 142 ATGGGAGTATGGAGGCGAGAATCCAAGATGGTGATGATAATRAGGAGGCTATTTCCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8692 GAGTTCAACAAATGTTGACCA 8712
                                                                                326 AȚGGTAAȚACTGCGATGATTAȚCCAGAAAGGTTCTGGTAAȚAAGCAAAȚAȚTACACAGT 385
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                                                                                                                                59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATACAGCTGATTTCAATTCAGAAAATGTTAAACCACAAA 289
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                                                                                                                            Conservative
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                                                                                                                                       6.8%;
54.6%;
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                                                                                                                       Score 30.8; DE Pred. No. 3; 1; Mismatches
                                                                                                                           1;
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Pred. No. 13;
0; Mismatches
                                                                                                                                                        DB 6;
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AGGATTATCATGTACATGATGAGGCAGAGCAGGAACAGAAAAAGCTTGG

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RESULT 14
US-10-767-471-501/c
US-10-767-471-501/c
Commence 501, Application US/10767471
                                                                                                                        RESULT 15
US-10-767-471-10718/c
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; LENGTH: 1227
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-501
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US-10-767-471-34493/c
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-34493
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SEQUENCE 501, Application US/10'/6'4'/1
SEQUENCE 501, APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
Sequence 10718, Application US/10767471
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION
FILE REFERENCE: CL001505
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Best Local Similarity. 54...
59; Conservative
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CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 34493
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Best Local Similarity 54.6%;
Matches 59; Conservative
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CURRENT FILING DATE: 2004-01-30
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TITLE OP INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001505
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                                                                                                                                                                                                                                                            386 ATGGTACTCAAAAAACGGCAATTGTAGTGCAGAGACAGTCGCAAATGG
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                                                                                                                                                                                                                                                                                                                                                 326 ATGGTAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGT 385
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                                                                                                                                                                                                                      AGGATTATCATGTACATGATGASGCAGAGCAGGAACAGAAAAAGCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 1227;
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(76573)
; OTHER INFORWATION: n = A
US-10-767-471-10718
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                                                                                                                                     Query Match
Best Local Similarity 54.6
Matches 59; Conservative
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CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10718
LENGTH: 76573
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
69761 AGGATTATCATGTACATGATGASGCAGAGCAGGAACAGAAAAAGCTGG 69714
                                                                           69821 ATGGGAGTATGGAGGCGAGAATCCAAGATGGTGATAATRAGGAGGCTATTTCCCAGG 69762
                                386 ATGGTACTCAAAAAACGGCAATTGTAGTGCAGAGACAGTCGCAAATGG 433
                                                                                                                326 ATGGTAATACTGCGATGATTATCCAGAAAGGTTCTGGTAATAAAGCAAATATTACACAGT 385
                                                                                                                                                                        6.8%;
54.6%;
                                                                                                                                                                                                                                                        A,T,C or G, or insertion/deletion polymorphism
                                                                                                                                                     ; Score 30.8; DE; Pred. No. 22; 1; Mismatches
                                                                                                                                                                                          DB 6;
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Search completed: March 17, 2004, 08:25:37 Job time: 72.6301 secs.

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Listing first 45 summaries
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Maximum DB seq length: 200000000
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'Cgn12_6/ptodata/2/pna/US08_COMB.seq:*
'Cgn12_6/ptodata/2/pna/US081_COMB.seq:*
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46: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/pna/USIOIA_COMB. seq: 41: /cgn2_6/ptodata/2/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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RESULT 1

US-09-543-407-9

Sequence 9, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043.406

CURRENT APPLICATION UNMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

SOFTWARE: FRESENGE FOR Windows Version 4.0

LENGTH: 48

TYPE: Days

TYPE: Days

Sequence 9, Application US/09543407
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TYPE: DNA
ORGANISM: Leishmania
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3 21 US-07-965-673A-9
3 21 US-09-528-237A-850
1 PCT-US97-22578-44
8 15 US-09-107-433-2456
8 15 US-09-107-433-2456
4 1 PCT-US93-27401-9
4 25 US-10-617-320-2456
4 1 PCT-US03-27401-9
5 US-10-640-833-77
7 48 US-10-640-833-77
7 62 US-60-681-175-437
8 64 US-10-158-844-7
9 162 US-60-61-998-613
9 27 US-60-621-998-613
9 28 US-60-029-960-47
9 29 US-99-555-240-34030
9 27 US-09-564-617-77662
9 21 US-10-424-599-11973
9 21 US-10-424-599-11973
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9 21 US-10-424-599-11973
9 21 US-09-585-440-3409-11973
9 21 US-09-585-439A-100294
9 21 US-09-685-439A-100294
9 21 US-09-684-016-237766
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US-09-543-407-52

US-09-543-407-13

US-09-543-407-13

US-09-543-407-17

US-09-543-407-17

US-09-543-407-19

US-09-543-407-21

US-09-543-407-23

US-09-543-407-25

US-09-543-407-25

US-09-543-407-29

US-09-543-407-29

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US-09-543-407-29

US-09-543-407-29

US-09-543-407-49
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                                                     Query Match
Best Local S
Matches 48
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Best Local S
Matches 48
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Best Local S
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Sequence 33, Application US/09543407
GENERAL IMFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Loran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR.
ITILE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP
FILE REFERENCE: 920043.406
CURRENT FILING DATE: 2000-04-05
INUMBER OF SEQ ID NOS: 59
SOFTMARE: FastSEQ for Windows Version 4.0
IENGTH: 78
TYPE: DNA
OPSANTEM: Assistant Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Security Se
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Sequence 52, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
CURRENT APPLICATION NUMBER: US/09/543,407

NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 78
TURE: NYA
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OTHER INFORMATION: PCR primer
US-09-543-407-52
                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: PCR primer
                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 48
                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 48
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Conservative
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                                                                                           Score 48; DB 23;
Pred. No. 1.1e-08;
); Mismatches 0;
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                                                                                                                                                       Length
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                                                                                           Indels
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APPLICANT: Doran, James L.
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043,406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 456
TYPE: DNA
ORDANISM: Artificial Sequence
RESULT 6
US-09-543-407-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-543-407-11
                                                                                                                                                                     Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L
APPLICANT: Collinson, S.
APPLICANT: Kay, William W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                          OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragmer OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 456
                                                                                                                                                                                       ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Loca 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        382 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 429
                                                                                                             1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 48
                                                                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 100.0%; Score 48; DB 23; Similarity 100.0%; Pred. No. 1.7e-08; 48; Conservative 0; Mismatches 0;
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Collinson, S. Karen
Kay, William W.
                                                                                                                                                                     Conservative
                                                                                                                                                              100.0%; Sc
100.0%; Pr
                                                                                                                                                                   Score 48; DB 23;
Pred. No. 1.7e-08;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEPTIDE SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEPTIDE SEQUENCES
                                                                                                                                                                                                         Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 456;
                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Sequence 15,

Application US/09543407

Sequence 19, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Asron P.
APPLICANT: Doran, James L.

APPLICANT:

Doran, James L. Collinson, S. Karen Kay, William W.

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APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEF
FILE REFERENCE: 920043, 406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
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US-09-543-407-19
                   RESULT 8
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Best Local S
Matches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09543407 GENERAL INFORMATION:
                                                                                                                                                                    Matches
                                                                                                                                                                                        Query Match
Best Local :
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SEQ ID NO 15
LENGTH: 456
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APPLICANT: KAY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: White, Aaron P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: White, Aaron P. APPLICANT: Doran, James L
                                                                                                                                                                                                                                                                                                                                                LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                     OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                              Local Similarity 100.
mes 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                      1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 48
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                                                                                 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA
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Collinson, S. Karen
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                                                                                                                                                                                    100.0%;
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                                                                                                                                                                Score 48; DB 23;
Pred. No. 1.7e-08;
; Mismatches 0;
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Pred. No. 1.7e-08;
; Mismatches 0;
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                                                                                                                                                                                                     Length 456;
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                                                                                                                                                                Gaps
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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043 406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 456
TYPER. NNA
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-09-543-407-23
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                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/09543407 GENERAL INFORMATION:
                         CURRENT FILING DATE:
                                                         APPLICANT: KAY, WILLIAM W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
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Best Local :
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US-09-543-407-21
                                                                                                                                                                                             APPLICANT: White, Aaron P.
APPLICANT: Doran, James L
APPLICANT: Collinson, S.
APPLICANT: Kay, William W
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Best Local S
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OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
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GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 19
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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APPLICATION NUMBER: US/09/543,407 FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262
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Collinson, S. Karen
Kay, William W.
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ilarity 100.0%;
Conservative 0
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ilarity 100.0%;
Conservative 0
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Pred. No. 1.7e-08;
Mismatches 0;
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Pred. No. 1.7e-08;
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                                                                              PEPTIDE SEQUENCES
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NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 456
TYPE: DNA
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US-09-543-407-27
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APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S.

APPLICANT: Kay, William W.
                                                                                              APPLICANT: DORAN, James L.

APPLICANT: COLLINGON, S. KAREN
APPLICANT: KAY, WILLIAM W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043.405
FILE REFERENCE: 920043.405
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
CURRENT FILING DATE: 2000-04-05
                                                                                                                                                                                                                                                                                                      Sequence
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Best Local
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CURRENT APPLICATION NUMBER: US/09/543,407
NUMBER OF SEQ ID NOS: 59
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 25
SEQ ID NO 25
SEQ ID NO 25
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US-09-543-407-25
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
ORTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: Sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25, Application US/09543407 GENERAL INFORMATION:
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APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 23
LENGTH: 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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les 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                     172 rárdárcadorderraccoordirárraccoardaáárdecacardoa 219
                                                                                                                                                                                                                                                                                                                                                                                             1 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 rárdárcagoriggriadocografirgirádocoárdadárdgeacargea 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                      Application US/09543407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 48; DB 23;
100.0%; Pred. No. 1.7e-08;
tive 0; Mismatches 0;
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Pred. No. 1.7,
0; Mismatches
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 456;
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ORGANISM: Artificial Sequence

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CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
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                                                                                                   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 48
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48, Application US/09543407 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
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Best Local Similarity
OTHER INFORMATION: PCR primer -09-543-407-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: White, Aaron P.
                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TATGATCAGCTGGTTACCCGTGTTACCCCATGAAATGGCACATGCA 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n 100.0%; Score 48; DB 23; Similarity 100.0%; Pred. No. 1.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 1.7e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 456;
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; APPLICANT: Doran, James L.
; APPLICANT: Collinson, S. Karen
; APPLICANT: Ray, William W.
; TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
; TITLE OF INVENTION: DRESENTATION OF HETEROLOGOUS PEI
; FILE REFERENCE: 920043.406
; CURRENT APPLICATION NUMBER: US/09/543,407
; CURRENT FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; SEQ ID NO 49
; SEQ ID NO 49
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US-09-543-407-49
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                                                                                                                                   US-09-543-407-49
                                                        Query Match
Best Local Similarity
Matches 43; Conserv
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Best Local :
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                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TATGATCAGCTGGTTACCCGTGTTACCCATGAAATGGCACATGC 47
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                   TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGC
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TATGATCAGCTCGTTACACGTGTTGTTACACATGAAATGGCTCATGC
                                                                 Conservative
                                                                              84.6%;
91.5%;
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Pred. No. 1.1e-05;
0; Mismatches 4;
                                                                               Score 40.6; DB 23;
Pred. No. 1.1e-05;
                                                                 Mismatches
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                                                               Indels
                                                                                                 Length 78; .
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Search completed: March 18, 2004, 02:46:57 Job time : 311.872 secs

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Run on:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D8
                                                                                                                                                                                                                                                                                                                                                           Score
                               seq
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length: 2000000000
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1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US00_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US00_NEW_COMB.seq:*
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Gapop 10.0 , Gapext 1.0
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US-10-767-795-1394
US-10-767-795-1392
US-10-767-701-129396
US-10-767-701-11493
US-10-767-701-14458
US-10-767-471-34311
US-10-767-471-31393
US-10-767-701-31393
US-10-765-790-41
US-10-765-790-41
US-10-765-790-41
US-10-783-271-34
US-10-783-271-34
US-10-783-271-34
US-10-783-271-34
US-10-783-271-34
US-10-783-271-34
US-10-783-271-34
US-10-783-271-34
US-10-783-271-3193
US-10-417-884A-2521
US-10-417-884A-2612
US-10-417-375A-31
US-10-767-701-657
US-10-779-543-5903
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2406.048 Million cell updates/sec
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Sequence 23396, A
Sequence 21396, A
Sequence 11493, A
Sequence 167, App
Sequence 34311, A
Sequence 34311, A
Sequence 14458, A
Sequence 10717, A
Sequence 10717, A
Sequence 31393, A
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                                          11899, A
2521, Ap
10553, A
30765, A
169, App
2612, Ap
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US-10-767-795-1394
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Matches
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                             TYPE: DNA
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Result No.

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19.6	19.88	19.8 19.8 19.8 19.8 19.8	20 20 20 19.8
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US-10-767-471-34488 US-10-767-471-34490 US-10-767-471-34556 US-10-767-701-12512	US-10-767-701-10879 PCT-US03-31941A-1 PCT-US03-31941A-2 PCT-US03-31941A-19	US-60-545-213-391 US-60-545-213-392 US-60-545-213-42 US-60-545-213-4663 US-60-545-213-4664 US-60-545-213-4664 US-10-100-683-5410	US-10-417-884A-62 US-10-100-683-11827 US-10-779-543-12187 US-10-417-884A-380
Sequence 34488, A Sequence 34490, A Sequence 34556, A Sequence 12512, A	Sequence 10879, A Sequence 1, Appli Sequence 2, Appli Sequence 19, Appl		Sequence 62, Appl Sequence 11827, A Sequence 12187, A Sequence 380, App

## ALIGNMENTS

Minimum Maximum

Searched:

Sequence:

Database

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US-10-767-795-1392, Application US/10767795

Sequence 1392, Application US/10767795

; GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

; APPLICANT: Zhou, Yihua

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

; FILE REFERENCE: 38-21 (53534) B

; CURRENT APPLICATION NUMBER: US/10/767,795

; CURRENT ELING DATE: 2004-01-30

; NUMBER OF SEQ ID NOS: 117596

; SEQ ID NO 1392

LENGTH: 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: uC-gsronu33B172b05b1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/767,795
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 117596
SEQ ID NO 1394
LENGTH: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1394, Application US/10767795 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53534)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kovalic, David K. APPLICANT: Cao, Yongwei APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Gossypium hirsutum
PEATURE:
FEATURE: OTHER INFORMATION: Clone ID: uC-geronu33B027f06b1
                                                  ORGANISM: Gossypium hirsutum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity hes 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 TGATCAGCTGGTTACCCGTGTTACCCATGAAATGGCACATG 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGATAAACTCATAACTCGTTTGGTTACCAAGGAAGAAGCACATG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.3%;
ilarity 70.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.2; DB Pred. No. 1.6; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>,</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 435;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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US-10-767-795-1392

Query Match

Similarity

48.3%;

\_DB 6; Length 539;

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APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53535) B
CURRENT APPLICATION NUMBER: US/10/767,701
RUMBER OF SEQ ID NOS: 63128
SEQ ID NO 29396
LENGTH: 545
FILE REFERENCE: 3004-01-29
SEQ ID NOS: 63128
CURRENT FILING DATE: 2004-01-29
SEQ ID NO 29396
LENGTH: 545
FYER: DNA
ORGANTON:
RESULT 5
US-10-781-014-167
                                                       밁
                                                                                                                                                                                                   APPLICANT: Zhou, Yihua
ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53535) B
CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 63128
LENGTH: 743
TYPE: DNs
                                                                                                                                            ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS45512_1
US-10-767-701-11493
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                                                                                                      Matches
                                                                                                                           Query Match
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US-10-767-701-29396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                              ORGANISM: Sorghum bicolor FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                          Local
                                    269 ATGTTTAGCTGGTTCCCCATCTTCTTCCCATTGAGAAAGCCCAT 312
                                                             2 ATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACAT 45
                                                                                                   31;
                                                                                                                                                                                                                                                                                                                                                                                                                        532 Archecreareaccarecadaracccareacede 497
                                                                                                         h 48.3%;
Similarity 70.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            5 ATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGÁTAMACTCATAACTCGTTTGGTTÁCCAÁGGAÁGAAGCÁCÁTG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48.3%;
                                                                                                        Score 23.2;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23.2; DB Pred. No. 1.7; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 23.2; DB Pred. No. 1.7; 0; Mismatches
                                                                                                                DB 6;
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                                                                                      13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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                                                                                                             Length 743;
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                                                                                 Gaps
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PRIOR APPLICATION NUMBER: 10/076,555
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 09/217,471
PRIOR FILING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/068,755
PRIOR FILING DATE: 1997-12-23
PRIOR APPLICATION NUMBER: 60/080,664
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-10-779-543-5864
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; LOCATION: (101)..(1012)
; OTHER INFORMATION: RXN02920
US-10-781-014-167
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5864, Appli
GENERAL INFORMATION:
                                                                                                                                                                                                               APPLICANT: WILLIAMS et al
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II
FILE REFERENCE: 2300-21302
CURRENT APPLICATION NUMBER: US/10/779,543
CURRENT FILING DATE: 2004-02-12
CURRENT FILING DATE: 2004-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 46.2%;
Best Local Similarity 69.8%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 784
LENGTH: 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: BGI-126CPCN
CURRENT APPLICATION NUMBER: US/10/781,014
CURRENT FILING DATE: 2004-02-17
PRIOR APPLICATION NUMBER: US 99/602,740
PRIOR APPLICATION NUMBER: 60/141,031
PRIOR PILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/143,208
PRIOR PILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/143,208
PRIOR PILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931412.8
PRIOR APPLICATION NUMBER: DE 19931413.6
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR APPLICATION NUMBER: DE 19931419.5
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
PRIOR PILING DATE: 1999-07-08
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PRIOR APPLICATION NUMBER: DE 19931424.1
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931428.4
PRIOR APPLICATION NUMBER: DE 19931428.4
PRIOR APPLICATION NUMBER: DE 19931428.4
PRIOR APPLICATION NUMBER: DE 19931428.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Corynebacterium glutamicum
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
TITLE OF INVENTION: PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 réarecécréérciagecerégrérecteanréagiaééciéer 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 TGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACAT 45
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                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10779543
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Pred. No. 5;
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FILING DATE: 1998-10-21

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PRIOR FILING DATE: 209-04-10
PRIOR APPLICATION NUMBER: PCT/US99/01619
PRIOR APPLICATION NUMBER: 60/072,910
PRIOR FILING DATE: 1999-01-28
PRIOR FILING DATE: 1998-01-28
PRIOR FILING DATE: 1998-02-24
PRIOR FILING DATE: 1998-02-24
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080,114
PRIOR APPLICATION NUMBER: 60/080,114
PRIOR PILING DATE: 1998-03-31
Remaining Prior Application data removed - Set NUMBER OF SEQ ID NOS: 23767
SOFTWARE: FASE/SEQ for Windows Version 4.0
SEQ ID NO 5864
LENGTH: 808
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                    ঠ
                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-767-471-34311
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US-10-767-471-34311
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001505
                                                                                                                                                                        NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34311
LENGTH: 201
                                                               Matches
                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 120, 1
LOCATION: 166, 1
LOCATION: 214, 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 639, 641, 643, 650, 660,
LOCATION: 762, 783, 784, 795, 801
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: n = A, T, C or G
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LOCATION: 3, 16, 20, 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ION: 120, 123, 129, 133, 138, ION: 166, 172, 173, 174, 180, ION: 214, 216, 217, 218, 219, INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                             333 TATGATNTTCTGCCCACCTGTGATNNTACCCATGAACACGC 373
155
                                                             30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TATGATCAGCIGGTTACCCGTGTTACCCATGAAATGGC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.8%;
Similarity 68.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357, 358, 375,
442, 448, 449,
497, 507, 510,
                 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACA 44
TTTGATCAGTTTCATATTCCTGTGGGTACTAATGAAAAGGAACA 198
                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246,
                                                                           45.0%;
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385,
451,
527,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 22; DB 6 ; Pred. No. 5.8; 0; Mismatches
                                                          Score 21.6; DB Pred. No. 6.2; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             283,
398,
470,
559,
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186,
226,
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192,
228,
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                                                                                            BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             681,
                                                            14; Indels
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147,
197,
236,
                                                                                         6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 808;
                                                                                         Length 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             722,
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156,
201,
238,
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                                                            0
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                                                            Gaps
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US-10-767-701-31393/c
US-10-767-701-31393/c
; Sequence 31393, Application US/10767701
; GENERAL INFORMATION:
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US-10-767-701-14458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOPTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 14458
LENGTH: 2895
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14458, Application US/10767701
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                       Matches
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yingwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5353)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (1)...(546025)
OTHER INFORMATION: n = A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS8018_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 546025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                        329443
                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1033 ATAAGCAACGGGTTGCAGTTGTTGTAGCTCATGAATTAGCTCAT 1076
                                                                                                                                                                                                                                                                                                                       30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                        TTTGATCAGTTTCATATTCCTGTGGGTACTAATGAAAAGGAACA
                                                                                                                                                                                                                                                                           TATGATCAGCTGGTTACCCGTGTTACCCATGAAATGGCACA 44
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10767471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Michele et al.
GENETIC POLYMORPHISMS ASSOCIATED WITH
RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                      45.0%;
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                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                        Score 21.6;
Pred. No. 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21.6;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                       Mismatches
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US-10-783-271-34
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-765-790-41
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          SOFTWARE: Patent
SEQ ID NO 34
LENGTH: 175737
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                                                                                                                                          Sequence 34, Application US/10783271
GENERAL INFORMATION:
APPLICANT: Veridex, LLC
APPLICANT: Wang, Yixin
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                          TITLE OF INVENTION: BREAST CANCER PROGNOSTICS
FILE REFERENCE: VDX-5003 USNP
CURRENT APPLICATION NUMBER: US/10/783,271
CURRENT FILING DATE: 2004-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 41
                                                          NUMBER OF SEQ ID NOS: 11
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Best Local 9
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CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 31393
LENGTH: 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/765,790
CURRENT FILING DATE: 2004-01-27
PRIOR APPLICATION NUMBER: US 10/737,082
PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Li, Zheng
TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
FILE REFERENCE: 1657/2035
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.2
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LOCATION: (1).. (607)
OTHER INFORMATION: unsure at all n locations
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                                          PatentIn version 3.2
                                                                                                                                                                                                                                                                          AAGCCCAGCTGGTGACTTGAGTGTCTCCCCAACAATAGAACATG 15867
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Lechner, John F.
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Gannon, Allison
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Pred. No. 32;
0; Mismatches
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Pred. No. 9.5;
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US-10-779-543-15761/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15761
APPLICANT: Reddy, Roopa
APPLICANT: Gueglar, Karl, J.
APPLICANT: Gueglar, Karl, J.
APPLICANT: Au-Young, Janice K.
TITLE OF INVENTION: COMPOSITION FOR DETECTION
FILE REFERENCE: PA-0014-1 CON
CURRENT APPLICATION NUMBER: US/10/781,469
CURRENT FILING DATE: 2004-02-17
PRIOR APPLICATION NUMBER: US 09/496,321
PRIOR FILING DATE: 2000-02-01
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Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1998-01-28
PRIOR APPLICATION NUMBER: 60/075,954
PRIOR FILING DATE: 1998-02-24
PRIOR APPLICATION NUMBER: 60/080,114
PRIOR FILING DATE: 1998-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/068,755
PRIOR FILING DATE: 1997-12-23
PRIOR APPLICATION NUMBER: 60/080,664
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CURRENT FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: 10/076,555
PRIOR FILING DATE: 2002-02-15
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/217,471 PRIOR FILING DATE: 1998-12-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Williams et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 421
TYPE: DNA
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FILING DATE: 1998-10-21
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                                                                                                                                                                                                                                                                                                     225 TTGTTAACTGTCCAGTTACCCATGAAAATTCACAT
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26; Conserv
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Pred. No. 19;
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Pred. No. 58;
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Twine, Natalie
APPLICANT: Twine, Natalie
APPLICANT: Towner, Andrew
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: ANIO1080 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEO ID NOS: 5278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 52
LENGTH: 198161
TYPE: DNA
ORGANISM: Homo sapiens
US-10-775-169-52
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PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 125
SOFTMARE: PERL Program
SEQ ID NO 49
LENGTH: 905
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 2832568
US-10-781-469-49
Search completed: March 17, 2004, 08:25:38 Job time: 8.32948 secs
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US-10-775-169-52
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                                                                                                                                                                         Query Match 42.9%; Score 20.6; DB 6; Length 198161; Best Local Similarity 67.4%; Pred. No. 72; Matches 29; Conservative 0; Mismatches 14; Indels 0;
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                                                                                         175379 TCACATGTGTTCTCATGTTCTTAACCACGAAATGTCTCAGGGA 175421
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OLASON WINTER JOYAL SIHIL

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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: /cgn2_6/ptodata/2/pna/
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CCURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 456
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US-09-543-407-11
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20 US-09-523-691-71
20 US-09-252-691-71
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  ALIGNMENTS
  PEPTIDE SEQUENCES
   Sequence 11, Appl Sequence 5, Appl Sequence 5, Appl Sequence 13, Appl Sequence 13, Appl Sequence 17, Appl Sequence 23, Appl Sequence 24, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 172, Appl Sequence 172, Appl Sequence 172, Appl Sequence 172, Appl Sequence 3, Appl Sequence 3, Appl Sequence 172, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 171, Appli Sequence 171, Appli Sequence 171, Appli Sequence 171, Appli Sequence 171, Appli Sequence 171, Appli Sequence 171, Appli Sequence 2434, Appli Seq
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Sequence 56, Application US/U0222002...
GENERAL INFORMATION:
APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
  US-08-233-642A-56
  US-09-543-407-11
   Query Match
Best Local S
Matches 456
  Aluxa
STREET: bocc
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
71P: 98104-7092
71P: 7810ABBE FO
SOFTWARE: PatentIn Release #1.0, ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
   FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
  421
   421
  361
   361
   301
  301
  241
   241
   181
  181
  121
   121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCCTTGCCAA
   456;
   61
  61
  μ
   1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  Similarity
  GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
   GCACATGCAAACAACGCCACGGCTAACCAGTATTAA
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCCGCCCAATACGGCGGT 360
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   E: Seed and Berry 6300 Columbia Center,
   100.0%; ilarity 100.0%; Conservative 0;
   ٥,
   Score 456; DB 23;
Pred. No. 7.6e-136;
Mismatches 0;
  701 Fifth
   Version
   #1.25
   456
   Indels
  Length 456;
   <u>,</u>
   Gaps
  420
   420
   360
  300
   300
   240
  240
   180
  180
   120
  120
  60
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   RESULT 3
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   US-08-233-642A-56
   REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMPUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6931
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
   Sequence 1, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Agron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
  Best Loc
Matches
  SEQ ID NO 1
  Query Match
LENGTH: 456
TYPE: DNA
ORGANISM: Salmonella enteritidis
   Local
  NAME/KEY:
LOCATION:
  STRANDEDNESS: single TOPOLOGY: linear
   LENGTH: 456 base pairs
  361
  301
  301
  241
   241
   181
   181
   121
   121
   421
   421
  424; Conservative
  61
  13
  _
   Similarity
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCCTAACGCTGCGCTTGCCTCTGCAA 180
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
  GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG 420
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GGCGTCGTTCCACAATGGGGCGGCGGCGAATACTAACGGCGGCGAATAGTTCCGGC 120
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   SdD
  1..456
   93.0%;
  Score 404.8; DB 6;
Pred. No. 2.6e-119;
0; Mismatches 32;
  Indels
  Length
  456;
  0
   180
  300
  60
  0
```

```
APPLICANT: DOTAIN, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
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   ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-13
  RESULT 4
US-09-543-407-13
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   US-09-543-407-1
   Sequence 13, Applica GENERAL INFORMATION:
  Query Match
Best Local Similarity
   Matches 424;
  Best Local Similarity
   Query Match
  LENGTH: 45
   APPLICANT: White, Aaron P. APPLICANT: Doran, James L
  ORGANISM: Artificial Sequence FEATURE:
  421
  361
  361
   301
   301
   241
   241
   181
  181
  121
  421
  121
  61
  61
   456
  1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAGTCGTAGTTTCTGGCAGTGCTCTGGCT
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC 120
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
                                     ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  Application US/09543407
   Conservative
   Conservative
  82.5%;
  93.0%;
   Score 376; DB 23;
Pred. No. 5.1e-110;
0; Mismatches 50;
   0; Mismatches
  Score 404.8; DB 23; Pred. No. 2.6e-119;
   PEPTIDE SEQUENCES
   Length 456
   Indels
   Indels
   Length
   <u>,</u>
   0,
   Gaps
   420
                                     60
   60
  420
   360
   360
   300
   300
  240
  240
  180
  120
   60
   60
   0
   0
```

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043.406
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version, 4.0
SEQ ID NO 19
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  ; FEATURE:
; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA;
; OTHER INFORMATION: sequence containing the replacement fragment;
; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-19
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  RESULT 5
US-09-543-407-19
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   Query Match
Best Local (
   Sequence 19, Application US/09543407 GENERAL INFORMATION:
  Matches
  LENGTH: 456
TYPE: DNA
  ORGANISM: Artificial Sequence
                                   181
   181
  121
  121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
   361
   301
  61
  421
  421
  361
  301
   241
  241
   181
   181
  121
  397;
   121
  61
   Similarity
                      AGCGATGCCCGTAAATCTGAAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  GGCGTCGTTCCACAATGGGGCGGCGGCGGCGAATAGTTCCGGC
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTTCTGGCAGTGCTCTGGCT
AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
   AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATG 420
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAAATGGTTTCAGAAATAAT 300
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   CTGGTTACCCGTGTTACCCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT 420
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG 360
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCCGAT 240
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCCTTGCTCTGCAA
  79.3%; ilarity 87.1%; Conservative
   Score 361.6; DB 23; Pred. No. 2.3e-105; 0; Mismatches 59;
   456
  PEPTIDE SEQUENCES
  Indels
  Length 456;
   0;
240
                                 240
  180
   120
  120
  60
  300
   180
  240
  120
```

```
Sequence 17, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043,406
CURRENT APPLICATION UNMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 456
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  ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragmen; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-17
  RESULT 6
US-09-543-407-17
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   δ
  Matches
  Query Match
Best Local :
   ORGANISM: Artificial Sequence FEATURE:
   TYPE: DNA
   301
   361
                                 361
   301
  241
  241
  181
  181
   121
   121
  393;
   421
   361
   361
  301
  301
  241
   421
  241
   61
   13
   μ.
  Similarity
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                       AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCCGTGTTGTTACCCCATGAAATG
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATACGGCGGT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GGCGTCGTTCCACAATGGGGCGGCGGCGGCAATAGTTCCCGGC
   GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCGGCAATAGTTCCGGC
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTTCTGGCAGTGCTCTGGCT 60
  CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCACTGCAA
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
  GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATG
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   Conservative
   77.9%;
   <u>.</u>
   Score 355.2; DB 23;
Pred. No. 2.6e-103;
0; Mismatches 63;
  DB 23;
   456
   PEPTIDE SEQUENCES
   Indels
   Length
   0
   Gaps
                               420
   360
   300
  180
  180
   360
  240
  120
   120
   60
   360
   420
   420
   360
   300
   300
```

```
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
RESULT 8
US-09-543-407-25
; Sequence 25, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
   ; FEATURE:
; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga; OTHER INFORMATION: sequence containing the replacement fragmen THER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-23
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  RESULT 7
US-09-543-407-23
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   Query Match
Best Local Similarity
Matches 392; Conserv
  Sequence 23, Application US/09543407 GENERAL INFORMATION:
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
  181
  181
  121
   121
  361
  301
   301
  241
   241
   421
   361
  421
  61
  61
  421
  _
  CATGAAATGGCACATGCAAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCCGGC
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   GCACATGCAAACAACGCCACGCTAACCAGTATTAA 456
  GCACATGCAAACAACGCCACGCTAACCAGTATTAA 456
   AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATG 420
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  GCCACCATCGACCAGTGGAACGCTAAAAACTATGATCAGCTGGTTACCCGTGTTGTTACC
   77.5%; llarity 86.0%; Conservative
  0
   Score 353.6; DB 23;
Pred. No. 8.6e-103;
0; Mismatches 64;
  PEPTIDE SEQUENCES
   Indels
   Length 456;
   0
   Gaps
   360
   240
  180
  240
   120
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  US-09-543-407-25
  Matches
   Query Match
Best Local
  TYPE: DNA
  Local Similarity
nes 392; Conserv
  361
  301
  301
  421
  421
   361
   241
  241
   181
  181
  121
   121
   61
   61
  Conservative
  77.5%;
86.0%;
  <u>.</u>.
```

```
RESULT 9

US-09-543-407-15

; Sequence 15, Application US/09543407

; Sequence 15, Application US/09543407

; GENERAL INFORMATION:

APPLICANT: Moite, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP

FILE REFERENCE: 920043-406

; CURRENT APPLICATION NUMBER: US/09/543,407

; CURRENT APPLICATION NUMBER: US/09/543,407

; CURRENT FILING DATE: 2000-04-05

; NUMBER OF SEQ ID NOS: 59

; SOFTWARE: FABLEEQ for Windows Version 4.0
   ; APPLICANT: Doran, James L.
; APPLICANT: Collinson, S. Karen
; APPLICANT: Kay, William W.
; TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
; TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
; FILE REFERENCE: 920043.406
; CURRENT APPLICATION UNMBER: US/09/543,407
; CURRENT FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 456
   ORGANISM:
ORGANISM:
ORGANISM:
Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragmen
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   1 ATGAAACTTTTAAAAGTGGCAGCAGTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG 420
  GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAGGTTATGGTAACGGCGCCGAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
   GCCTCCTTCCACAATGGGCCGCCGCCGTAATCATAACGGCGGCGCAATAGTTCCCGGC
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTTATGATCAG
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
  Pred. No. 8.6e-103;
   Mismatches
  456
   PEPTIDE SEQUENCES
   PEPTIDE SEQUENCES
   Indels
   Length
  <u>,,</u>
  Gaps
   240
   180
   120
  360
   300
  60
  360
   60
```

```
Sequence 21, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 456
TYPE: DNA
REALTHEE.
   ; OTHER INFORMATION:
; OTHER INFORMATION:
; OTHER INFORMATION:
US-09-543-407-21
  RESULT 10
US-09-543-407-21
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 Query Match
Best Local Similarity
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  Query Match
  FEATURE:
  OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
  TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
  LENGTH: 456
   Local Sim hes 391;
  361
   301
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   241
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  181
  181
   121
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  61
   61
   ب
   Similarity
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  GCACATGCAAACAACGCCACGGCTAACCAGTATTAA
   AATAACGCCGCGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG 420
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTTCAGAAATAAT
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC 120
   GGCGTCGTTCCACAATGGGGGGGGGGGGGGGAATAGTTCCGGC 120
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAGTCGTAGTTTCTGGCAGTGCTCTGGCT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   Conservative
  Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
  Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
 76.8%;
85.5%;
   77.2%;
   0;
Score 350.4; DB 23; Pred. No. 9.3e-102;
   Score 352; DB 23;
Pred. No. 2.8e-102;
0; Mismatches 65;
   65;
  456
  456
  PEPTIDE SEQUENCES
  Length 456;
   Indels
                Length 456;
   0
   Gaps
  240
   360
   420
   360
  300
   240
   180
  60
  60
   0
```

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PE
FILE REFERENCE: 920043,406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 27
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  RESULT 11
US-09-543-407-27
Sequence 27, Applica
GENERAL INFORMATION:
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   Best Loca
Matches
   Query Match
   Matches
  ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Recombinant OTHER INFORMATION: sequence oc OTHER INFORMATION: encoding PI
  TYPE: DNA
  LENGTH: 456
   Local
   390;
  361
121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  361
  301
  241
  421
  421
  301
   241
  181
   181
  121
                                     61
   61
   121
   390;
   61
   61
   μ
  Similarity
   GGCGTCGTTCCACAATGGGGCGGCGGCGGCGAATAACGGCGGCGGCGGCAATAGTTCCGGC
                                 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  ATGAAACTTTTAAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG
  GCACATGCAGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCCGAT
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GTAGGCCAGGGTGCGGATAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCCAATAGTTCCGGC
   GGCGTCGTTCCACAATGGGGCGGCGGCGCTAATCATAACGGCGGCGCAATAGTTCCGGC
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  Application
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCCGAT
   Conservative
   Conservative
  Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragmer encoding PT3 from GP63 of Leishmania major.
  76.8%;
85.5%;
  US/09543407
  Score 350.4; DB 23;
Pred. No. 9.3e-102;
0; Mismatches 66;
   ٥,
   Mismatches
   66;
  456
  PEPTIDE SEQUENCES
   Indels
   Indels
  Length
  456;
  0;
  0
  Gaps
  Gaps
  120
   60
                                 120
  420
   420
   360
   300
   180
  360
   240
   240
   300
   120
   120
   60
   60
  0
```

```
Sequence 29, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Asaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEF
FILE REFERENCE: 920043.406
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
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  RESULT 12
US-09-543-407-29
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  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga; OTHER INFORMATION: sequence containing the replacement fragmer; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major US-09-543-407-29
  NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 456
  Query Match
Best Local Similarity
   Matches
  ORGANISM: Artificial Sequence
   FEATURE:
   TYPE: DNA
           241
  181 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCCGAT
   181
  181
  121
   121
  361
  361
   301
   301
  241
   421
   421
   241 TATGATCAGCTGGTTACCCGTGTTGTTÄCCCATGAAATGGCACATGCATTCAGAAATAAT
   181
   121
   61
  13
   388; Conservative
  1
  μ
GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  GGCGTCGTTCCACAATGGGGCGGCGGCGGCAATAGTTCCGGC
   ATGAAACTITTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
  ATGAMACTTTTAMAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATG
   76.1%;
85.1%;
   0,
   Score 347.2; DB 23;
Pred. No. 1e-100;
0; Mismatches 68;
   DB 23;
   PEPTIDE SEQUENCES
   Indels
   Length 456;
   ٥,
   Gaps
   300
  240
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  RESULT 13
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   US-08-233-642A-54
  Sequence 54, Application US/08233642A
GENERAL INFORMATION:
APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
  Query Match
Best Local Similarity
Matches 317; Conserv
   APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND C
TITLE OF INVENTION: BASED VACCINE
NUMBER OF SEQUENCES: -8
NUMBER OF SEQUENCES: -8
   TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 54:
  ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622,4900
   COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
   TOPOLOGY: 1i
   SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
   FEATURE:
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
  STREET: 6300 C
CITY: Seattle
STATE: Washing
   NAME/KEY:
LOCATION:
   APPLICATION NUMBER: US/0 FILING DATE: 26-APR-1994 CLASSIFICATION: 424
   STATE: Washington COUNTRY: U.S.A.
  STRANDEDNESS:
   301
  361
   361
   301
                   124 GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC 183
  421
61
  64
  98104-7092
  nucleic acid
   GTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCG
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
   GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420
  AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG 420
   GCCACCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAGGCGGT
   GCCACCATCGACCAGTGGAACGCTAAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
   6300 Columbia Center,
   Conservative
   linear
   CDS
   DNA (genomic)
   double
  69.1%;
  BASED VACCINES
58
  METHODS AND COMPOSITIONS FOR SALMONELLA-
   US/08/233,642A
   0
   920043.403C3
  Score 315.2; DB
Pred. No. 2e-90;
   Mismatches
  701 Fifth Avenue
   Version
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   Indels
  Length 361;
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  ; SEQ ID NO 172
, LENGTH: 477
; TYPE: DNA
; ORGANISM: Enterobacter cloacae
US-09-252-691-172
  RESULT 14
US-09-252-691-172
US-09-252-691-172
US-09-252-691-172
GENERAL INFORMATION:
HAPPLICANT: Keith G. Weinstock et al.
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  Query Match 48.8
Best Local Similarity 68.0
Matches 310; Conservative
  APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND
FILE REFERENCE: 107196.135
CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILLING DATE: 1999-02-18
CURRENT FILLING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
  421
  382
   361
   322
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  241
  202
  181
   142
  121
  364
  241
  181
   82
  61
   22
   301
   304
  244
   121
   184
   1
GGCTTTGGCAACAACGCGACCGCACACCAGTACTGA
   GCACATGCAAACAACGCCACGCTAACCAGTATTAA 456
  GGCAACGGCGCGGTAGACCAGACAGCGTCCGGCTCAACGGTGACTGTGCACCAGGTT
  AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG
  GCCACCATCGACCAATGGAATAGCAAAGACTCTGTTATCAACGTGAAACAGTTCGGCGGC
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   GTTGGCCAGGGCTCTGATGACAGTTCTATCGATCTGCTGCAAAAAAGGCTTTGGTAACAGC
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   ACGGACGCCCGAGATTCTGAATTGACCATTACCCAGCATGGTGGTGGTAACGGCGCAGAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   cereaere a de constant de cons
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  GGTGCGGTACCACATTTGGCGGCGGCCACGGTGGTGGCTGGGGTGGCGGCAATAACGGC
   GGCGTCGTTCCACAATGGGGCGGCGGCGGCGAATAGTTCCGGC
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   ATGAAACTTTTCAAAGTGGCAGTTATTGCAGCAATCGTAGTTTCTGGCAGTGCTTTCGCA
  AACGCCGCGCTGGTTAATCA 320
   AACGCCGCGCTGGTTAATTA 383
  ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAAT 363
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   GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC
  GATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTA
  GATGCCGGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCCGATGTA
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  48.8%;
  Score 222.4; DB 17; Length Pred. No. 1.9e-60; O; Mismatches 146; Indels
  SEQUENCES RELATING THERAPEUTICS
   Length
   477;
   0;
   Gaps
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   441
  ENTEROBACTER
   381
   360
   321
   300
  261
   81
  240
   201
   141
  120
   60
   300
  303
  240
  180
  243
   0
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Sequence 172, Application US/09252691C

GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO E TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
CURRENT APPLICATION NUMBER: US/09/252,691C
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,145
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR PILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 11326
SEQ ID NO 172
LENGTH: 477
ORGANISM: Enterobacter cloacae
US-09-252-691C-172
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   Matches
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Best Local
442
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   142
   121
   310;
   61
   82
   22 ATGAAACTTTTCAAAGTGGCAGTTATTGCAGCAATCGTAGTTTCTGGCAGTGCTTTCGCA
  1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  Similarity
                               GCACATGCAAACAACGCCACGGCTAACCAGTATTAA
  GGCAACGGCGCCGGTAGACCAGACAGCGTCCGGCTCAACGGTGACTGTGCACCAGGTT 441
   AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATG 420
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
  ĠŤTĠĠĊĊĀĠĠĠĊŦĊŦĠĀŤĠĀĊĀĠŤŦĊŤĀŤĊĠĀŦĊŤĠĊŦĠĊĀĀĀĀĀĠĠĊŤŤTĠĠŢĀĀĊĀĠĊ
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCGCTCTGCAA 180
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  ĠĊĊŔĊĊŔŤĊĠŔĊĊŔŖŤĠĠŔŔŦŖĠĊŔŔŔĠŔĊŤĊŦĠŦŤŔŤĊŔŖĊĠŤĠŖŖŖŖĊŔĠŤŢĊĠĠĊĠĠĊ 381
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
  CCTGACTCAACCCTGAGCATTTACCAGTACGGCGGCGGTAACTCCGCGCCTTGCTTTGCAG 201
  ACGGACGCCCGAGATTCTGAATTGACCATTACCCAGCATGGTGGTGATAACGGCGCAGAT
   GGTGCGGTACCACAATTTGGCGGCGGCGCCACGGTGGTGGCTGGGGTGGCGGCAATAACGGC
   48.8%; ilarity 68.0%; Conservative
   0
   Score 222.4; DB 17;
Pred. No. 1.9e-60;
0; Mismatches 146;
                                 456
   Indels
   Length
   477;
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   Gaps
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  ENTEROBACTER
  321
  261
  141
   120
   81
   0
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Search completed: March 18, 2004, 02:46:58 Job time : 2923.24 secs

RESULT 15 US-09-252-691C-172

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Result
   Minimum DB
Maximum DB
   Total number of hits satisfying chosen parameters:
  Sequence:
  Title:
  OM nucleic - nucleic search, using
  Scoring table:
  Perfect score:
   იიიი
  0.0
  0000
  0000
  9
    22222221111111111
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Score
  length: 0
length: 2000000000
   Match Length
  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
   456
   March 16, 2004, 15:39:56 ; Search time 69.6301 Seconds (without alignments) 2406.048 Million cell updates/sec
  Query
  Pending_Patents_NA_New:*

| (cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*
| (cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*
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| (cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq:*
   637880 seqs, 183698769 residues
   US-09-543-407-11
   Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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  Copyright
   3990
1355
150223
  1588
290892
1326
24900
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11400
  GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
  8
          US-09-741-873C-3
US-09-741-873C-1
US-09-870-230A-629
US-10-624-149A-1
US-10-767-7701-14522
US-10-767-471-10809
US-10-767-471-10736
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US-10-767-701-28437
US-60-545-213-2135
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US-60-545-213-1313
US-60-545-213-1313
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US-60-545-213-1585
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  SUMMARIES
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Sequence
Sequence
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Sequence
Sequence
   Description
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Sequence
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Sequence
  Sequence 14522, A Sequence 10809, A Sequence 257, App
   Sequence 629, App
Sequence 593, App
Sequence 1, Appli
  Sequence
  Sequence
   Sequence
  Sequence
   Sequence
10736, A
2134, Ap
2135, Ap
6407, Ap
1030, Ap
1030, Ap
291, App
5725, Ap
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31417, A
1313, Ap
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| C 28 28 28 6.1 2148 6 US-10-775-972-134 29 27.8 6.1 749 6 US-10-767-701-12516 30 27.8 6.1 1580 6 US-10-767-701-12516 31 27.6 6.1 201 6 US-10-767-701-12607 32 27.6 6.1 1052 6 US-10-767-701-12607 33 27.6 6.1 4697 6 US-10-767-701-12607 34 27.6 6.1 6224 6 US-10-763-372-1187 35 27.6 6.1 6224 6 US-10-453-372-1187 37 27.4 6.0 12982 6 US-10-767-701-1287 38 27.4 6.0 1295 6 US-10-767-701-1287 39 27.4 6.0 1295 6 US-10-100-683-5480 39 27.4 6.0 3416 6 US-10-100-683-397 39 27.4 6.0 8206 6 US-10-101-683-3529 42 27.4 6.0 8206 6 US-10-021-698A-3529 42 27.4 6.0 186449 6 US-10-021-698A-715 43 27.2 6.0 959 6 US-10-767-701-1446 45 27.2 6.0 959 6 US-09-461-537A-3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                  |                    |                     |                    | _                   | _                  |                 | _                  | ^                  | _                   |                    |                    |                    |                     | _                   |                    |                     | _                 |                |
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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | US-09-461-537A-3 | US-10-767-701-1446 | PCT-US04-05654-1515 | US-10-021-698A-715 | US-10-021-698A-3529 | US-10-100-683-3397 | US-10-151-553-1 | US-10-100-683-5480 | US-10-767-701-1287 | US-10-767-471-10679 | US-10-453-372-1187 | US-10-453-372-1173 | US-10-453-372-1185 | US-10-767-701-12607 | US-10-767-471-28293 | US-10-451-467A-239 | US-10-767-701-12516 | US-10-775-972-154 | CC FC 7.F FULL |
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## ALIGNMENTS

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   PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR PPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1999-05-04
PRIOR PILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
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   NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
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PRIOR FILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR FILING DATE: 1992-11-03
PRIOR PPLICATION NUMBER: US 08/187,865
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  APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
CURRENT ENVENTION: Pibronectin Binding Protein As Well As Its Preparation
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR PILING DATE: 1998-05-06
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PRIOR FILING DATE: 1997-11-26
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   GCTÁCTCTTGÁTCÁGTGGÁÁCGGCAÁÁÁATTCTGÁAÁTGÁCGGTTAAACÁGTTCGGTGGT 442

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SOFTWARE: PatentIn Ver. 2.0

SSEQ ID NO 629

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ORGANISM: Homo sapiens
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PRIOR FILING DATE: 1997-06-20
PRIOR APPLICATION NUMBER: 60/050,359
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  CURRENT FILING DATE: 2001-09-27
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   APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Lyme Disease Vaccines
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PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
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  Query Match 7.3%;
Best Local Similarity 47.4%;
Matches 100; Conservative
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APPLICANT: HOGENBOOM, HENDRICUS R. J. M.
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TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMI
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
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  APPLICANT: LADNER,
  APPLICANT:
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COHEN, EDWARD H.
NASTRI, HORACIO G.
ROOKEY, KRISTIN L.
  TTTGCTGTGAAGAGTAATGATGGTGAGAAAG 3643
  GCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATCTGAAAACGACCATTACCCAG
  YGGYWSYGGRGGYGGYWSYGGYWSYGGYGAYTTYGAYTAYGARAARATGGCWAAYGCYAA 887
   AAGAAGGATGATCAGATTGCTGCTGCTATTGCTTTGAGGGGGATGGCTAAGGATGGAAAG 3612
   GTTACGGCTGCGGCTGCTGAGCAGGATGGAGAGAGCCTGCAGAGGCTACAAATCCG
   ATTGCTGCTATTGGGAAGGGTAATGAGGATGCTGCGGATTTTGGTAAGGATGAGATG
   AGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTG
   ATTACTGTCGGCCAATACGGCGGTAATAACG 367
  ACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGAT 336
   Application US/10045674A
  0; Mismatches 111; Indels
  Score 33.4; DB 5; Pred. No. 0.37;
   Length 1355;
   Length 3990;
  Indels
  0
  0;
   Gaps
  FAMILY
   276
   216
   3492
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CURRENT APPLICATION NUMBER: US/10/624,149A
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: 60/403,282
PRIOR FILING DATE: 2002-08-14
PRIOR PILING DATE: 2002-08-14
PRIOR PILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: DE 10337008
PRIOR APPLICATION NUMBER: DE 10317008
PRIOR APPLICATION NUMBER: DE 10317008
PRIOR PILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 1
SEQ ID NO 1
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  RESULT 5
US-10-624-149A-1
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   5
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   Ś
  US-10-624-149A-1
  LENGTH: 150223

TYPE: DNA
ORGANISM: Equine herpesvirus 1
PUBLICATION INFORMATION:
AUTHORS: Telford, E.A.
AUTHORS: Watson, M.S.
AUTHORS: MCBride, K.
AUTHORS: Davison, A.J.
TITLE: The DNA sequence of equ
   Sequence 1, Application US/10624149A GENERAL INFORMATION:
  Matches
  Query Match
Best Local Similarity
   APPLICANT: Ziegler, Christina
TITLE OF INVENTION: gM-Negative EHV-Mutants without Heterologous Elements
FILE REFERENCE: 1/1372
  APPLICANT: Neubauer, Antonie APPLICANT: Ziegler, Christi
  VOLUME: 189
ISSUE: 1
PAGES: 304-316
DATE: JUL-1992
DATABASE ACCESSION NUMBER: NC 001491,
DATABASE ENTRY DATE: 2000-08-01
   JOURNAL:
  95542 CTGTGGTAACGGTGGGCCTTAGTTTTGATACGGCTCATTTCCACACGCATGTTTGCCTACG
   948 RYTWGAYWSYGTCGCYACWGAYTAYGGTGCTGCYATCGAYGGYTTYATYGGYGAYGTYWS 1007
  258 TAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTG 317
   Virology
   YGGYCTKGCTAAYGGYAAYGGWGCYACYGGWGAYTTYGCWGGYTCKAATTCYCARATGGC 1067
GAGAGCTTATTCACAACGAGCTGTTG 95687
                                      GAAATAATGCCACCATCGACCAGTGG 318
  GCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCA
   CTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACG
   YCARGTYGGWGAYGGKGAYAAYWSWCCKYTWATGAAYAAYTTYMGWCA 1115
  TCAAGCCCATGAGCCACGGACCGGATATGGTTTCTGTATACCAGTCTCTGGGGCGCGTCA
  GAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGT 377
   TAATTATGATCAGCTGGTTACCCGTGTTACCCATGAAATGGCACA 425
  Conservative
  7.1%;
51.4%;
  Christina
  equine herpesvirus-1
   Score 32.4; DI
Pred. No. 3.5;
0; Mismatches
  0;
  5
   DB 6;
  71;
   Length 150223;
  Indels
  0;
  Gaps
   292
  9566
  9560
   232
  0
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US-10-767-701-14522

Sequence 14522, Application US/10767701 GENERAL INFORMATION: APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua

```
NAME/KEY: misc feature; LOCATION: (1)...(290892); LOCATION: (1)...(290892); OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables US-10-767-471-10809
  RESULT 7
US-10-767-471-10809/c
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  US-10-767-701-14522
   NUMBER OF SEQ ID NOS: 50231

SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 10809

LENGTH: 290892

TYPE: DNA
ORGANISM: Homo sapiens
   Sequence 10809, Application US/10767471
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES
FILE REFERENCE: CL001505
  Query Match
Best Local Similarity
Matches 123; Conserv
  APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REPERENCE: 38-21(535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 14522
LENGTH: 1588
  Query Match 6.9
Best Local Similarity 44.9
Matches 125; Conservative
   CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
  OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS2100_1
  ORGANISM: Sorghum FEATURE:
        234073
   515
   220
   575
   160 ААСССТССССТТССТССАААСССАТССССТАААТСТСАААССАСТТАСССАСАСС 219
   100
   455 GGTGGTGGCGGCTTCGGTGGTGGTGGCTATGGCGGTGGCGGTGGCTATGGTGGTGGC
  40 GTTTCTGGCAGTGCTCTGGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAAC
  GATTATGATGATGATGGTAATGGTGATGATGGTGATGGTGATAGTTACAGTAGTGAT
GTTGGTAATGATAGTGGTGACGACGGTGATGCTAATGATTATGATGATGATGGTGGT
  AGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTG
  фсталесестессттестеслалесентессетильного в потратителение в потратите 
  CAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAA
   GGTTATGGTAACGGCGCGGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACT
   GGTGGTGGTGTTGGTGATTATGGAGCTGCAGGTGGAGCTGGAGGCAACTTTGCTGCTGGA
  GCTGGTAGCTTTGGCGGTGGTTCCACTGGCGCCGAGAAGGA
   GGCGGCGGCAATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCT 159
  GGTAGTAACAGCTTTGCCAGCAGTAACTTCGGTGCTGACAGTGGTTTTGGTGGAAACCCCT
   GGCGGTGGCTATGGTGGCTATGGTGGCAACTACGGCAACAGGGGTGGCGATGGCTAT
  Conservative
  bicolor
  6.8%;
  6.9%;
  Score 31.4; DB 6; Length 1
Pred. No. 1.2;
0; Mismatches 156; Indels
  Score 31.2;
Pred. No. 11;
  Mismatches
  DB 6;
  153;
  Length 290892
  Length 1588;
  Indels
  735
  320
  <u>,,</u>
  0;
  Gaps
  Gaps
  276
    234014
  234074
   279
   574
   514
  694
   634
   THEREOF
  0
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GTACTGCTTCAGCATGTCTCGGTCGTCTGGAGTGTTGAT 277

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  FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(489)
OTHER INFORMATION: FRXA02596
US-10-781-014-257
  RESULT 8
US-10-781-014-257/c
   밁
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  밁
   PRIOR APPLICATION NUMBER: US 09/602,740
PRIOR FILING DATE: 2000-06-23
PRIOR PEPLICATION NUMBER: 60/141,031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/143,208
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 60/151,572
PRIOR APPLICATION NUMBER: 60/151,572
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
  δ
   Query Match
Best Local 9
   SEQ ID NO 257
LENGTH: 512
  Sequence 257, Applic GENERAL INFORMATION:
  Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 784
  PRIOR
  FILE REFERENCE: BGI-126CPCN
CURRENT APPLICATION NUMBER: US/10/781,014
CURRENT FILING DATE: 2004-02-17
   PRIOR APPLICATION NUMBER: DE 19931428.4
PRIOR FILING DATE: 1999-07-08
  PRIOR
  APPLICANT: Zelder, Óskar
APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORVEBBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: INVOLVED IN CARBON METABOLISM AND ENERGY
TITLE OF INVENTION: PRODUCTION
   APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwi
  TYPE: DNA ORGANISM: Corynebacterium
   APPLICATION NUMBER: DE 19931420.9
FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931424.1
  APPLICATION NUMBER: DE 19931419.5
FILING DATE: 1999-07-08
  FILING DATE: 1999-07-08
  APPLICATION NUMBER: DE 19931413.6 FILING DATE: 1999-07-08
  310 GACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAATAACGCC 369
   277
   Similarity
                                GCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTT 408
   AAGGATGGTAATGAAAÁTGÁTÁATGCTGÁTGCTAÁC 233858
   GGGAATGTTGGTGAAGATCGTGGCTGTGATGGTGATGATGATGATGATGATGAT 233894
  ATTACTGTCGGCCAATACGCGGGTAATAACGCCGCGCTGGTTAATTATGATCAGCTGGTT
  ACCCGTGTTGTTACCCATGAAATGGCACATGCAAAC 432
  ACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGAT
   Schroder, Hartwig
Zelder, Oskar
   Application US/10781014
  Conservative
   56.6%;
  glutamicum
  0; Mismatches
   Score 30.2; D
Pred. No. 1.8;

    See File Wrapper or PALM

  DB 6;
  43;
   Length 512;
   Indels
   0;
   Gaps
  396
   0,
```

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RESULT 10
US-10-767-471-10736/c
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   RESULT 9
US-10-781-014-255/c
   Sequence 10736, Appl: GENERAL INFORMATION:
  Remaining Prior Application
NUMBER OF SEQ ID NOS: 784
SEQ ID NO 255
   Sequence 255, Application US/10781014 GENERAL INFORMATION:
  Matches
  Query Match
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS
TITLE OF INVENTION: REPUMATION ARTHRITIS,
FILE REFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
  FEATURE:

NAME/KEY: CDS

LOCATION: (101)..(1303)

OTHER INFORMATION: RXN02596

-10-781-014-255
  PRIOR APPLICATION NUMBER: US 09/602,740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/141,031
   CURRENT APPLICATION NUMBER: US/10/781,014
CURRENT FILING DATE: 2004-02-17
  APPLICANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUT
TITLE OF INVENTION: INVOLVED IN CARBON
  FILE REFERENCE: BGI-126CPCN
  TITLE OF INVENTION:
  APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
  TYPE: DNA ORGANISM: Corynebacterium glutamicum
   ENGTH:
  rocar
   FILING DATE: 1999-07-08
APPLICATION NUMBER: DE 19931424.1
FILING DATE: 1999-07-08
  APPLICATION NUMBER: DE 19931428.4 FILING DATE: 1999-07-08
  APPLICATION NUMBER: 60/143,208
FILING DATE: 1999-07-09
APPLICATION NUMBER: 60/151,572
FILING DATE: 1999-08-31
APPLICATION NUMBER: DE 19931412.8
FILING DATE: 1999-07-08
  APPLICATION NUMBER: DE 19931420.9
  APPLICATION NUMBER: DE 19931419.5
FILING DATE: 1999-07-08
  APPLICATION NUMBER: DE 19931413.6 FILING DATE: 1999-07-08
   FILING DATE: 1999-06-25
  1189 GCCCAGTCGACCGCCGAACAGCACCTTATTATTAGCAGCCTCTTCAGCAGCCAGAAGGCG 1130
  310 GACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAATAACGCC 369
  6.6%;
1 Similarity 56.6%;
56; Conservation
   1326
   GCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTT 408
   GTACTGCTTCAGCATGTCTCGGTCGTCTGGAGTGTTGAT 1091
  Schroder, Hartwig
Zelder, Oskar
   Application US/10767471
  PRODUCTION
  data removed -
  Score 30.2; DB 6;
Pred. No. 2.7;
0; Mismatches 43;
  GLUTAMICUM GENES
   ASSOCIATED WITH METHODS OF DET
  See
  43;
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  Length 1326;
  AND ENERGY
  Indels
   DETECTION
  0,
  PROTEINS
   AND
   USES
   THEREOF
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US-60-545-213-2134/c
; Sequence 2134, Application US/60545213
; GENERAL INFORMATION:
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  밁
   5
  RESULT 12
  ; OTHER INFORMATION: Clone ID: 7551688 US-10-767-701-28437
   . OTHER INFORMATION: n=A,T,C or G, or insertion/deletion polymorphism (see Tables 1-US-10-767-471-10736
   Query Match
Best Local
  SEQ ID NO 10736
LENGTH: 24900
APPLICANT: Wyeth
APPLICANT: Mounts, William Martin
APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
   Matches
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  Query Match
Best Local
   LENGTH: 24
TYPE: DNA
  ORGANISM: Sorghum bicolor FEATURE:
   NAME/KEY: misc_feature
  ORGANISM: Homo sapiens
  LOCATION:
  Match 6.4%;
Local Similarity 54.1%;
  10048 CAGCATCCTGACTGCTTTTAGTGTCTCAAAAGTCCTGGGTCAAGTGGTGCATAATTGGTG 9989
  183
   327
  267
  207
  74
   1 Similarity
65; Conserv
  GTAAGGGCGGCGGTTATGGCGGCGGCGGCGGTTACGGTGGCAACCGGG
   AATGGGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGCCCGG 124
  AAGAAGGCGGTTACGAAGCCGGTGGTTACGGTGGCGGCGGCGGCGGTTACGGCGGTCCCCC 182
  AATC 9925
   TCCTGAACCCAAACTGTATGGTACTAAAAATAGTGCAATCCTGGTTTGTTATATTTAA
  CATTACCCAGAGCGGTTATGGTAACGGCCCCGATGTAGGCCAGGGTGCGGATAATAGTAC 266
  AAAC 330
   TATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAA 326
   Conservative
   Conservative
   6.5%;
   .
  Score 29.6; D
Pred. No. 14;
0; Mismatches
   ٥.
   Score 29.4; Di Pred. No. 2.7;
   Mismatches
   BB
  DB 6;
   51;
   59;
  6
  Length 300;
  Length 24900;
   Indels
   Expression
   0
  0
  Gaps
  Gaps
   Profiles
   9929
   유
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RESULT 14
US-60-545-213-6406/c
; Sequence 6406, Application US/60545213;
; GENERAL INFORMATION:
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  ; ORGANISM: Homo sapiens
US-60-545-213-2135
  US-60-545-213-2135/c
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  뭕
   δ
  RESULT 13
   ; TYPE: DNA
; ORGANISM: Homo
US-60-545-213-2134
  SOFTWARE: PatentIn version 3.2
SEQ ID NO 2135
LENGTH: 1400
   Sequence 2135, Application US/60545213 GENERAL INFORMATION:
   Matches
   Query Match
Best Local Similarity
   APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays f.
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
  SOFTWARE: PatentIn
SEQ ID NO 2134
LENGTH: 1400
  Query Match
Best Local
  Matches 108;
   APPLICANT: Wyeth APPLICANT: Moun'
   TYPE: DNA
  392 TGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAACAACGCCACGGCTAACCAG
  392
  212
  317
   332
  437
   108;
  257
   272 ААСТGАСТСАGAATGGTTŢCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACT
  Similarity
  CCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGTTAATTATGATCAGC
   TTGGGGTTCTCCATCCACTGCTTGAAAAGGCCAGAGACCATCTCCTCACACTCTGGAACT
   AACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACT
   CCCTGGGCGATAGCGTTGCAGTAGACGGTGGACCGCAGGTTGGGGTGGATCGGGTTATTA
  CCCAGAGCGGTTATGGTAACGGCGCGATGTAGGCCAGGGTGCGGATAATAGTACTATTG
  CCGTTGGAGCAGGCGGTGCTGATGGCATTAACCTCGCTGTACTGGTCCATCAGGTTTTCT 258
   TGGTTACCCGTGTTACCCATGAAATGGCACATGCAAACAACGCCACGGCTAACCAG
  CCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCGAGGGTGCGGATAATAGTACTATTG 271
  CCGTTGGAGCAGGCGGTGCTGATGGCATTAACCTCGCTGTACTGGTCCATCAGGTTTTCT 258
  CCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGTTAATTATGATCAGC
  TTGGGGTTCTCCATCCACTGCTTGAAAAGGCCAGAGACCATCTCCTCACACTCTGGAACT
   CCCTGGGCGATAGCGTTGCAGTAGACGGTGGACCGCAGGTTGGGGGTGGATCGGGTTATTA 378
  Conservative
   Conservative
   sapiens
   version
   45.2%;
  45.2%;
   3.2
  ٥,
   <u>;</u>
  Score 29.4; DB 7;
Pred. No. 5.1;
0; Mismatches 131;
  Score 29.4; DB 7;
Pred. No. 5.1;
0; Mismatches 131;
  for Monitoring
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  Length 1400;
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  0
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   199
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   199
   391
   331
   378
  271
  318
   318
   331
  Drug
```

```
; APPLICANT: Mounts, William Martin; TITLE OF INVENTION: Nucleic Acid Arrays for Moi TITLE OF INVENTION: Target Genes; FILE REFERENCE: AM101083 (031896-042099); CURRENT APPLICATION NUMBER: US/60/545,213; CURRENT FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6406
; SEQ ID NO 6406
; TYDEN: NON.
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  ; TYPE: DNA
; ORGANISM: Homo
US-60-545-213-6407
   RESULT 15
US-60-545-213-6407/c
; Sequence 6407, Application
; GENERAL INFORMATION:
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   S
   ; TYPE: DNA
; ORGANISM: Homo
US-60-545-213-6406
   Matches 108;
  Query Match
  SEQ ID NO 6407
  APPLICANT: Mounts, Milliam Martin
TITLE OF INVENTION: Nucleic Acid Arrays fo
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILLING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
  Matches 108;
  Query Match
   APPLICANT: Wyeth
   LENGTH: 1400
   Local
  Local
                                  392
  377
  272 AACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACT
  437
  212 CCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTG 271
   392
   317
   377
  212 CCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTG 271
  437
   Similarity
  Similarity
TGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAACAACGCCACGGCTAACCAG 450
  CCGTTGGAGCAGGCGGTGCTGATGGCATTAACCTCGCTGTACTGGTCCATCAGGTTTTCT
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   TTGGGGTTCTCCATCCACTGCTTGAAAAGGCCAGAGACCATCTCCTCACACTCTGGAACT
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   CCCTGGGCGATAGCGTTGCAGTAGACGGTGGACCGCAGGTTGGGGTGGATCGGGTTATTA
  CCGTTGGAGCAGGCGGTGCTGATGGCATTAACCTCGCTGTACTGGTCCATCAGGTTTTCT
   CCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGTTAATTATGATCAGC 391
  TTGGGGTTCTCCATCCACTGCTTGAAAAGGCCAGAGACCATCTCCTCACACTCTGGAACT
  CCCTGGGCGATAGCGTTGCAGTAGACGGTGGACCGCAGGTTGGGGTGGATCGGGTTATTA
   Conservative
   Conservative
   sapiens
   6.4%;
  6.4%;
45.2%;
  US/60545213
  Score 29.4; DB 7;
Pred. No. 5.1;
0; Mismatches 131;
  0
  Score 29.4;
Pred. No. 5.
   red. No. 5.1;
Mismatches 131;
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  Monitoring
  DB 7;
   Monitoring
   Length
   Indels
  Length 1400;
   Indels
  Expression
  Expression
  0
   0;
  Profiles
   Gaps
   Profiles
   199
   378
  331
   331
  318
  378
   0
  of.
   유
  Drug
  Drug
```

Search completed: March 17, 2004, 08:25:40 Job time : 71.6301 secs

OLISH WINTER FLOWER SHILL

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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  Minimum DB
Maximum DB
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   Title:
Perfect score:
   Run on:
  OM nucleic - nucleic search, using sw model
   Total number of hits satisfying chosen parameters:
  Scoring table:
  Sequence:
  Beq
   length: 0
length: 2000000000
  IDENTITY_NUC
   March 17, 2004, 16:50:01; Search time 2921.94 Seconds (without alignments) 5491.177 Million cell updates/sec
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  Gapop 10.0 , Gapext 1.0
  US-09-543-407-13
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cgn2_6/ptodata/2/pna/US081_COMB.seq:*
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cgn2_6/ptodata/2/pna/US099B_
  atgaaacttttaaaagtggc.....ccacggctaaccagtattaa 456
  GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
  /pna/PCTUS
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   75154660
```

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44. (cgn2 6/ptcdata/2/pna/US100B COMB. seq; 47. (cgn2 6/ptcdata/2/pna/US101B COMB. seq; 47. (cgn2 6/ptcdata/2/pna/US101B COMB. seq; 47. (cgn2 6/ptcdata/2/pna/US101B COMB. seq; 47. (cgn2 6/ptcdata/2/pna/US101B COMB. seq; 48. (cgn2 6/ptcdata/2/pna/US101B COMB. seq; 59. (cgn2 6/ptcdata/2/
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

```
RESULT 1

US-09-543-407-13

Sequence 13, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 13
SEQ ID NO 13
LENGTH: 456
TYPE: DNA
ORGANISM: Astificial - 1
   Result
No.
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ORGANISM: Artificial Sequence
   404.8
404.8
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2751
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13 US-09-543-407-3
13 US-09-741-8738-3
11 US-09-741-8738-3
12 US-60-352-946-1
10 US-60-352-946-1
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11 US-09-741-8738-1
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13 US-09-543-407-4
13 US-09-543-407-4
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24 US-09-252-691-172
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   Sequence 13, Appl
Sequence 56, Appl
Sequence 1, Appli
Sequence 23, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 21, Appl
Sequence 27, Appl
Sequence 29, Appl
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Sequence 172, Appl
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  Description
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; FEATURE:
; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
; OTHER INFORMATION: sequence containing the replacement fragment
; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
US-09-543-407-13
   US-08-233-642A-56
  Sequence 56, Applicat GENERAL INFORMATION:
   Query Match
Best Local :
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, \
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642;
PILLING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
  Matches
  APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
TITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
   ADDRESSEE: Seed STREET: 6300 CC CITY: Seattle STATE: Washingt CCUNTRY: U.S.A.
  421
  301
  421
   361
   361
  301
   241
   241
  181
  181
   121
   121
  456;
  61
  23
   Similarity
   Washington f: U.S.A.
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
  CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   CTGGTTACCCGTGTTGCTCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCCGATATTACTGTCGGCCAATATGATCAG
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   3E: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
  Application US/08233642A
  Conservative
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   US/08/233,642A
  0
   #1.0,
  Score 456; DB 23;
Pred. No. 7.1e-135;
  Mismatches
   Version
   #1
  456
  0
  Length 456;
  Indels
  0
   120
   420
   420
  360
   300
   300
  240
   180
   180
  360
   60
  240
  120
```

```
Sequence 1, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
FILE REFERENCE: 920043-406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT TILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
  RESULT 3
US-09-543-407-1
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   ; NAME/KEY:
; LOCATION:
US-08-233-642A-56
   REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 9200
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 56:
  Query Match
Best Local Similarity
   Matches
             LENGTH: 45
TYPE: DNA
ORGANISM: Salmonella enteritidis
   SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   TOPOLOGY:
   361
   361
   301
   301
   241
   241
  181
  421
   181
  121
  121
   424; Conservative
  61
  61
                                  456
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   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG 360
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCAATAGTTCCGGC 120
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
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  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT 420
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
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  1..456
   linear
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  920043.403C3
   Score 404.8; DB 6; Pred. No. 1.9e-118; 0; Mismatches 32;
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   0
   Gaps
  180
  120
  60
   420
   300
   0
```

```
; APPLICANT: White, Aaron P.
; APPLICANT: Doran, James L.
; APPLICANT: COllinson, S. Karen
; APPLICANT: Kay, William W.
; TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
; TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PE
; FILE REFERENCE: 920043,406
; CURRENT APPLICATION NUMBER: US/09/543,407
; CURRENT APPLICATION NUMBER: US/09/543,407
; CURRENT FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 23
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  RESULT 4
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  US-09-543-407-23
   US-09-543-407-1
  Sequence 23, Application US/09543407 GENERAL INFORMATION:
  Matches
   Query Match
Best Local Similarity
  Matches 424; Conservative
   Best Local Similarity
   Query Match
  ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   TYPE: DNA
  421
  361
  361
   301
   301
   181
   181
  121
  410;
  421
   241
   241
  121
  61
  61
  456
   1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   CTGGTTACCCGTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATATGATCAG
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCGAT 240
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC 120
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCCT
  Conservative
   83.9%;
   88.8%;
93.0%;
  Score 382.4; DB 23;
Pred. No. 2.8e-111;
0; Mismatches 46; 1
   Score 404.8; DB 23;
Pred. No. 1.9e-118;
0; Mismatches 32;
  456
   PEPTIDE SEQUENCES
  Indels
  Length
   Length 456;
  0
  °.
  Gaps
  Gaps
  420
  60
                                      9
   360
  120
  420
   300
   300
   240
   180
  60
  60
  0
```

```
Sequence 11, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron p.

APPLICANT: Doran, James L.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

ITILE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEF

ITILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/99/543,407

CURRENT APPLICATION NUMBER: US/99/543,407

NUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 456

TYPE: DNA

ORGANISM: Artificial Sequence

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   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-11
   RESULT 5
US-09-543-407-11
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   Matches
  Local Similarity
                          181
   181
  121
   121
  406;
   61
  61
  421
  361
   361
   301
   301
  421
  241
  241
   181
  181
  121
  121
  61
AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  atgaaactritiaaaaagiggeageatricgeageaaregtagtrictiggeagigereger
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  CATGAAATGGCACATGCAAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
  GCCACCATCGACCAGTGGAACGCTAAAAACTATGATCAGCTGGTTACCCCGTGTTGTTACC
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   ccedactica a certica de la respecta de la constante de la cons
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTACGCTTAACGCTGCGCCTTGCTAACGLTGCGCTTGCAA
   Conservative
  82.5%;
  Score 376; DB 23;
Pred. No. 3.2e-109;
0; Mismatches 50;
   Length 456;
  PEPTIDE
  Indels
   SEQUENCES
   <u>,</u>
   Gaps
  240
   180
  120
  120
   60
  60
  420
  420
   360
   360
   300
  300
  240
  240
  180
   180
  120
  0
```

```
Sequence 19, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

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   US-09-543-407-19
  RESULT 6
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   Matches
   Query Match
Best Local
                  361
  301
  301
   241
   241
   181
  181
  121
   121
  397;
  61
   61
  421
   421
  361
  361
   301
  301
   241
   ш
   241
   n 79.3%;
Similarity 87.1%;
97; Conservative
AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATATGATCAG 360
   CTGGTTACCCGTGTTGCTTACCCATGÀAATGGCACATGCAAGGCGTAATGGTGCGTCAGGTT
  GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
  AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
   GGCGTCGTTCCACAATGGGGCGGCGGCGGCAGTAATCATAACGGCGGCGGCAATAGTTCCGGC
   ĠĊĊĀĊĊĀŤĊĠĀĊĊĀĠĪĠĠĀĀĊĠĊŤĀĀĀĀĀĊŤĊĊĠĀŤĀŤŤĀĊŤĠŤĊĠĠĊĊĀĀŤĀĊĠĠCGGT
   AGCGATGCCCGTAAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTGCAA
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAGTCGTAGTTTCTGGCAGTGCTCTGGCT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
  AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATG
   CTGGTTACCCGTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
  GCACATGCAAACAACGCCACGGCTAACCAGTATTAA
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCCGATATTACTGTCGGCCAATATGATCAG
   ĠŦĀĠĠĊĊĀĠĠĠŦĠĊĠĠĀŦĀĀŦĀĠŦĀĊŦĀŦŦĠĀĀĊŦĠĀĊŦĊĀĠĀĀŦĠĠŦŦŦĊĀĠĀĀĀŦĀĀŦ
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
   Score 361.6; | Pred. No. 1.3e
   0;
   5; DB 23;
l.3e-104;
  59;
   456
   456
   PEPTIDE SEQUENCES
   Indels
  Length
   0,
   Gaps
   420
   360
  180
  300
   240
  240
  120
   120
  60
   60
  420
  420
   360
   360
  300
   300
  0,
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RESULT 8
US-09-543-407-25
; Sequence 25, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
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   ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragmen; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major: US-09-543-407-17
  RESULT 7
US-09-543-407-17
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   ş
  Sequence 17, Application GENERAL INFORMATION:
   Matches
   Query Match
Best Local !
  SEQ ID NO 17
LENGTH: 456
  TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
   APPLICANT: White, Aaron
APPLICANT: Doran, James
APPLICANT: Collinson, S
APPLICANT: Kay, Willian
   SOFTWARE: FastSEQ for Windows Version
   NUMBER OF SEQ ID NOS: 59
  TYPE: DNA
ORGANISM: Artificial
FEATURE:
  181
   181
   121
   421
  361
   301
  301
  241
   241
  121
   361
   393;
  421
  61
   13
  421
   _
   Similarity
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCCGGC
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  CCGGACTATGATCAGCTGGTTACCCGTGTTACCCCATGAAATGGCACATGCACTGCAA
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGC
  ATGAAACTTTTAAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
   CTGGTTACCCGTGTTACCCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   Doran, James L.
Collinson, S. Karen
Kay, William W.
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  77.9%; ilarity 86.2%; Conservative
   Sequence
   US/09543407
  Score 355.2; DB 23; Pred. No. 1.5e-102; O; Mismatches 63;
  456
  PEPTIDE SEQUENCES
   Indels
   Length
  fragment
  456;
  0
  420
  360
  240
   240
  420
   300
   180
   120
  60
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   RESULT 9
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   US-09-543-407-25
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
  Matches
  Query Match
Best Local
  ORGANISM: Artificial Sequence FEATURE:
  TYPE: DNA
   LENGTH: 456
  Local Similarity
   421
   361
   361
  301
   301
  241
   181
   181
   121
   121
   421
   241
   392;
  61
   61
  Conservative
  77.5%;
86.0%;
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```
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH ASSETS OF SEC ID NOS: 59
LENGTH ASSETS OF SEC ID NOS: 59
LENGTH ASSETS OF SEC ID NOS: 59
LENGTH ASSETS OF SEC ID NOS: 59
LENGTH ASSETS OF SEC ID NOS: 59
LENGTH ASSETS OF SEC ID NOS: 59
Sequence 15, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
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APPLICANT: KAY,
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTTATGATCAG 180
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT 420
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  CTGGTTACCCGTGTTACCCATGAAATGGCACATGCAGGTTATGGTAACGGCGCCGAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  Score 353.6; DB 23; Pred. No. 4.8e-102;
   Mismatches
  456
                            PEPTIDE SEQUENCES
   PEPTIDE SEQUENCES
   Indels
  Length 456;
   0,
  Gaps
  240
   300
   300
  120
   60
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; OTHER INFORMATION:
; OTHER INFORMATION:
; OTHER INFORMATION:
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  US-09-543-407-21
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   ; LENGTH: 456
; TYPE: DNA
; ORGANIZM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Recombinant :
; OTHER INFORMATION: sequence con!
; OTHER INFORMATION: encoding PT3
US-09-543-407-15
  Sequence 21, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
   Query Match
Best Local Similarity
   SEQ ID NO 21
LENGTH: 456
   Query Match 77.2%;
Best Local Similarity 85.7%;
Matches 391; Conservative
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
  FEATURE:
  TYPE: DNA
ORGANISM: Artificial Sequence
  421
   421
  361 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   361
  301
   301
  241
   241
  181
   181
  121
  121
   61
  61
  ۳
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
   CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
  Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
   Recombinant Salmonella enteritidis 3b afga sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
   76.8%;
85.5%;
   0
Score 350.4; DB 23; Pred. No. 5.1e-101;
   Score 352; DB 23;
Pred. No. 1.6e-101;
0; Mismatches 65;
  456
   PEPTIDE SEQUENCES
  Length 456;
                   Length 456;
   0
   420
   360
  180
  420
  360
  300
   300
  240
  240
   180
   120
  120
   60
   0
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   US-09-543-407-27
  RESULT 11
US-09-543-407-27
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  Best Loc
Matches
  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 27
   Query Match
  Sequence 27, Applica GENERAL INFORMATION:
   Matches
  APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.466
   APPLICANT: White, Aaron P
APPLICANT: Doran, James I
  OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
   TYPE: DNA
ORGANISM: Artificial
  FEATURE:
  LENGTH: 456
  Local
121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  390;
  421
   361
   361
  301
  181
   421
   301
   241
  241
   181
   121
  121
                                    61
  61 GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACCGGCGGCGAATAGTTCCGGC 120
  61
   390;
   61 GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCGGCAATAGTTCCGGC
   Similarity
                                GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   ATGAAACTTTTAAAAGTGGCAGCAGTCGCAGCAGTCGTAGTTTCTGGCAGTGCTCTGGCT
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GCACATGCAGACCAGTGGAACGCTAAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCCGGCCAATATGATCAG
   GTAGGCCAGGGTGCGGATAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCCAATAGTTCCGGC 120
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  Application US/09543407
  Conservative
   Conservative
  Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
   Sequence
   76.8%;
   Score 350.4; DB 23;
Pred. No. 5.1e-101;
0; Mismatches 66;
   0;
   Mismatches
   66;
   456
  PEPTIDE SEQUENCES
  Indels
   Indels
   Length 456;
   0;
   0
   Gaps
   60
  60
  360
  300
  180
   420
   420
   360
   300
  180
  240
   120
  60
   0
   0
```

```
APPLICANT: White, Aaron P.
APPLICANT: Collingon, S. Karen
APPLICANT: Collingon, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 456
TYPE: DNA
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   ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-29
   RESULT 12
US-09-543-407-29
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  Sequence 29, Application US/09543407 GENERAL INFORMATION:
   Matches
   Query Match
Best Local Similarity
  ORGANISM: Artificial Sequence FEATURE:
   361
  301
   181
   389;
   421
  361
   301
  241
  181
241
                                  241
  181
   121
   121
   241 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATTCAGAAATAAT
  121
   181
  61
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  μ
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
   GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCGAATAGTTCCCGGC 120
   CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
                                GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCGAT 240
   Conservative
   76.5%;
   0
   Score 348.8; DB 23;
Pred. No. 1.7e-100;
0; Mismatches 67;
   Indels
  Length 456;
   0
   Gaps
  300
  240
   360
   240
   180
  420
   420
  360
   300
  180
   0
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RESULT 13
US-08-233-642A-54
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   S
   US-08-233-642A-54
   Sequence 54, Applicat
GENERAL INFORMATION:
   Matches 289;
  Query Match
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWALE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
   TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-6031
TELEX: 3723936 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 54:
   APPLICANT: Kay, William w.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James along AND
   MOLECULE TYPE:
FEATURE:
   SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
TYPE: nucleic acid
   REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92/
TELECOMMUNICATION INFORMATION:
   ATTORNEY/AGENT INFORMATION: NAME: King, Joshua
  NUMBER OF SEQUENCES:
   CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
  TITLE OF INVENTION:
  NAME/KEY:
  STATE: W
  STRANDEDNESS:
TOPOLOGY: li
   FILING DATE: 26-APR-1994
CLASSIFICATION: 424
   STREET: 6300 C
  ZIP: 98104-7092
  Local Similarity
  301
   421
  421
   361
   361
   301
61
  64 GTCGTTCCACAATGGGGCGGCGGCGATAATCATAACGGCGGCGGCAATAGTTCCGGCCCG 123
                             GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC 183
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
 GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCCAAAGC
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT 420
  GCCACCTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCAGGCGGT 360
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
  Washington : U.S.A.
  Application
  6300 Columbia
   63.0%; ilarity 99.0%; Conservative
   linear
   Sdo
  DNA (genomic)
   double
  BASED VACCINES
  METHODS AND COMPOSITIONS FOR SALMONELLA-
  US/08/233,642A
  US/08233642A
  Center, 701
  920043.403C3
   0
   Score 287.2; DB 6
Pred. No. 8.7e-81;
   Mismatches
  Version
  Fifth Avenue
  6
   456
   Indels
   Length 361;
   0;
   Gaps
 120
   60
  420
   360
```

```
RESULT 15
US-09-252-691C-172
; Sequence 172, Application US/09252691C
; GENERAL INFORMATION:
; APPLICANT: Keith G. Weinstock et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
  B
  ; SEQ ID NO 172
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Enterobacter cloacae
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   US-09-252-691-172
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   Sequence 172, Application US/09252691B
GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
   Best Local Similarity Matches 313; Conserv
  Query Match
  181
   304
  121
  442
  361
  322
   301
  262
  241
   202
  181
   142
   121
  184
  82
   61
  22
  1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  GATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTA
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   ACGGACGCCCGAGATTCTGAATTGACCATTACCCAGCATGGTGGTGGTAACGGCGCAGAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  GGTGCGGTACCACAATTTGGCGGCGGCCACGGTGGTGGCTGGGGTGGCGGCAATAACGGC
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  ATGAAACTTTTCAAAGTGGCAGTTATTGCAGCAATCGTAGTTTCTGGCAGTGCTTTCGCA
   ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACG
   ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATG
  GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC
   GGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCC
  GATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTA
  CTGGTTACCCGTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT 420
  GCCACCATCGACCAATGGAATAGCAAAGACTCTGTTATCAACGTGAAACAGTTCGGCGGC
  GTTGGCCAGGGCTCTGATGACAGTTCTATCGATCTGCTGCAAAAAAGGCTTTGGTAACAGC
   Conservative
   49.8%; Score 227.2; DB 1 68.6%; Pred. No. 1.6e-61; tive 0; Mismatches 143
  DB 17;
   143;
  Length
   0
   292
  355
  TO ENTEROBACTER
  240
  243
   360
   300
  261
   201
  180
  141
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  180
   120
  81
   441
   0
```

```
FILE REFERENCE: 107106.135
CURRENT APPLICATION NUMBER: US/09/252,691C
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,145
PRIOR APPLICATION NUMBER: US 60/094,787
PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 11326
SEQ ID NO 172
LENGTH: 477
TYPE: DNA
RORGANISM: Enterobacter cloacae
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   US-09-252-691C-172
  Query Match 49.8
Best Local Similarity 68.6
Matches 313; Conservative
   262
   142
   382
  361
  322
   301
   241
  202
  181
   121
442
                            421
  82
   61
  Н
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
   ATGAAACTTTTCAAAGTGGCAGTTATTGCAGCAATCGTAGTTTCTGGCAGTGCTTTCGCA
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   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
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  CTGGTTACCCGTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
  GCCACCATCGACCAATGGAATAGCAAAGACTCTGTTATCAACGTGAAACAGTTCGGCGGC 381
   GTTGGCCAGGGCTCTGATGACAGTTCTATCGATCTGCTGCAAAAAGGCTTTGGTAACAGC
  ACGGACGCCCGAGATTCTGAATTGACCATTACCCAGCATGGTGGTGGTAACGGCGCAGAT
   GGTGCGGTACCACAATTTGGCGGCGCCACGGTGGTGGTGGCTGGGGTGGCGGCAATAACGGC 141
GGCTTTGGCAACAACGCGACCGCACACCAGTACTGA
   GGCAACGGCGCGGCGGTAGACCAGACAGCGTCCGGCTCAACGGTGACTGTGCACCAGGTT
  49.8%;
  Score 227.2; DB 17;
Pred. No. 1.6e-61;
0; Mismatches 143;
  DB 17;
   AND THERAPEUTICS
   477
   Indels
  Length
  477
  0
  Gaps
  240
  81
  441
   420
  360
  201
   60
  321
   261
   0
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Search completed: March 18, 2004, 02:46:59 Job time : 2923.24 secs

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Result
   Minimum
   Total number of hits satisfying chosen parameters:
   Scoring table:
  Sequence:
   Perfect score:
   OM nucleic - nucleic search, using sw model
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   ö
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  30...
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44...
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       length: 0
length: 2000000000
  US-09-543-407-13
456
1 atgaaacttttaaa
  March 16, 2004, 15:39:56; Search time 69.6301 Seconds (without alignments)
   Match
  637880 seqs, 183698769 residues
  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
   Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
   Pending Patents_NA_New:*

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5 31875
4 300
4 1790242
4 670
4 861
3 1851
3 1853
3 1853
3 1463
4 634
2 1543
2 1543
2 1543
2 1543
2 798
   7 196083
7 196083
7 2007
2148
1355
2159
  3990
150223
   Length DB
   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
  σ
                   US-09-741-873C-3
US-09-830-230A-629
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US-10-021-698A-970
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Sequence 14522, A
Sequence 892, App
Sequence 153, App
Sequence 154, App
Sequence 153, App
Sequence 10730, A
Sequence 10735, A
Sequence 1085, A
Sequence 1085, A
Sequence 28437, A
Sequence 15726, A
Sequence 15726, A
Sequence 15726, A
Sequence 1782, Appl
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Sequence 1782, Appl
Sequence 5725, Ap
Sequence 5725, Ap
Sequence 5725, Ap
Sequence 5725, Ap
Sequence 5725, Ap
Sequence 5725, Ap
  Description
   Sequence 629,
  Sequence 1,
   Sequence
  Appli
Appli
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|--------------------|--------------------|-----------------|--------------------|---------------------|---------------------|-----------------------------|--------------------|--------------------|--------------------|----------|---------------------|---------------------|--------------------|---------------------|---------------------|---------------------|--------------------|--------------------|
| 45                 | 44                 | 43              | 42                 | 41                  | 40                  | 39                          | 38                 | 37                 | 36                 | 35       | 34                  | ü                   | 32                 | 31                  | 30                  | 29                  | 28                 | 27                 |
| 27                 | 27                 | 27.4            | 27.4               | 27                  | 27                  | 27                          | 27                 | 27.6               | 27.6               | 27.6     | 27                  | 27.6                | 27                 | 27                  | 27.8                | 27.8                |                    |                    |
| N                  | 'n                 | Α.              | 4                  | 4.                  | 4.                  | 0                           | o                  |                    |                    | o        | o                   | o                   | o                  | o                   |                     | &                   | 28                 | 28                 |
| 6.0                | 6.0                | 6.0             | 6.0                | 6.0                 | 6.0                 | 6.1                         | 6.]                | 6.1                | 6.1                | 6.1      | 6.]                 | 6.1                 | 6.1                | 6.1                 | 6.1                 | 6.1                 | 6.1                | 6.1                |
| _                  | _                  | _               | Ī                  | Ü                   |                     | -                           |                    |                    |                    |          |                     |                     |                    |                     |                     |                     |                    |                    |
| 547                | 543                | 2000            | 883                | 823                 | 819                 | 232882                      | 10251              | 6494               | 6224               | 4697     | 1052                | 564                 | 402                | 201                 | 749                 | 390                 | 714                | 237                |
| 6                  | ш                  | σ               | σ                  | 0                   | σ                   | σ                           | σ                  | σ                  | σ                  | σ        | σ                   | σ                   | σı                 | 0                   | σ                   | σ                   | σ                  | Φ                  |
| us-                | PCT                | -Sn             | us-                | us-                 | -Sn                 | us-                         | -Sn                | US-                | -SD                | -SD      | us-                 | -Sn                 | us-                | US-                 | us-                 | -Sn                 | -Sn                | -Sn                |
| US-10-767-701-2454 | PCT-US04-05654-151 | US-10-151-553-1 | US-10-767-701-1287 | US-10-767-701-20007 | US-10-417-884A-2244 | <b>US-10-767-471-1067</b> 9 | US-10-045-674A-582 | US-10-453-372-1187 | US-10-453-372-1173 | 10-      | US-10-767-701-12607 | US-10-767-701-16629 | US-09-969-034-1464 | US-10-767-471-28293 | US-10-767-701-12516 | US-09-796-692B-3647 | US-10-779-543-2346 | US-10-767-701-3141 |
| 767-               | 0-10               | 151-            | 167-               | 767-                | 117-                | 167-                        | )45-               | 153-               | 153-               | 153-     | 767-                | 767-                | -69                | 767-                | 167-                | 796-                | 179-               | 167-               |
| 701                | 565                | 553             | 701                | 701                 | 884                 | 471                         | 674                | 372                | 372                | 372      | 701                 | 701                 | 034                | 471                 | 701                 | 692                 | 543                | 701                |
| -24                | 4-1                | Ļ               | -12                | -20                 | A-2                 | -10                         | A-5                | -11                | -11                | -11      | -12                 | -16                 | -14                | -28                 | -12                 | B-3                 | -23                | -31                |
| 545                | 515                |                 | 87                 | 007                 | 244                 | 679                         | 82                 | 87                 | 73                 | 85       | 607                 | 629                 | 64                 | 293                 | 516                 | 647                 | 469                | 417                |
|                    |                    |                 |                    |                     |                     |                             |                    |                    |                    |          |                     |                     |                    |                     |                     |                     |                    |                    |
| Se                 | Se                 | Se              | Se                 | Se                  | Se                  | Se                          | Se                 | Se                 | Se                 | Se       | Se                  | Se                  | Se                 | Se                  | Se                  | Se                  | Se                 | Se                 |
| Sequence           | Sequence           | Sequence        | Sequence           | Sequence            | Sequence            | Sequence                    | Sequence           | Seguence           | Sequence           | Sequence | Sequence            | Sequence            | Sequence           | Sequence            | Sequence            | Sequence            | Sequence           | Sequence           |
|                    |                    | ő               |                    |                     |                     |                             |                    |                    |                    | e<br>C   | õe                  |                     |                    |                     |                     |                     |                    |                    |
| 24545,             | 1515               | 1, ,            | 1287               | 20007               | 2244                | 10679                       | 582,               | 1187               | 1173,              | 1185,    | 12607               | 16629               | 1464,              | 28293               | 12516               | 3647                | 23469              | 31417              |
| 5                  | .∵<br>≽            | tďď,            | ."<br>A            | 7                   | , AI                | 9                           | Apr                | ."<br>A            | ,<br>A             | ,<br>A   | ĭ,                  | •                   | i, Ap              | ű,                  | 9                   | ,<br>A              | ,                  | 7,                 |
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ALIGNMENTS

## ; TYPE: DNA; ORGANISM: Escherichia coli; FEATURE: ; NAME/KEY: CDS; LOCATION: (83)..(538) US-09-741-873C-3 FILE REFERENCE: 012889-084 CURRENT APPLICATION NUMBER: US/09/741,873C CURRENT FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: SE 8801723-1 PRIOR FILING DATE: 1998-05-06 PRIOR APPLICATION NUMBER: US 08/978,878 PRIOR FILING DATE: 1997-11-26 PRIOR FILING DATE: 1997-11-26 PRIOR REPLICATION NUMBER: US 07/347,189 PRIOR FILING DATE: 1999-05-04 PRIOR APPLICATION NUMBER: US 07/789,437 PRIOR APPLICATION NUMBER: US 07/789,437 PRIOR APPLICATION NUMBER: US 07/789,437 PRIOR APPLICATION NUMBER: US 07/970,846 PRIOR APPLICATION NUMBER: US 07/970,846 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/187,865 PRIOR APPLICATION NUMBER: US 08/318,519 PRIOR APPLICATION NUMBER: US 08/318,519 PRIOR APPLICATION DATE: 1994-01-28 PRIOR APPLICATION NUMBER: US 08/318,519 PRIOR APPLICATION NUMBER: US 08/318,519 RESULT 1 US-09-741-873C-3 ; Sequence 3, Applicati ; GENERAL INFORMATION: NUMBER OF SEQ ID NOS: 11 SOFTWARE: PATENTIN VERSION 3.0 SEQ ID NO 3 LENGTH: 675 APPLICANT: Normark, Staffan APPLICANT: Olsen, Arne TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation Application US/09741873C

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> 61 83

121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180

GGCGTCGTTCCACAATGGGGCGGCGGCGGCGAATACGTTAACGGCGGCGGCGGCAATAGTTCCGGC 120

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Query Match 49.5%; Best Local Similarity 68.4%; Matches 312; Conservative

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Mismatches

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Indels Length 675;

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Gaps

Score 225.6; DB Pred. No. 1.4e-66

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US-09-741-873C-1
   US-09-741-873C-1
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   APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein
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FILING DATE: 1991-11-06
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  GGCTTTGGTÄÄCÄÄCGCGÄCCGCTCÄTCÄGTÄCTÄÄ 538
  CTGGTTACCCGTGTTACCCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
  ĠĊTĀCTCTTĠĀTĊĀĠTĠĠĀĀĊĠĠĊĀĀĀĀĀTŤĊTĠĀĀĀŤĠĀĊĠĠŤTĀĀĀĊĀĠŤTCĠĠŤĠĠT
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Pred. No. 8.4e-52;
0; Migmatches 134
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PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 756
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 629
  PRIOR APPLICATION NUMBER: PCT/US98/12718
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/057,483
PRIOR FILING DATE: 1997-09-03
PRIOR APPLICATION NUMBER: 60/053,344
PRIOR FILING DATE: 1997-07-22
  PRIOR APPLICATION NUMBER: 60/053,377 PRIOR FILING DATE: 1997-07-22 PRIOR APPLICATION NUMBER: 60/050,359
  APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Lyme Disease Vaccines
FILE REFERENCE: PB481US
CURRENT APPLICATION NUMBER: US/09/830,230A
CURRENT FILING DATE: 2001-09-27
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LOCATION: (1210)
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  GGCAACGGTGCTGCAGTTGACCÁGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT
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Query Match Best Local

n 7.2%; Similarity 47.8%;

96;

Conservative

GCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAG 216

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Score 33; DB 5 Pred. No. 0.43;

DB 5; Length 3990

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95662 GAGAGCTTATTCACAACGAGCTGTTG 95687

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; DATABASE ACCESSION NUMBER: NC 001491,
; DATABASE ENTRY DATE: 2000-08-01
US-10-624-149A-1
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ORGANISM: Equine herpesvirus 1
PUBLICATION INFORMATION:
AUTHORS: Telford, E.A.
AUTHORS: Watson, M.S.
AUTHORS: Watson, A.J.
AUTHORS: Davison, A.J.
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   APPLICANT: Neubauer, Antonie
APPLICANT: Ziegler, Christina
TITLE OF INVENTION: 9M-Negative EHV-Mutants without Heterologous Elements
FILE REPERENCE: 1/1372
   ISSUE: 1
PAGES: 304-316
  JOURNAL: Virology VOLUME: 189
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293 GAAATAATGCCACCATCGACCAGTGG 318
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  CTGTGGTAACGGTGGGCCTTAGTTTTGATACGGCTCATTTCCACAGCATGTTTGCCTACG
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  TTTGCTGTGAAGAGTAATGAT 3633
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  GCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCA 292
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  95601
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   APPLICANT: DEL MASTRO, RICHARD
APPLICANT: SIMON, JASON
APPLICANT: ALLEM, KRISTINA
APPLICANT: PANDIT, SUNIL
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: 2976-4044US1
   APPLICANT: Kovalic, Davi
   APPLICANT: KEITH,
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CURRENT FILING DATE: 2004-01-29
   APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
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  APPLICANT:
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ORGANISM: Sorghum
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   455 GGTGGTGGCGGCTTCGGTGGTGGTGGCTATGGCGGTGGCGGTGGCTATGGTGGC 514
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Conservative
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  PAUL
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NAME/KEY: modified base
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OTHER INFORMATION: a, t, c or g
US-10-021-698A-892
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Best Local (
  Matches
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PRIOR FILING DATE: 2000-06-14
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VAN EERDEWEGH, PAUL
DUPUIS, JOSEE
DEL MASTRO, RICHARD
  SIMON, JASON
ALLEN, KRISTINA
   Conservative
   MIT
   SUNIL
t, c or g
   48.6%;
  or g
  or g
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US-10-775-972-153
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   SOFTWARE: Fa
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CURRENT FILING DATE: 2004-02-10
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   APPLICANT: Bangur, Chaitanya S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
   APPLICANT: Henderson, Robert A. APPLICANT: Wang, Tongtong APPLICANT: Bangur, Chaitanya S
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LOCATION: (195354)
OTHER INFORMATION: a, t,
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Windows Version 4.0
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48.6%;
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  Score 30.6;
Pred. No. 17;
  Mismatches
  DB 6;
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RESULT 9

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Best Local Similarity 45.8%;
   PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
   APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEFTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
   APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Compositions AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIACHOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C21
CURRENT APPLICATION NUMBER: US/10/775,972
CURRENT FILING DATE: 2004-02-10
NUMBER OF SEQ ID NOS: 563
SOFTWARE: FASTSEQ for Windows Version 4.0
   CURRENT APPLICATION NUMBER: US/10/045,674A
CURRENT FILING DATE: 2001-10-25
  TITLE OF INVENTION:
  APPLICANT:
  TITLE OF INVENTION: LIBRARIES FILE REFERENCE: DYAX/002 CIP2
   APPLICANT: Henderson, Robert A.
   TYPE: DNA ORGANISM: Artificial Sequence
  OTHER INFORMATION:
OTHER INFORMATION:
  PEATURE:
                      FEATURE:
NAME/KEY: CDS
OCATION: (1)..(1305)
  ENGTH:
   1429
  1549
   INFORMATION:
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  200 AAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCATGTAGGCCAGGGTGCGGATA 259
  140 TTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAAGCGATGCCCGTAAATCTG 199
  1355
   AGGGCTTGAAATTACTCACCCAGGAGAAATCCCAGTATAATCTGCCCTCCCATTÄGTGGT 1370
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  AGGAGAGAAGCTCCAAGTTCCGAGGCTTCTCATTTTACCAAACAGTT 1323
   ACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAGCTGGTT
  ATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGA 319
  TTCCCCAGAAAATTCTCTACAAAGATGTTCATTTTTTAAGTTAAAAGTACTTAAAAGTT
  NASTRI, HORACIO G. ROOKEY, KRISTIN L.
  RENE
  ROBERT C.
EDWARD H.
  Description of Artificial Sequence: M13-III nucleotide sequence
  0; Mismatches 123; Indels
   Score 30.2; DI
Pred. No. 2.9;
   DB 6;
  Length 2148;
   366
  0
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   RESULT 11
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  US-10-767-701-13730
   US-10-045-674A-593
   APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(33535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 11730
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  TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
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   682 TTACACTATTCATGACACCGAGGACACGGAAAACTGCCAAAAAAAGATGATACAAGTTATGA
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   288 TTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGG 347
  888 YAARGGSGCYATGACYGARAAYGCYGAYGARAAYGCRCTRCARWSTGAYGCYAARGGYAA 947
  177 GCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGC 236
  828 YGGYMSYGGRGGYGGYMSYGGYGAYTTYGAYTAYGARAARATGGCWAAYGCYAA
  117 CGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCT 176
  768 KGGYGGYGGYMSYGGYGGWGGYMSYGGYGGYMSYGARGGYGGWGGYMSYGARGGWGG
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   84;
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GCGTGGTGATGTTAGAGTTCACCCAAATGCTACAGAAATCATGT
                                   GGTGCGTCAGGTTTGGGCAACAACGCCACGGCTAACCAGT 451
   CCAGCAGGGGAGCAAGCCCCTGTGTGATTTCTCAAATTTTAGAGCAAATGTGTGCGAGAT
   TAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGA 356
   TCAGCTGGTTACCCGTGTTGTTACCCCATGAAATG
  Conservative
   Conservative
  Application US/10767701
  David K.
   48.8%;
  6.6%;
25.1%;
  6.5%;
   80; Mismatches 170;
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   Score 29.6; D
Pred. No. 4.6;
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  887
  827
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  With
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RESULT 12 US-10-767-471-10736/c

Sequence 10736, Application US/10767471 GENERAL INFORMATION:

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  US-10-767-471-10553
  US-10-767-471-10553
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  Query Match 6.5%;
Best Local Similarity 52.4%;
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETI
FILE REFERENCE: CL001505
  Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10736
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   CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
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LOCATION: (1)...(318752).
OTHER INFORMATION: n = A,
  FILE REFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
   APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: REGUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
  TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
LOCATION: (1) ... (24900)
OTHER INFORMATION: n = A,T,C or G,
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254959 AATG 254962
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   327 AAACTCCGATATTACTGTCGGCCAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGA
  9928
   267 TATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAA
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  AAAC 330
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  A,T,C or
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Pred. No. 4
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   Score 29.6; DB 6;
Pred. No. 14;
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  DB 6;
  59;
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   Length 24900;
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  Gaps
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   326
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   0
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS AS:
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, M
FILE REFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10805
LENGTH: 1790242
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Search completed: March 17, Job time: 73.6301 secs
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   US-10-767-471-10805
   RESULT 15
US-10-767-471-10805/c
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US-10-767-701-28437
; Sequence 28437, Application US/10767701
; GENERAL INFORMATION:
  ; OTHER INFORMATION: Clone ID: US-10-767-701-28437
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   TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(5355)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128 SEQ ID NO 28437 LENGTH: 300
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Best Local Similarity
  APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
   OTHER INFORMATION: n = A, T, C or G, or insertion/deletion polymorphism (see Tables
  NAME/KEY: misc_feature
LOCATION: (1)...(1790242)
  FEATURE:
  ORGANISM: Homo sapiens
   TYPE: DNA
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ORGANISM: Sorghum bicolor
   FEATURE:
  Local Similarity 53.9
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  326 AAAACTCCGATATTACTGTCGGCCAATATGATCAGCTGGTTACCCGTGTTGTTA 379
   266
  183
   123 AAGAAGGCGGTTACGAAGCCGGTGGTTACGGTGGCGGCGGCGGCGGTTACGGCGGTCCCC
   74 AATGGGGCGGCGGTAATCATAACGGCGGCGAATAGTTCCGGCCCGG 124
  60;
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  GTAAGGGCGGCGGTTATGGCGGCGGCGGCGGTTACGGTGGCAACCGGG
  Zhou, Yinua
Cao, Yongwei
   Conservative
  Michele et al.
GENETIC POLYMORPHISMS ASSOCIATED WITH
RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
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53.5%;
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  Title:
Perfect score:
   Run on:
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456
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.

Score

Length

DB IJ

% Query Match

| DE SEQUENCES                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Sequence 6264, Ap<br>Sequence 6264, Ap<br>Sequence 6264, Ap<br>Sequence 20532, A<br>Sequence 24330, A<br>Sequence 24340, A<br>Sequence 24948, A<br>Sequence 3383, Ap<br>Sequence 3383, Ap | Sequence 19, App<br>Sequence 171, App<br>Sequence 171, App<br>Sequence 171, App | Sequence 78, Appl<br>Sequence 48, Appl<br>Sequence 79, Appl<br>Sequence 79, Appl | Sequence 77, Appl<br>Sequence 52, Appl<br>Sequence 9, Appli<br>Sequence 9, Appli | Sequence 1, Appli<br>Sequence 170, App<br>Sequence 170, App<br>Sequence 170, App | Sequence 3, Appli<br>Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 1, Appli | Sequence 172, App<br>Sequence 172, App<br>Sequence 172, App<br>Sequence 3, Appli | Sequence 27, Appl<br>Sequence 29, Appl<br>Sequence 54, Appl<br>Sequence 3, Appli | Sequence 13, Appl<br>Sequence 23, Appl<br>Sequence 25, Appl<br>Sequence 21, Appl | 1,<br>19,<br>17,                                                                                                                                                 | Description Sequence 15, Appl Sequence 56, Appl                                                                                                                                                                                |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------|----------------------------------------------------------------------------------|----------------------------------------------------------------------------------|----------------------------------------------------------------------------------|----------------------------------------------------------------------------------|----------------------------------------------------------------------------------|----------------------------------------------------------------------------------|----------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| APPLICANT: DISTRIBUTION: METHODS AND COMPOSITIONS FOR SALMONELLA- TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA- TITLE OF INVENTION: BASED VACCINES NUMBER OF SEQUENCES: 58 NUMBER OF SEQUENCES: - CORRESPONDENCE ADDRESS: ADDRESSEE: Seed and Berry STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle STATE: Washington COUNTRY: U.S.A. ZIE: 98104-7092 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIN Release #1.0, Version #1.25 APPLICATION NUMBER: US/08/233,642A FILING DATE: 26-APR-1994 CLASSIFETCATION: 424 ATTORNEY/AGENT INFORMATION: NAME: King, Joshua | SULT 2 -08-233-642A-56 Sequence 56, Application ( GENERAL INFORMATION: APPLICANT: Kay, Willia APPLICANT: Collinson, APPLICANT: Collinson                                                  | 456                                                                             |                                                                                  |                                                                                  | Qy 241 GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGAGTATGGTTTCAGAATAAT 300               | QY 181 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240          | QY 121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180          | QY 61 GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC 120           | QY 1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60             | Query Match 100.0%; Score 456; DB 23; Length 456; Best Local Similarity 100.0%; Pred. No. 2.1e-139; Matches 456; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | ; FEATURE: ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA ; OTHER INFORMATION: sequence containing the replacement fragment ; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-15 |

RESULT 1

US-09-543-407-15

Sequence 15, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT APPLICATION NUMBER: US/09/543,407

SUDMBER OF SEQ ID NOS: 59

SEQ ID NO 15

SEQ ID NO 15

SEQ ID NO 15

LENGTH: 456

TYPE: DNA ORGANISM: Artificial Sequence

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ALIGNMENTS

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456
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350.3
352.3
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348.8
348.8
348.6
64.8
64.8

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571 US-09-252-691-172
571 US-09-252-691-172
571 US-09-252-691-172
571 US-09-252-691-172
571 US-09-252-691-172
571 US-09-252-691-170
571 US-09-252-691-170
571 US-09-252-691-171
571 US-09-252-691-171
571 US-09-252-691-171
571 US-09-252-691-171
571 US-10-146-492B-78
573 US-09-543-407-49
574 US-10-146-492B-78
575 US-10-146-492B-78
575 US-10-146-492B-78
575 US-10-146-492B-78
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575 US-10-146-492B-78
577 US-09-252-691-171
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577 US-09-252-691-171
577 US-09-252-691-171
577 US-09-252-691-171
577 US-

```
SEQUENCE 1, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Asron P.
APPLICANT: White, Asron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PE
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 1
   RESULT 3
US-09-543-407-1
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  US-08-233-642A-56
   TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
TYPE: nucleic acid
STEAMDENNESS: 41016
  Matches 423;
  Query Match
Best Local Similarity
ORGANISM: Salmonella
                 LENGTH: 456
TYPE: DNA
  NAME/KEY:
LOCATION:
  STRANDEDNESS: 611
TOPOLOGY: linear
   REFERENCE/DOCKET NUMBER:
   REGISTRATION NUMBER: 35,570
  301
  181
  361
   361
   301
  241
   241
   181
  121
   421
   121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCGAA
  61
   61
   -
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  ATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC 120
   AATAACGCCGCGCTGATTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  Conservative
  1..456
  single
 enteritidis
  92.8%;
  Score 403.2; DB 6;
Pred. No. 6.1e-122;
0; Mismatches 33;
   920043.403C3
   PEPTIDE SEQUENCES
   Length 456;
  0,
   360
   240
   180
   420
   420
  360
  300
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  120
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   RESULT 4
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  US-09-543-407-19
   US-09-543-407-1
  Sequence 19, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
  Query Match
Best Local Simi
Matches 396;
   FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FRETSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 456
  Best Local
   Query Match
  LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   421
  421
  361
  361
  301
   301
   241
   241
   181
   181
  121
  121
  61
   61 GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC 120
   1 ATGANACTTTTANAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   Similarity
  Similarity
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCCAGCGTAATGGTGCGTCAGGTT
 GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC 120
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCCGATATTACTGTCGGCCAATACGGCGGT 360
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  GGCGTCGTTCCACAATGGGGCGGCGGCGCAATCATAACGGCGGCGCAATAGTTCCGGC
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAGTCGTAGTTTCTGGCAGTGCTCTGGCT
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   AGCGATGCCCGTAAATCTGAAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  78.9%; ilarity 86.8%; Conservative
   Conservative
  92.8%;
  Score 360; DB 23;
Pred. No. 1.2e-107;
0; Mismatches 60;
   Score 403.2; DB 23; Length Pred. No. 6.1e-122; O; Mismatches 33; Indels
   456
  PEPTIDE SEQUENCES
  Length 456;
  Indels
  0
   0
  Gaps
   Gaps
  420
   300
  60
   240
   240
  120
                                      60
  420
  360
  180
   60
```

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043,406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 17
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  RESULT 5
US-09-543-407-17
   US-09-543-407-17
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  Matches
   Best Local
   Query Match
   Sequence 17, Applica GENERAL INFORMATION:
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   LENGTH: 456
TYPE: DNA
ORGANIEM: Artificial Sequence
PEATURE:
        181
                                       181
  121
  301
  61
   61
  392;
  421
   421
   361
  361
   301
   241
  241
  181
   181
   121
  121
   61
  Similarity
AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
                         AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGCAA
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  GGTTTTGGCAACAACGCCACGCTAACCAGTATTAA
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   AATÄACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  AATAACGCCGCGTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGGGGT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   CGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGC
   AGCGATGCCCGTĂAĂTATGĂTCAĠCTGGTTĂCCCGTGTTĞTTACCCATGĂAATGĠCACĂT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGGT
  Application US/09543407
  Conservative
  77.5%;
   0; Mismatches
  Score 353.6; DB 23; Pred. No. 1.6e-105;
   64;
  456
  PEPTIDE SEQUENCES
   Indels
   Length
   0;
   Gaps
                                240
   180
  180
   240
   120
  120
  60
   60
  240
   180
  420
   420
   360
  360
  300
   300
   240
  180
   120
```

```
Sequence 11, Application US/09543407

GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: RESERVATION FOR TITLE OF INVENTION: PRESERVATION OF HETEROLOGOUS PEF
FILE REFERENCE: 920043,406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 456
TYPE: DNA
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  ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major: US-09-543-407-11
  US-09-543-407-11
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  Query Match
Best Local Similarity
Matches 391; Conserv
   ORGANISM: Artificial Sequence FEATURE:
       361
                                    361
   301
  241
  301
  241
   181
   181
  121
  121
   61
   421
   421
  361
   361
   301
   61
  301
  241
   241
  \vdash
                     AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC 120
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGC 120
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   AATAACGCCGCGTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  77.2%;
milarity 85.7%;
Conservative
   <u>,</u>
  Score 352; DB 23;
Pred. No. 5.3e-105;
0; Mismatches 65;
   PEPTIDE SEQUENCES
   Length 456;
   Indels
  0;
  Gaps
  180
   420
                               420
  360
  360
   300
   300
  240
   180
  240
   60
  420
  420
   360
   360
   300
  0
```

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421

GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA

456

```
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PE
FILE REFERENCE: 920043, 406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
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   US-09-543-407-13
  밁
  RESULT 7
   Query Match
Best Local S
Matches 391
  Sequence 13, Application GENERAL INFORMATION:
  FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
-09-543-407-13
  APPLICANT: White, Aaron
   LENGTH: 456
TYPE: DNA
ORGANISM: Artificial
  361
  181
   181
   121
                               421
   361
   301
  301
   241
  241
  121
   391;
  421
  61
  61
   \vdash
  Similarity
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
                             GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
  CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCATCCGGC
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  GCACATGCAAACAACGCCACGGCTAACCAGTATTAA 456
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
   Conservative
   Sequence
  77.2%;
85.7%;
   US/09543407
  Score 352; DB 23;
Pred. No. 5.3e-105;
O; Mismatches 65;
                               456
456
  PEPTIDE SEQUENCES
   Length 456;
   Indels
   0
   Gaps
   420
   240
  360
  180
   300
  240
   120
   60
```

RESULT 8
US-09-543-407-23
; Sequence 23, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: COllinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
   APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 456
  RESULT 9
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  US-09-543-407-23
   Sequence 25, Application US/09543407 GENERAL INFORMATION:
   Matches
  Query Match
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  ORGANISM: Artificial Sequence FEATURE:
   TYPE: DNA
   Local Similarity
   361
   361
  301
   421
  421
   301
  241
  241
   181
  181
   121
   121
   391;
  61
   61
  1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAGTCGTAGTTTCTGGCAGTGCTCTGGCT
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
  GGTTTTGGCAACAACGCCACGCTAACCAGTATTAA 456
   CATGAAATGGCACATGCAAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GCCACCATCGACCAGTGGAACGCTAAAAACTATGATCAGCTGGTTACCCGTGTTGTTACC
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTTACGGTTCCGCTTAACGCTGCGCTTCGCTTCGCAA
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  GGCGTCGTTCCACAATGGGGCGGCGGCGGCGAATAGTTCCGGC
   GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCATCCGGC 120
   Conservative
   77.2%;
85.7%;
   0,
   Score 352; DB 23;
Pred. No. 5.3e-105;
0; Mismatches 65;
   456
   PEPTIDE SEQUENCES
   PEPTIDE SEQUENCES
  Length 456;
   Indels
   0,
   Gaps
   420
  240
   180
  360
   360
  300
   240
  120
   60
  60
```

```
SEQUENCE 21, Application US/09543407

SEQUENCE 21, Application US/09543407

SEQUENCE 21, Application US/09543407

APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP
FILE REFERENCE: 920043.406

CURRENT APPLICATION NUMBER: US/09/543,407

CURRENT FILING DATE: 2000-04-05

NUMBER OF SEQ ID NOS: 59

SOSTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 21
  US-09-543-407-21
  RESULT 10
US-09-543-407-21
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   ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-25
       Best Local Similarity
                            Query Match
  Query Match
Best Local Similarity
Matches 391; Conser
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
   FEATURE:
   TYPE: DNA ORGANISM: Artificial Sequence
   361
  361
   301
   421
  421
  301
   241
   241
  181 CTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCAGGTTATGGTAACGGCGCCGAT
  181 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
   121
   121
   61
   61
   ATGAAACTTTTAAAAGTGGCAGCAGTTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  GGTTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTTATGATCAG
  GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCATCCGGC
  GGCGTCGTTCCACAATGGGGGGGGGGGGGGGGGGAATAGTTCCGGC
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   Conservative
       76
85
   77.2%;
85.7%;
   Score
Pred.
   0,
   Score 352; DB 23;
Pred. No. 5.3e-105;
  Mismatches
348.8; DB 23;
No. 6.1e-104;
   65;
  PEPTIDE SEQUENCES
  Length 456;
                 Length
  Indels
  ۰,
  Gaps
  420
  420
  360
  360
  300
  300
  240
  120
  180
  120
  60
  60
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  US-09-543-407-27
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   В
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 27
   5
   밁
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   Matches
   Query Match
  Sequence 27, Application US/09543407 GENERAL INFORMATION:
  TITLE OF INVENTION: BACTERIAL FIMBRIAL FITLE OF INVENTION: PRESENTATION OF HE FILE REFERENCE: 920043 406
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
   Matches
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  TYPE: DNA
ORGANISM: Artificial
FEATURE:
   LENGTH: 456
  Local
  61
   61
   389;
   361
  421
  421
   361
   301
  301
   241
  241
  181
  181
  121
   121
   61
   61
  Similarity
  389; Conservative
CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCATCCGGC
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAGTCGTAGTTTCTGGCAGTGCTCTGGCT
                              GÉCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GCACATGCAGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GTAGGCCAGGGTGCGGATAATTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATG
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   GGCGTCTATGATCAGCTGGTTACCCCGTGTTGTTACCCCATGAAATGGCACATGCATCCGGC 120
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  ccedactcaacerreaecatriateaeraceerrececraacecrececricerecaa
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
   ATGAAACTTTTÄÄÄÄGTGGCÄGCÄTTCGCÄGCÄÄTCGTÄGTTTCTGGCÄGTGCTCTGGCT
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   Conservative
   Sequence
   76.5%;
  Score 348.8; DB 23;
Pred. No. 6.1e-104;
Viematches 67;
  0,
  Mismatches
  HETEROLOGOUS
  SYSTEM
  FOR
  67;
  PEPTIDE SEQUENCES
  Indels
  Length
   Indels
  0,
   0,
  Gaps
   Gaps
                              120
  120
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   360
  420
  360
   300
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   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major: US-09-543-407-29
  RESULT 12
US-09-543-407-29
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  APPLICANT: white, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: KBY, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FASTSEQ for Windows Version 4.0
  Sequence 29, Application US/09543407 GENERAL INFORMATION:
  Query Match
Best Local (
  Matches
  LENGTH: 45
TYPE: DNA
   ORGANISM: Artificial Sequence FEATURE:
        241
   181
  181
  361
  121
   121
   421
   361
  301
   301
  241
   241
   181
   421
  181
   121
  61
   61
  387;
  456
  Н
  Similarity
 GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA.180
   GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   TATGATCAGCTGGTTACCCGTGTTACCCATGAAATGGCACATGCATTCAGAAATAAT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCGAT 240
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   Conservative
  75.8%;
84.9%;
   0,
   Score 345.6; DB 23;
Pred. No. 6.9e-103;
0; Mismatches 69;
  DB 23;
   Indels
  Length 456;
   <u>,,</u>
   Gaps
   240
  180
  120
  60
  360
   240
   240
   420
  420
   360
  300
  300
   180
   0
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   RESULT 13
US-08-233-642A-54
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   US-08-233-642A-54
   Sequence 54, Application GENERAL INFORMATION:
  Matches
  Query Match
   ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILLNG DATE: 26-APR-1994
CLASSIFICATION: 424
CLASSIFICATION: 424
   TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 54:
  SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
TYPE: nucleic acid
  ATTORNEY/AGENT INFORMATION:
NAME: King, Joshua
REGISTRATION NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 920043.403C3
TELECOMMUNICATION INFORMATION:
  FEATURE:
  MOLECULE TYPE:
   TITLE OF INVENTION: METHODS AND CONTITLE OF INVENTION: BASED VACCINES NUMBER OF SEQUENCES: -
  APPLICANT:
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
   STREET: Seattle
  APPLICANT: Doran, James L.
   APPLICANT:
   NAME/KEY:
LOCATION:
  Local Similarity
les 286; Conserv
  TOPOLOGY:
  STRANDEDNESS:
   STATE: Washington COUNTRY: U.S.A.
   361
  301
  421
   421
  361
   301
   47
  ATGCATCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGC
                                 TTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTA
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420
   ATAGTTCCGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGC
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GCCACCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAGGCGGT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
  6300 Columbia Center, 701
   Kay, William w.
Collinson, S. Karen
Clouthier, Sharon C.
  Conservative
  linear
  CDS
  DNA (genomic)
   double
  62.3%;
  METHODS AND COMPOSITIONS FOR SALMONELLA-
  US/08/233,642A
   US/08233642A
  Score 284.2; DB 6;
Pred. No. 1.3e-82;
0; Mismatches 3;
   Version
  Fifth
  Avenue
  456
  Length 361;
  Indels
  0
  Gaps
                                 229
  169
   106
  360
   420
  0
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  ; TYPE: DNA
; ORGANISM: E.
US-09-543-407-3
   RESULT 14
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  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 456
   Query Match
Best Local Similarity
Matches 310; Conserv
   Sequence 3, Applicat: GENERAL INFORMATION:
  APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
  APPLICANT: White, Aaron APPLICANT: Doran, James
  361
421
  361 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGGCGTAATGGTGCGTCAGGTT
  301
   301
   241
   241
   181
  181
  121
  121
  61
   61
  350
   287
   227
  167
  290
  230
   GGCAACGGTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT
                  GGTTTTGGCAACAACGCCACGCTAACCAGTATTAA
   GCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGTGGT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  ĠŦŦĠĠŦĊĀĠĠĠĊŦĊĀĠĀŦĠĀĊĀĠĊŦĊĀĀŦĊĠĀŦĊŤĠĀĊĊĊĀĀĊĠŤĠĠĊŤŤĊĠĠŦĀĀĊĀĠĊ
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   CCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAA
   ACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGCAGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
   GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC
  GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  ATGAAACTTTTAAAAGTAGAAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCTCTGGCA
   Application US/09543407
   AATACGGCGTAATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTC
  AATACGGCGGTAATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTC 398
  TĊĀĠĀĀĀĪĀĀĪĠĊĊĀĊĊĀĪĊĠĀĊĊĀĠĪĠĠĀĀĊĠĊĪĀĀĀĀĀĊĪĊĊĠĀĪĀĪTĀĊĪĠĪĊĠĠĊĊ
   TCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCC
   ACGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTT
  Conservative
   48.8%;
   0
  Score 222.4; DB 23; Length Pred. No. 3.9e-62; O; Mismatches 146; Indels
                      456
   PEPTIDE
  Length
   335
  °.
  Gaps
   420
  300
  420
   360
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   300
  240
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   349
   226
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   US-09-252-691-172
  Sequence 172, Application US/09252691B
GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
SEQ ID NO 172
LENGTH: 477
TYPE: DNA
ORGANISM: Enterobacter cloacae
   Matches
  Query Match
   Local
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                                    421
  382
   361
  322
   301
   262
  241
  142
   202
  181
   121
   310;
  82 GTGCGGTACCACAATTTGGCGGGGGCCACGGTGGTGGCTGGGGTGGCGGCAATAACGGC 141
   61 GGCGTCTATGATCAGCTGGTTACCCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC 120
  1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
   Similarity
                      GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
GGCTTTGGCAACAACGCGACCCGCACACCAGTACTGA
  GGCAACGGCGCGGTAGACCAGACAGCGTCCGGCTCAACGGTGACTGTGCACCAGGTT
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   ĠĊĊĀĊĊĀŦĊĠĀĊĊĀĀŦĠĠĀĀTAGCĀĀĀGĀĊŦĊŦĠŦŦĀŦĊĀACĠŦGAĀĀĊĀGŦŦĊĠĠĊĠĠĊ
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GTTGGCCAGGGCTCTGATGACAGTTCTATCGATCTGCTGCAAAAAAGGCTTTGGTAACAGC
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   ACGGACGCCCGAGATTCTGAATTGACCATTACCCAGCATGGTGGTAACGGCGCAGAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  ĆĊTĠĀĊŤĊĀĀĊCĊŤĠĀĠĊĀŤŤŤĀĊĊĀĠŤĀĊĠĠCGGĊĠGŤĀĀĊTĊCĠĊĠĊŤŤĠĊŤŢŤĠĊĀG
  Argaaacttiticaaagtggcagtaattgcagcaatcgtagtitictggcagtgctttcgca
  Conservative
  48.8%;
   Score 222.4; 1
Pred. No. 4e-6:
0; Mismatches
  0,
  .4; DB 17;
4e-62;
   146;
                              456
  Length
   0,
   Gaps
   240
  441
   381
   321
  300
  201
  261
   81
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Search completed: N Job time : 2924.24 March 18, 4 secs 2004, 02:47:01

477

RESULT 15 US-09-252-691-172

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Result
  Database
   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  Minimum
   Title:
Perfect score:
  OM nucleic - nucleic search, using sw
   Total number of hits satisfying chosen parameters:
   Searched:
  Scoring table:
   Sequence:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   DB seq length: 0
DB seq length: 2000000000
    27.8
27.8
27.8
27.8
  Query
  Pending_Patents_NA_New:*

1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq:*

3: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

4: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

6: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*

7: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq:*
   456
   637880 seqs, 183698769 residues
   IDENTITY_NUC
  March 16, 2004, 15:39:56 ; Search time 69.6301 Seconds (without alignments) 2406.048 Million cell updates/sec
  Gapop 10.0 , Gapext 1.0
   US-09-543-407-15
   48.8
39.5
7.3
   atgaaacttttaaaagtggc.....ccacggctaaccagtattaa
  Copyright
  8 3990
3 3990
3 150223
1 150223
5 1400
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4 757
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   Length DB
  GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
US-09-741-873C-3
US-09-741-873C-3
US-09-330-230A-629
US-09-330-230A-629
US-10-624-149A-1
US-10-788-792-27
US-10-788-792-27
US-10-545-213-213-6406
US-60-545-213-6407
US-60-545-213-6407
US-60-545-213-6407
US-60-545-213-6407
US-10-771-241-117
US-10-771-241-117
US-10-417-375A-143
PCT-US04-05654-2123
US-10-021-698A-869
US-60-548-091-5258
US-60-548-091-22688
US-10-100-683-3549
US-10-100-683-3549
US-10-775-972-154
US-10-775-972-154
US-10-767-701-7904
US-10-767-701-74458
   SUMMARIES
   model
   Description
  Sequence
Sequence
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Sequence
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  Sequence
Sequence
   629, Appli 27, Appli 27, Appli 2134, Appli 2134, Appli 2134, Appli 2137, Appli 213, Appli 213, Appli 213, Appli 213, Appli 213, Appli 213, Appli 213, Appli 213, Appli 213, Appli 213, Appli 213, Appli 213, Appli 213, Appli 213, Appli 213, Appli 2329, Appli 23
  , Appli
, Appli
29, App
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|--------------------|---------------------|-------------------|--------------------|---------------------|-------------------|---------------------|---------------------|-------------------|-------------------|--------------------|-------------------|--------------------|--------------------|--------------------|---------------------|---------------------|---------------------|-------------------|
| <b>.4</b><br>5     | 44                  | 43                | 42                 | 41                  | 40                | 39                  | 38                  | 37                | 36                | 35                 | 34                | 33                 | 32                 | 31                 | 30                  | 29                  | 28                  | 1                 |
| 27                 | 27                  | 27.2              | 27.2               | 27.4                | 27.4              | 27.4                | 27.6                | 27.6              | 27.6              | 27.6               | 27.6              | 27.6               | 27.6               | 27.6               | 27.6                | 27.8                | 27.8                | 47.0              |
| 5.9                | 5.9                 | 6.0               | 6.0                | 6.0                 | 6.0               | 6.0                 | 6.1                 | 6.1               | 6.1               | 6.1                | 6.1               | 6.1                | 6.1                | 6.1                | 6.1                 | 6.1                 | 6.1                 | ٥. ٢              |
| 987                | 511                 | 998               | 959                | 318752              | 868               | 201                 | 232882              | 3035              | 2571              | 1662               | 1523              | 1498               | 600                | 600                | 201                 | 1126118             | 32372               | T0007             |
| 0                  | 6                   | ர                 | 0                  | σ                   | σ                 | 6                   | σ                   | σ                 | v                 | 0                  | 0                 | σ                  | 7                  | 7                  | 6                   | 6                   | σ                   | a                 |
| US-10-100-683-3090 | US-10-767-701-18763 | US-09-461-537A-3  | US-10-767-701-1446 | US-10-767-471-10553 | US-10-767-701-167 | US-10-767-471-11899 | US-10-767-471-10679 | US-10-786-892-279 | US-09-999-183A-4  | US-10-100-683-5106 | US-10-100-683-750 | US-10-100-683-5108 | US-60-545-213-6292 | US-60-545-213-2020 | US-10-767-471-28293 | US-10-767-471-10615 | US-10-767-471-10611 | 5, COT-1/5-/0/-01 |
| Sequence 3090, Ap  | Sequence 18763, A   | Sequence 3, Appli | Sequence 1446, Ap  | Sequence 10553, A   | Sequence 167, App | Sequence 11899, A   | Sequence 10679, A   | Sequence 279, App | Sequence 4, Appli | Sequence 5106, Ap  | Sequence 750, App | Sequence 5108, Ap  | Sequence 6292, Ap  | Sequence 2020, Ap  | Sequence 28293, A   | Sequence 10615, F   | Sequence 10611, A   | sequence tos/4, A |

ALIGNMENTS

```
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1997-11-26
PRIOR PILING DATE: 1999-05-04
PRIOR PILING DATE: 1991-11-06
PRIOR PILING DATE: 1991-11-06
PRIOR PILING DATE: 1992-11-03
PRIOR PILING DATE: 1992-11-03
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR PILING DATE: 1992-11-03
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR PILING DATE: 1994-01-28
PRIOR PILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-01-28
PRIOR FILING DATE: 1994-10-05
NUMBER OF SEQ ID NOS: 11
US-09-741-873C-3
   US-09-741-873C-3
   Sequence 3, Application US/09741873C
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well
  SOFTWARE: PatentIn version 3.0 SEQ ID NO 3 LENGTH: 675
                      FEATURE:
NAME/KEY: CDS
LOCATION: (83)..(538)
  TYPE: DNA
ORGANISM: Escherichia coli
   Αß
  Its Preparation
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121

CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCCTCTGCAA 180 GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC 202 61 83 Н

ATGAAACTITTAAAAGTAGCAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCTGTGGGCA 142 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60

GGCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC 120

Query Match 48.8
Best Local Similarity 68.0
Matches 310; Conservative

48.8%;

0; Mismatches 146; Score 222.4; DB 5; Pred. No. 8.7e-67;

Indels Length 675;

0

Gaps

```
TITLE OF INVENION. Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
PRIOR APPLICATION NUMBER: US/09/741,873C
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1989-05-04
PRIOR FILING DATE: 1991-11-06
PRIOR FILING DATE: 1992-11-03
PRIOR FILING DATE: 1992-11-03
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
  밁
  NUMBER OF SEQ ID NOS: 11-05
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 396
TYPE: DNA
ORGANISM: Escherichia coli
US-09-741-873C-1
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  В
   Ś
   Query Match
Best Local Similarity 70.6%;
  RESULT 2
US-09-741-873C-1
  Matches
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   Sequence 1, Application US/09741873C GENERAL INFORMATION:
  PRIOR APPLICATION NUMBER: US 08/318,519
PRIOR FILING DATE: 1994-10-05
  APPLICANT: Normark, Staffan APPLICANT: Olsen, Arne
297 TAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGG 356
   177 AGATGTTGGTCÁGGGCTCAGATGACÁGCTCAATCGATCTGÁCCCÁACGTGGCTTCGGTAA 236
  117 CGGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCT 176
   57 ČGGCCCAAATŤCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCT 116
   443 GGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT 502
   361
  383
   301
  323
  241
   263
   GCÁAÁCTGÁTGCCCGTAACTCTGÁCTTGÁCTÁTTÁCCCAGCATGGCGGCGGTAÁTGGTGC
  GCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGC 236
  181
   203
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCTGGTTAATCAAACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420
  GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA 538
  ĠĊŦĀĊŦĊŤŦĠĀŦĊĀĠŦĠĠĀĀĊĠĠĊĀĀĀĀĀŦŦĊŦĠĀĀĀŤĠĀĊĠĠŤŦĀĀĀĊĀĢŦŦĊĠĠŦĠĠŤ 442
  GCCACCATCGACCAGTGGAAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
  GÍTTGGTCÁGGGCTCAGÁTGÁCÁGCTCAÁTCGÁTCTGÁCCCÁACGTGGCTTCGGTÁÁCÁGC 382
   ограсссасын аймалық тартастаттеластелет сасаттесттелелелет зоо
  Acroaroccernakericioakerrokeratrakecekakearokecokokorakirokerokeakar 322
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
  CCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAA 262
  Conservative
  Score 180; DB 5; Length 396;
Pred. No. 2.7e-52;
0; Mismatches 100; Indels
  ٥,
  Gaps
   176
```

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0,

Gaps

0

```
; NAME/KEY: misc feature
; LOCATION: (1251)
; OTHER INFORMATION: n equals
US-09-830-230A-629
     Query Match 7.3
Best Local Similarity 47.4
Matches 100; Conservative
  APPLICATION NUMBER: 60/053,377
FRIOR PELLING DATE: 1997-07-22
PRIOR APPLICATION NUMBER: 06/053,377
FRIOR APPLICATION NUMBER: 06/053,377
FRIOR APPLICATION NUMBER: 06/053,377
FRIOR APPLICATION NUMBER: 60/053,377
FRIOR FILING DATE: 1997-07-22
PRIOR PELING DATE: 1997-07-22
PRIOR APPLICATION NUMBER: 60/053,377
FRIOR FILING DATE: 1997-07-22
PRIOR APPLICATION NUMBER: 60/053,377
FRIOR FILING DATE: 1997-07-2
   RESULT 3
US-09-830-230A-629
  FEATURE:
FEATURE:
NAME/KEY: misc_feature
NAME/KEY: (1148)
  PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 756
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 629
SEQ ID NO 629
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   문
   FEATURE:
  LOCATION: (1250)
OTHER INFORMATION: n equals
  NAME/KEY: misc feature
LOCATION: (1250)
  LOCATION: (1247)
OTHER INFORMATION: n equals a,t,g,
  Sequence 629, Application US/09830230A GENERAL INFORMATION:
   NAME/KEY: misc feature
LOCATION: (1247)
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  NAME/KEY: misc feature
LOCATION: (1244)
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OTHER INFORMATION: n equals
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   FEATURE:

NAME/KEY: misc feature

LOCATION: (1139)

OTHER INFORMATION: n equals
   NAME/KEY: misc feature
LOCATION: (1210)
   LOCATION: (1143)
OTHER INFORMATION: n equals
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  TYPE: DNA
ORGANISM: Homo sapiens
   LENGTH: 3990
   357
  417
   357 CGGTAATAACGCCGGGGTGGTTAATCAGACGGCATCTGATTCCAGCGTAATGGTGCGTCA 416
   237 CAGCGCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAAATGACGGTTAAACAGTTCGG
  ddrigdcritiddraacaacdcaaccdcicarcardagtactaa 396
   GGTTGGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  rédregcáacegrécrecaerreaccadacerecarecratera
                    7.3%;
  60/050,359
   a,t,g,
  a,t,g,
Score 33.4; DB 5;
Pred. No. 0.23;
0; Mismatches 111;
   a,t,g,
  a,t,g,
  a,t,g,
   a,t,g,
   or
Or
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   or
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  or
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  or
                           Length 3990;
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  US-10-624-149A-1
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   Sequence 1, Application US/10624149A
GENERAL INFORMATION:
APPLICANT: Neubauer, Antonie
APPLICANT: Ziegler, Christina
TITLE OF INVENTION: gm-Negative EHV-Mutants without Heterologous Elements
FILE REFERENCE: 1/1372
CURRENT APPLICATION NUMBER: US/10/624,149A
CURRENT FILING DATE: 2003-07-21
   SOFTWARE:
   Query Match
  LENGTH: 150223

TYPE: DNA

ORGANISM: Equine herpesvirus 1

PUBLICATION INFORMATION:

AUTHORS: Telford,E.A.

AUTHORS: Watson, M.S.

AUTHORS: Davison, A.J.

TITLE: The DNA sequence of equine herpesvirus-1
  PRIOR APPLICATION NUMBER: 60/403,282
PRIOR FILING DATE: 2002-08-14
PRIOR APPLICATION NUMBER: DE 10233064
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: DE 10317008
PRIOR FILING DATE: 2003-04-11
   NUMBER OF SEQ ID NOS: 2
  ISSUE: 1
PAGES: 304-316
DATE: JUL-1992
DATABASE ACCESSION NUMBER: NC 001491, NCBI
DATABASE ENTRY DATE: 2000-08-01
  JOURNAL: VI:
VOLUME: 189
  Local
95662
   277
  157
   ch 7.1%;
l Similarity 51.4%;
75; Conservative
   Virology
  Patentin Version 3.0
GAGAGCTTATTCACAACGAGCTGTTG 95687
  TCAAGCCCATGAGCCACGGACCGGATATGGTTTCTGTATACCAGTCTCTGGGGGCGCGTCA
  GCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCA
  CTGTGGTAACGGTGGGCCTTAGTTTTGATACGGCTCATTTCCACAGCATGTTTGCCTACG
   CTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACG 232
                                    GAAATAATGCCACCATCGACCAGTGG 318
  TTTGCTGTGAAGAGTAATGATGGTGAGAAAG 3643
   AAGAAGGATGATCAGATTGCTGCTGCTATTGCTTTGAGGGGGGATGGCTAAGGATGGAAAG
  ATTACTGTCGGCCAATACGGCGGTAATAACG 367
   ACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGAT 336
  AGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTG 276
  GCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATCTGAAACGACCATTACCCAG
   ATTGCTGCTGCTATTGGGAAGGGTAATGAGGATGGTGCGGATTTTGGTAAGGATGAGATG
   Score 32.4; Di
Pred. No. 2.8;
0; Mismatches
   DB 6;
   71;
   Length 150223;
   Indels
   0
   Gaps
  95601
   0
```

RESULT 5

RESULT 7

```
Sequence 10736, Application US/10767471
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, ME
FILE REFERENCE: CL001505
CURRENT APPLICATION NUMBER: US/10/767,471
CURRENT FILING DATE: 2004-01-30
NUMBER OF SEQ ID NOS: 50231
SOFTWARE: FastSEQ for Windows Version 4.0
   ; LENGTH: 1575
; TYPE: DNA
; ORGANISM: HOMO s
US-10-788-792-27
  ; FEATURE:
, NAME/KEY: misc feature
; LOCATION: (1)...(24900)
; OTHER INFORMATION: n = A,T,C or G,
US-10-767-471-10736
   US-10-788-792-27/c

Sequence 27, Application US/10788792

GENERAL INFORMATION:

APPLICANT: Bayer Pharmaceuticals Corporation

APPLICANT: Bigwood, Douglas

APPLICANT: Bigwood, Douglas

APPLICANT: Bigwood, Douglas

APPLICANT: Bigwood, Douglas

CURRENT APPLICATION NUMBER: US/10/788,792

CURRENT APPLICATION NUMBER: US/10/788,792

CURRENT FILING DATE: 2004-02-27

PRIOR APPLICATION NUMBER: US 60/450,655

PRIOR FILING DATE: 2003-02-28

NUMBER OF SEQ ID NOS: 254

SOTTWARE: Patentin version 3.2
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   밁
  US-10-767-471-10736/c
   SEQ ID NO 10736
LENGTH: 24900
  Matches
   Query Match
  SEQ ID NO 27
   Matches
  Query Match 6.8%;
Best Local Similarity 55.7%;
  ORGANISM: Homo sapiens
  TYPE: DNA
   6.5%;
Local Similarity 52.4%;
hes 65; Conservative
  9928
   267
   207 CATTACCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTAC 266
AATC 9925
                                       AAAC 330
  TCCTGAACCCAAACTGTATGGTACTAAAAATAGTGCAATCCTGGTTTGTTGTATATTTAA
   TATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAA
  CAGCATCCTGACTGCTTTTAGTGTCTCAAAAGTCCTGGGTCAAGTGGTGCATAATTGGTG 9989
   GGATTTCCATACAGTCTGACCGTGCAGTTGCTCAGTTCGGTCAAAAGAACGTCGCGCTGG
  GGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGG 376
   TGCAACTCGCTGGCTCTTCTCCCAAGACTTGGGACTCCAGGTTGG
   TTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTTGG 422
   Conservative
   Score 30.8; DB Pred. No. 1.2; 0; Mismatches
  0,
   0
  Score 29.6;
Pred. No. 11;
  Mismatches
  or insertion/deletion polymorphism (see Tables 1-2
  ASSOCIATED, METHODS OF
   DB 6;
  DB 6;
   47;
  59;
   Length 24900;
  OF DETECTION
  Length 1575;
  Indels
   Indels
  HITH
  0;
   0,
  AND USES
  Gaps
   Gaps
   629
  USE
  THEREOF
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   TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION UNMBER: US/60/545,213
NUMBER OF SEQ ID NOS: 303284
SEQ ID NO 2135
LENGTH: 1400
Typer. ....
  밁
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   ; TYPE: DNA
; ORGANISM: Homo sapiens
US-60-545-213-2135
  Query Match
Best Local Similarity 45.2
108; Conservative
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  В
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   ; TYPE: DNA; Homo sapiens US-60-545-213-2134
  US-60-545-213-2134/c

; Sequence 2134, Application US/60545213

; GENERAL INFORMATION:
  Query Match
Best Local Similarity
Matches 108; Conserv
   APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Uncleic Acid Arrays for Monitoring Expression Profiles of
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
LENGTH: 1400
TYPE TIME TO THE TIME
  APPLICANT: Wyeth APPLICANT: Mount
  332 CCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGTTAATCAGACCGCAT 391
  377 TTGGGGTTCTCCATCCACTGCTTGAAAAGGCCAGGAGCATCTCCTCACACTCTGGAACT
   272 AACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACT 331
   212 CCCAGAGCGGTTATGGTAACGGCGCCGATGTAGGCCAGGGTGCGGATAATAGTACTATTG 271
  392
  377
  437
  212
CCGTTGGAGCAGGCGGTGCTGATGGCATTAACCTCGCTGTACTGGTCCATCAGGTTTTCT
  CCCTGGGCGATAGCGTTGCAGTAGACGGTGGACCGCAGGTTGGGGTGGATCGGGTTATTA 378
  GGGÀTCTCCCTCCÀGTTGTTGGTATTATTTCTGAAGTGÀATGAAGAGGGGTGTGÀCCTG 199
   creartccaeceraareerecercaeerreerrreecaacaacaaceccaceeraaccae
  CCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGTTAATCAGACCGCAT 391
   TTGGGGTŤCTCCATCCACTGCTTGÅAÄÄGĠĊCAGAGAČĆĀTČTCCTCÁCACTCTGGÄÄĊŤ
  AACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACT
   сссаран с денежения проставляющий проставляю
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   Conservative
  45.28;
  6.4%;
  Score 29.4; DB 7;
Pred. No. 3.4;
0; Mismatches 131;
  0,
  Score 29.4; DE Pred. No. 3.4;
  Mismatches 131;
  DB 7;
  Length 1400;
  Indels
  Length 1400;
   Indels
   0;
   ,
,
   Gaps
  318
  318
   331
  Drug
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   RESULT 10
US-60-545-213-6407/c
US-60-645-213-6407/c
The control of the control of
   ; ORGANISM: Homo sapiens US-60-545-213-6407
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  Query Match
Best Local Similarity
Matches 108; Conserv
  CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT FILING DATE: 2004-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6407
TYPE: DNA
TYPE: DNA
   GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: MOUNTS, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
   В
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   밁
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  ; ORGANISM: Homo sapiens
US-60-545-213-6406
   RESULT 9
US-60-545-213-6406/c
; Sequence 6406, Application US/60545213; GENERAL INFORMATION:
  밁
   Ś
   APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042099)
CURRENT APPLICATION NUMBER: US/60/545,213
CURRENT APPLICATION NUMBER: US/60/545,213
NUMBER OF SEQ ID NOS: 303264
SOFTWARE: Patentin version 3.2
LENGTH: 1400
TYPE: 13.1
   Matches 108;
  Query Match
Best Local
  APPLICANT: Wyeth APPLICANT: Mount
  TYPE: DNA
437 CCCTGGGCGATAGCGTTGCAGTAGACGGTGGACCGCAGGTTGGGGTGGATCGGGTTATTA
  212
   392 CTGAȚTCCAGCGTAAȚGGTGCGTCAGGTTGGTTTTGGCAACAACGCCCACGGCTAACCAG 450
   377
   272 AACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGAACGCTAAAAACT 331
   437
   212 CCCAGAGCGGTTATGGTAACGGCGCGGATGTAGGCCAGGGTGCGGATAATAGTACTATTG 271
  392 CTGATTCCAGCGTAATGGTGCGTCAGGTTGGTTTTGGCAACAACGCCCACGGCTAACCAG 450
  CCCAGAGCGGTTATGGTAACGGCGCGATGTAGGCCAGGGTGCGGATAATAGTACTATTG 271
  257
  Similarity
   CCGTTGGAGCAGGCGGTGCTGATGGCATTAACCTCGCTGTACTGGTCCATCAGGTTTTCT
   CCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGTTAATCAGACCGCAT 391
  TTGGĠGTTĊTCCĂŤCCACŤGCTTGĀĀĀĀĠĠĊĀGĀGĀĊĀTĊTCCTCĀCACTCTGGĀĀĊŤ
   CCCTGGGCGATAGCGTTGCAGTAGACGGTGGACCGCAGGTTGGGGTGGATCGGGTTÄTTA 378
  GGGÄTCTCCCTCCÁGTTGTTGGTATTATTTCTGAAGTGAATGÅAGAGGGGTGTGÁCCTG 199
   Conservative
  Conservative
   6.48;
45.28;
   45.2%;
   ٥,
   Score 29.4; DB 7;
Pred. No. 3.4;
0; Mismatches 131;
  Score 29.4; DB 7; Length 1 Pred. No. 3.4; O; Mismatches 131; Indels
   Monitoring Expression Profiles of
   Length 1400;
   Length 1400;
   0,
  Gaps
  258
  318
  Drug
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378

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  ঠ
  US-10-771-241-29
  Ś
  밁
  문
   ; LENGTH: 249
; TYPE: DNA
; ORGANISM: E. Coli
US-10-771-241-117
  RESULT 11
US-10-771-241-117/c
  ঠ
   밁
   ঠ
  문
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 29
LENCTH: 757
TYPE: DNA
  NUMBER OF SEQ ID NOS: 485
SOPTWARE: FASTSEQ for Windows Version
SEQ ID NO 117
   Sequence 29, Application US/10771241 GENERAL INFORMATION:
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   Sequence 117, Application US/10771241
   PRIOR APPLICATION NUMBER: 09/492,709
PRIOR TILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
   APPLICANT: FORBYTH, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION
TITLE OF INVENTION: ESCHERICHIA COLI
FILE REFERENCE: ELITRA.001C1
CURRENT APPLICATION NUMBER: US/10/771,241
CURRENT FILING DATE: 2004-02-03
  APPLICANT: Zyskind, Judith APPLICANT: Forsyth, R. Al
  PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
  FILE REFERENCE: ELITRA.001C1
CURRENT APPLICATION NUMBER: US/10/771,241
CURRENT FILING DATE: 2004-02-03
  APPLICANT: FOTSYTH, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION
TITLE OF INVENTION: ESCHERICHIA COLI
   APPLICANT: Zyskind, Judith APPLICANT: Forsyth, R. Al
  332
  392 CTGATTCCAGCGTAATGGTGCGTCAGGTTGGTTTTGGCAACAACGCCACGGCTAACCAG 450
  415 CA 416
   355 GGCGGTAATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGT 414
  295 AATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATAC 354
  377
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   60
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   GGCACCGACTATCCCCAGCAGGATAGTCATAAAGAATCCACCTCCATCTTTACCTGGCAT
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  TTGGGGTTCTCCATCCACTGCTTGAAAAGGCCAGAGACCATCTCCTCACACTCTGGAACT
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  58;
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  Indels
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; LOCATION: (1)...(757)
; OTHER INFORMATION: n = A
US-10-771-241-29
RESULT 14
PCT-US04-05654-2123
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; HAME/KEY: misc feature

; LOCATION: (1)... (83009)

; OTHER INFORMATION: n =

US-10-417-375A-143
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   RESULT 13
US-10-417-375A-143/c
   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 143
   Sequence 143, Application US/10417375A GENERAL INFORMATION:
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  Query Match
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   CURRENT APPLICATION NUMBER: US/10/417,375A
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
   APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets
   FILE REFERENCE: 529452001600
  ORGANISM: Mus musculus
   TYPE: DNA
  ENGTH:
  Local Similarity 48.8
  13996
  14056 AGAATATTAAAAGAATGCATAATATCCTCAAAAAGAACATTGACTAGTATTCCTTTATTC 13997
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   384 GA 385
   415 CA 416
  324 GGCACCGACTATCCCCAGCAGGATAGTCATAAAGAATCCACCTCCATCTTTACCTGGCAT 383
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Pred. No. 3
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Sequence 2123, Application PC/TUS0405654 GENERAL INFORMATION: APPLICANT: Sherman, Bradley K

Riechmann, Jose Luis Jiang, Cai-Zhong Heard, Jacqueline E Haake, Volker

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

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Matches
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  SOFTWARE: Patentin version 3.2
SEQ ID NO 2123
LENGTH: 2511
TYPE: DNA
ORGANISM: Arabidopsis thaliana
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TYPE: DNA
ORGANISM: Homo sapiens
  10-021-698A-869/c
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NAME/KEY: modified base
LOCATION: (6103)
THER INFORMATION: a, t, c or g
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   CURRENT APPLICATION NUMBER: PCT/US04/05654
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: 10/374,780
PRIOR FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 10/675,852
PRIOR FILING DATE: 2003-09-30
NUMBER OF SEQ ID NOS: 2950
  FEATURE:
OTHER INFORMATION: G1548 Predicted polypeptide sequence is paralogous to G390, G391
   PULICANT: Broun, Pierré E
PLICANT: RAMMENTO, ROGETICK W
PPLICANT: Pilgrim, Marsha L
TLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES IN PLANTS
TREENT APPLICATION WINDER
TREENT APPLICATION WINDER
   PPLICANT:
  Local Similarity
  ICANT
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DUPUIS, JOSEE
DEL MASTRO, RICHARD
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  SIMON, JASON
ALLEN, KRISTINA
   Reddie James
Dubell III, Arnold N
Pineda, Omaira
Repetti, Peter
Century, Karen
   Ratcliffe, Oliver Adam, Luc J
   Conservative
   Sutterson, Neal
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   Lynne
   Score 28.4; DB Pred: No. 9.8; 0; Mismatches
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   0
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US-10-021-698A-869
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Best Local Similarity 56.4%;
Matches 53; Conservative
  NAME/KEY: modified base LOCATION: (20008)
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                           69 Геатсаестветрасссететтетрасссатела 102
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0;

Gaps

Search completed: March 17, 2004, 08:25:46 Job time: 71.6301 secs

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Title:
Perfect score:
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  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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(Gen2_6
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   COMB. seq: *
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45: (***)** (***)** (***)** (***)** (***)** (***)*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

0,

Gaps

60

```
APPLICANT: White, Asron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: CALLINSON, S. Karen
ITILE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITILE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING.DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 456
TYPE: NNA
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  Description
APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson
TITLE OF INVENTION: METHODS AND COMPOSITIONS
INDMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: 701 Fifth Ave
STREET: 6300 Columbia Center, 701 Fifth Ave
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 8304 Columbia Center, 701 Fifth Ave
CORTERS: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION: 424
ATTORNEY/AGENT INFORMATION:
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US-08-233-642A-56
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   Sequence 56, Application US/08233642A GENERAL INFORMATION:
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   В
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; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-17
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  ĠĊĊĀĊĊĀŤĊĠĀĊĊĀĠŤĠĠĀĀĊĠĊŤĀĀĀĀĀĊŤĊĊĠĀŤĀŤŤĀĊŤĠŤĊĠĠĊĆĀĀŤĀĊĠĠĊĠĠŤ
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTTCAGAAATAAT
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   decerreirre a charte de ce de 
   GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  árgadácttríthadadstigickigckittegekigedáttegrádstrótigickigtigetetigiset.
  METHODS AND COMPOSITIONS FOR SALMONELLA-BASED VACCINES
58
   100.0%; Score 456; DB 23; 100.0%; Pred. No. 2.2e-133;
  0,
  Mismatches
   #1
   Indels
```

360

300 300 240 240 180 180 120

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APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTMARE: FastSEQ for Windows Version 4.0
IENGTH: 456
TYPE: DNA
  RESULT 3
US-09-543-407-1
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  REFERENCE/DOCKET NUMBER: 35,570
REFERENCE/DOCKET NUMBER: 92004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEFAX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY.
  밁
  밁
  US-08-233-642A-56
  Sequence 1, Application US/09543407 GENERAL INFORMATION:
  Matches 425;
  Query Match
Best Local Similarity
 ORGANISM: Salmonella
  FEATURE:
  NAME/KEY:
  361
  301
  241
  421
  361
  301
  241
  181
  181
  121
  121
   421
  61
  13
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  μ.
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCCGAT
   CCGGACTATGATCAGCTGGTTACCCGTGTTTACCCCATGAAATGGCACATGCACTGCAA
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  GGCGTCGTTCCACAATGGGGCGGCGGCGGCGATAGTTCCCGGC
  ATGANACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  Conservative
  CDS
enteritidis
  89.1%;
  920043.403C3
  0;
  Score 406.4; DB 6;
Pred. No. 1.2e-117;
0; Mismatches 31;
  PEPTIDE SEQUENCES
  Indels
  Length
  456;
  0,
  240
  180
  120
  420
  360
  360
  300
  300
  240
  180
  60
  60
  0
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APPLICANT: White, Aaron P.
APPLICANT: Dozan, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
APPLICANT: Ray, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 92043.406
FULL REFERENCE: 92043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 19
TENGTH: 456
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  US-09-543-407-1
   Sequence 19, Application US/09543407 GENERAL INFORMATION:
  Matches
  Query Match
Best Local Similarity
  Query Match
   Matches 425;
   Best Local
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
  398;
  421
  421
  361
  361
   301
   301
   241
   241
  181
  181
  121
  121
  61
   61
   1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   Similarity
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCCGATATTACTGTCGGCCAATACGGCGGT
GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC 120
                                ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCCAATAGTTCCGGC
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  CCGGACTATGATCAGCTGGTTACCCGTGTTACCCATGAAATGGCACATGCACTGCAA
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  Conservative
   Conservative
   79.6%;
   89.1%;
  Score 363.2; DB 23;
Pred. No. 6e-104;
0; Mismatches 58;
   0; Mismatches
   Score 406.4; DB 23; Pred. No. 1.2e-117;
  PEPTIDE SEQUENCES
  Indels
   Length
   Indels
  Length
  0
   <u>.</u>
  Gaps
  Gaps
                                  60
  60
  420
  240
  180
  180
   360
   360
  420
   300
  240
  120
   120
   60
   60
  0
```

RESULT 5

US-09-543-407-11

Sequence 11, Application US/09543407

APPLICANT: Mitte, Aaron P.
APPLICANT: Collinson, S.
APPLICANT: Collinson, S.
APPLICANT: Marcon P.
APPLICANT: Marcon P.
APPLICANT: Collinson, S.
APPLICANT: Marcon P.
APPLICANT: Marcon P.
APPLICANT: Nalliam W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
CURRENT FILING DATE: 920043-406

CURRENT FILING DATE: 2008-405

SOPTWARE: FBG ID NOS: 5900-04-05

SEQ ID NO 11 SIESEQ for Windows Version 4.0 LENCTH: 456

TYPE: DNA
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
US-09-543-407-11
US-09-543-407-11

Equation of the replacement fragment
US-09-543-407-11

THER INFORMATION: encoding PT3 from GP63 of Leishmania major. 181 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGAT 240
181 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGGAT 240 121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCCTAACGCTGCGCTTGCTCTGCAA 180 121 CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGCAA 180 61 GGCGTCGTTCCACAATGGGGCCGGCGGCGGTAATCATAACGGCGGCGAATAGTTCCGGC 120 atch
cal Similarity 77.9%; Score 355.2; DB 23; Length 456;
393; Conservative 0; Mismatches 63; Indels 0; Gaps 1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60 1 ATGAAACTTTTAAAAGTGGCAGCAFTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 421 GGTTTTGGCAACAACGCCACGCTAACCAGTATTAA 456 421 GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456 361 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420 361 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420 301 GCCACCATCGACCAGTGGAACGCTAAAAACTCCGGTATATTACTGTCGGCCAATACGGCGGT 360 301 GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360 241 GCAGGCCAGGGTGCGGATAATAGTAGTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300 241 GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAATAAT 300 181 AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTACCCCATGAAATGGCACAT 240 181 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGGCGAT 240 121 CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180 121 CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGCAA 1|80 61 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC | 20 us-09-543-407-17.rnpm В Ş D, Ş DЬ Ş DЪ Ş Db WESULT 6

WES-09-543-407-13

Sequence 13, Application US/09543407

APPLICANT MILE, ABRON P.

APPLICANT COLLINGUE M.

TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR CURRENT APPLICATION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES: 92004 M.406

CURRENT APPLICATION M. MADER: US/09/543,407

FULD REFERENT APPLICATION M.406

CURRENT APPLICATION M.406

CURRENT APPLICATION M.406

SOFTWARE: FASE ID MOSE: 2000-04-05

SEQ ID NO 13

LENGTH: 456 Ś В Ş Query Match Best Local Similarity 77.9%; Matches 393; Conservative OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga ; OTHER INFORMATION: Sequence containing the replacement fragment US-09-543-407-13 361 CTGGTTACCCGTGTTGTTACCCCÁTGAAATGGCACÁTGCAÁGCGTAÁTGGTGCGTCÁGGTT 420 361 AATAACGCCGCCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420 301 GCCACCATCGACCAGTGGAAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG 360 301 GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360 241 GTAGGCCAGGGTGGGATAATAGTAGTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300 241 GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAATAAT 300 LENGTH: 456
TYPE: DNA
ORCANISM: Artificial Sequence 181 Addangecegraaatetgaaacgaecattaeceagagegettatggtaliiiiiiiiiiii 181 AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240 121 COGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180 121 CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGCAA 180 S В Ş 61 GGCGTCGFTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGACAATAGTTCCGGC 120 Дb Ş DЪ Ş 421 GCACATGCAÁACAÁCGCCÁCGCTAÁCCAÁGTÁTTTÁA 456 421 GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456 361 AATAACGCCGCGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG 420 361 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420 301 decaecaregacoagragaaaceerraaaaacreegararracreregeeaaracraccageeaaracraccageeaaracageeggr 360 301 GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCGATACGGCGGT 360 241 GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300 241 GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGGCTCAGAATGGTTTCAGAATAAT 300 77.9%; Score 355.2; DB 23; Length ative 0; Mismatches 63; Indels Length 456;

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В Ş В Ś DЪ Ś 8

Page 4

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RESULT 8
US-09-543-407-25
; Sequence 25, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
  APPLICANT: White, Naron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE: TURNON TO THE TOWN TO THE TOWN TO THE TOWN TO THE TURNON TO 
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   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-23
   RESULT 7
US-09-543-407-23
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  Sequence 23, Application GENERAL INFORMATION:
  Matches
   Query Match
Best Local Similarity
   421
   361
   361
   301
  301
   241
  241
  181
   181
   121
   121
  421
   393;
  421
   61
   61
  421
   _
  _
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   CATGAAATGGCACATGCAAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
   CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCACTGCAA
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGC
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420
  GCCACCATCGACCAGTGGAACGCTAAAAACTATGATCAGCTGGTTACCCGTGTTGTTACC
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  Conservative
  77.9%;
86.2%;
   US/09543407
   0; Mismatches
  Score 355.2; DB 23; Pred. No. 2.1e-101;
  63;
  PEPTIDE SEQUENCES
  Indels
  Length
   456;
  0
   Gaps
   240
   180
   180
  120
   120
   60
RESULT 9
US-09-543-407-15
Sequence 15, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PREFILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTMARE: FastSEQ for Windows Version 4.0
   APPLICANT: Doran, James L.
APPLICANT: Kay, William W.
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PE
FILE REFERENCE: 920043, 406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
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  S
   US-09-543-407-25
   Matches
  Query Match
Best Local Similarity
   FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leighmania major.
  LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
  361
   361
   301
  421
  421
   301
   241
   241
   181
   181
   121
  121 CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGCAA 180
  393;
  61
   61
   -
  1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT 420
   GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCGAATAGTTCCGGC
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAGGTTATGGTAACGGCGCCGAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTTATGATCAG
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   Conservative
   77.9%;
86.2%;
  0,
   Score 355.2; DB 23; Pred. No. 2.1e-101;
   Mismatches
  456
   PEPTIDE SEQUENCES
   PEPTIDE
   Indels
  Length 456;
   SEQUENCES
  0
```

360

300 300

360

240 240 180

120 60

120

Gaps

```
Sequence 21, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEF
FILE REFERENCE: 920043.406
   OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-09-543-407-21
   RESULT 10
US-09-543-407-21
      Query Match
Best Local Similarity
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   Вb
  SEQ ID NO 21
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  CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
   US-09-543-407-15
  LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
   Matches 392;
   Query Match
Best Local !
   LENGTH: 456

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Recombinant
OTHER INFORMATION: sequence con
OTHER INFORMATION: encoding PT3
   421
   421
  361
   361
  301
   301
  241
  241
   181
  181
   121
  121
   61
  61
  н
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  ĠĊĊĀĊĊĀŤĊĠĀĊĊĀĠŤĠĠĀĀĊĠĊŦĀĀĀĀĀĊŤĊĊĠĀŤĀŤŤĀĊŤĠŤĊĠĠĊĊĀĀŦĀĊĠĠĊĠĠŤ
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCCGATATTACTGTCGGCCAATACGGCGGT 360
  GTAĞĞCCAĞĞĞTĞCĞĞATAATAĞTACTATTĞAACTĞACTCAĞAATĞĞTTTCAĞAAATAAT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  Similarity
  aGCGATGCCGGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCGAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
   сседастатеатсаестветтасссететтеттасссатеааатеесасатесастесаа
  ccedactcaacetteagcatttatcaetacegritccectaacectecetectectacaa
  GÓCGTCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGAATAGTTCCCGGC
  ATGAAACTTTTAAAAGTGGCAGCATTCGGAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  ATGAAACTTTTAAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  Conservative
   Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
        77.2%;
85.7%;
   Recombinant Salmonella enteritidis 3b afga sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
   77.5%;
Score 352; DB 23;
Pred. No. 2.2e-100;
  Score 353.6; DB 23
Pred. No. 6.7e-101;
0; Mismatches 64;
   DB 23;
            Length
  PEPTIDE SEQUENCES
  Indels
  Length 456;
   0;
   Gaps
  420
   420
  360
  300
   300
  240
  180
   180
  120
   120
   60
  60
```

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RESULT 11
US-09-543-407-27
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   Ś
  밁
   Ş
   Matches
  421
   421
   361
  361
   301
   301
  241
   241
  181
  181
   121
  121
  61
  391; Conservative
   61
  1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTTCTGGCAGTGCTCTGGCT
  ĠĠŦŦŦŦĠĠĊĀĀĊĀĀĊĠĊĊĀĊĠĠĊŦĀĀĊĊĀĠŦĀŦŦĀĀ
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GCACATGCAGÁCCÁGTGGÁÁCGCTAAAAACTTCGGATÁTTACTGTCGGCCAATÁCGGCGGT
   ĠŦĀĠĠĊĊĀĠĠĠŦĠĊĠĠĀŦĀĀŦŦAŤGAŦĊAGCTGGŦŦĀĊCĊGTGŦŦĞŦŦACĊCATGĀAĀTG
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGCCGCCGAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
  ccedactcaacgrteagcattrateagracegrteccgctaacgctecctectrecteaa
   CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGCAA 180
   ĠĠĊĠŦĊĠŦŤĊĊĂĊĂĂŤĠĠĠĠĠĠĠĠĠĠĠĠĠĠĠŦĂĂŤĊĂŤĂĂĊĠĠĊĠĠĊĠĠĊĂĂŤĂĠŦŦĊĊĠĠĊ
  GCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
   a Teala a critria a a la decide de carrece ca esta de carrece de carrece de crite de crite de crite de crite de carrece d
  <u>,</u>
  Mismatches
  456
   456
  65;
  Indels
  ٥,
  Gaps
  420
   420
   360
  360
   300
  240
  180
   120
  120
   60
   60
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APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043,406
FILE REFERENCE: 920043,406
CURRENT APPLICATION NUMBER: US/09/543,407
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
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   US-09-543-407-27
  Query Match
Best Local Similarity
Matches 391; Conserv
   Sequence 27, Application US/09543407 GENERAL INFORMATION:
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
   FEATURE:
                      121
   61
   61
  μ
CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCACTGCAA 180
                                  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGACAATAGTTCCCGGC
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC
  argaaactritiaaaacigecageatricecaecaarceractricieecaerecreecr
   ATGAPACTTTTAAAAGTGGCAGCACTTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  Conservative
  77.2%;
85.7%;
   0,
  Score 352;
Pred. No. 2
   Mismatches
   DB 23;
2.2e-100;
es 65;
   Length 456;
   Indels
   0
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120 120 60 60 0

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   ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragmen OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-29
  RESULT 12
US-09-543-407-29
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   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 29
  Sequence 29, Application US/09543407 GENERAL INFORMATION:
  Matches
   Query Match
Best Local (
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
FILE REFERENCE: 920043.406
   LENGTH: 456
TYPE: DNA
  ORGANISM: Artificial Sequence FEATURE:
241
                                241
  181
   181
   121
  361
  361
   301
   301
  241
   181
  121 CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCACTGCAA 180
   421
   421
  241 TATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATTCAGAAATAAT
   181
   121
  61
  389; Conservative
   61
   -
  μ
   Similarity
  GGCGTCGTTCCACAATGGGGCGGCGGCGAATAGTTCCCGGC
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                              GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCGAT 240
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCGAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT 240
   76.5%;
  0
   Score 348.8; DB 23;
Pred. No. 2.2e-99;
0; Mismatches 67;
   67;
  PEPTIDE SEQUENCES
  Indels
   Length
   456;
   0;
   Gaps
  120
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   300
   240
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   240
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   120
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  420
   360
  300
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   US-08-233-642A-54
   US-08-233-642A-54
   RESULT 13
   8
  Sequence 54, Application US/08233642A GENERAL INFORMATION:
APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
APPLICANT: Doran, James L.
  Best Local Similarity Matches 302; Conserv
   Query Match
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-LOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
FILING DATE: 26-APR-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
   TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 54:
  MOLECULE TYPE:
  SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
  FEATURE:
   TELECOMMUNICATION INFORMATION:
   CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
   TITLE OF INVENTION:
  NAME/KEY:
LOCATION:
  ADDRESSEE:
STREET: 63
   NAME: King, Joshua
REGISTRATION NUMBER: 35.
REFERENCE/DOCKET NUMBER:
  COUNTRY: U.S.Ā.
ZIP: 98104-7092
   TOPOLOGY:
   STRANDEDNESS:
   361
  361
   301
   421
  421
  301
                             124 GACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCACTGCAAAGC 183
61
  64
   Seattle
   nucleic acid
   GTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGAATAGTTCCGGCCCG
   ANTAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAGGCGGT
   Washington
  B: Seed and Berry
6300 Columbia Center,
   Doran, James L
  Conservative
   CDS
   linear,
  DNA (genomic)
   double
  61.9%;
  BASED VACCINES
58
   METHODS AND COMPOSITIONS FOR SALMONELLA-
  35,570
  0,
  920043.403C3
  Score 282.2; DB 6;
Pred. No. 2.8e-78;
0; Mismatches 33;
  701
  Version
  Fifth Avenue
  Indels
   Length
   361;
  0
  Gaps
  123
  420
   360
 120
  60
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   US-09-543-407-3
  RESULT 14
US-09-543-407-3
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   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
  Matches 315;
  Query Match
Best Local Similarity
  Sequence 3, Application US/09543407 GENERAL INFORMATION:
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
  TYPE: DNA ORGANISM: E.
   LENGTH: 456
      421
  361
  361 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGGCGTAATGGTGCGTCAGGTT
  301
   301
  241
   241
  181
  181
  121
   121
   61
  61
   301
   364
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  304
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   GGCAACGGTĠĊTGCAĠŤŤĠACĊĀĠĀĊTĠĊĀŤĊŤAĀCŤĊĊTCĊĠŤĊĀACĠŤĠACŤĊĀĠĠŤŤ
               GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
  GCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGTGGT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  ĠŦŦĠĠŦĊĀĠĠĠĊŦĆĀĠĀŦĠĀĊĀĠĊŦĊĀĀŤĊĠĀŦĊŦĠĀĊĊĊĀĀĊĠŦĠĠĊŤŤĊĠĠŦĀĀĊĀĠĊ
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
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   CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCACTGCAA
   ATGAAACTITTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
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   GETGTTGTTCCTCAGTACGCCGCCGCCGCTAACCACGGTGGTGGCGGTAATAATAGCGGC
   ATGAĂĂĊTTTTAAAAAGTAGAAGCAATTGCAGCAATCGTATTCTCCGGTAGCGCTCTGGCA
  AACGCCGCGCTGGTTAATCAGACCGCATCTGATTC 335
  AACGCCGCGCTTGATCAGACCGCATCTGATTC 398
  ACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAAT
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   Score 230.4; DB 23; Length Pred. No. 8.2e-62; O; Mismatches 141; Indels
456
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  180
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   180
  120
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   300
   363
  240
   303
  180
   243
   0
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   EARLIER FILING DATE: 1989-05-04
FEARLIER REPLICATION NUMBER: US 07/789,437
FEARLIER REPLICATION NUMBER: US 07/789,437
FEARLIER REPLICATION NUMBER: US 07/970,846
FEARLIER APPLICATION NUMBER: US 08/187,865
FEARLIER APPLICATION NUMBER: US 08/187,865
FEARLIER APPLICATION NUMBER: US 08/318,519
FEARLIER FILING DATE: 1994-01-28
FEARLIER FILING DATE: 1994-10-05
FEARLIER APPLICATION NUMBER: US 08/318,519
FEARLIER APPLICATION NUMBER: US 08/495,959
FEARLIER APPLICATION NUMBER: US 08/495,959
FEARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOPTWARE: PATENTIN Ver. 2.0
FEARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOPTWARE: PATENTIN VER. 2.0
FEARLIER FILING DATE: 1995-06-28
NUMBER OF SEQ ID NOS: 10
SOPTWARE: PATENTIN VER. 2.0
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   US-08-978-878-3
   RESULT 15
US-08-978-878-3
   Query Match
Best Local Similarity
   Matches
   APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL AS
FILE REFERENCE: 012889-081
CURRENT APPLICATION NUMBER: US/08/978,878
CURRENT FILING DATE: 1997-11-26
EARLIER APPLICATION NUMBER: SE 8801723-1
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ORGANISM: Escherichia
FEATURE:
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LOCATION: (83
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   203
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   143
   315;
   e 3, Application US/08978878 INFORMATION:
   61
   83
   Н
GGTTTTGGCAACAACGCCACGCTAACCAGTATTAA 456
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   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCTÁCTCTTGÁTCÁGTGGAÁCGGCÁÁÁÁATTCTGÁAÁTGÁCGGTTAAACAGTTCGGTGGT
   occaccarcaerogaaeceraaaaaerrecgararraerogeceaaraegecegr
   GTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTCGGTAACAGC
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   GGTGTTGTTCCTCAGTACGGCGGCGGCGGTAACCACGGTGGTGGCGGTAATAATAGCGGC
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   CCAPATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTGCAA
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Pred. No. 9.4e-62;
0; Mismatches 141;
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   420
                                 502
   442
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   262
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   120
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Search completed: March 18, 2004, 02:47:06 Job time: 2927.24 secs

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Result
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  Title:
Perfect score:
   Database
  Minimum
   Total number of hits satisfying chosen parameters:
   Scoring table:
   Sequence:
  Run on:
   OM nucleic -
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  230.4
186.4
34.2
31.4
31.4
31.4
31.2
   Score
    seq
   nucleic search, using
  length: 0
length: 2000000000
   Pending_Patents_NA_New:*

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2: /cgn2_6/ptodata/2/pna/USO6_NEW_COMB.seq:*

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4: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*

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7: /cgn2_6/ptodata/2/pna/USO8_NEW_COMB.seq:*
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Match
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   March 16, 2004, 15:39:56; Search time 69.6301 Seconds (without alignments) 2406.048 Million cell updates/sec
  637880 seqs, 183698769 residues
   Gapop 10.0 , Gapext 1.0
   IDENTITY_NUC
   US-09-543-407-17
  70.5
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   atgaaacttttaaaagtggc.....ccacggctaaccagtattaa
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  99 2007
9 2148
8 1099
8 150223
8 150223
6 1203
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7 1203
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7 1400
7 1400
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145597
145597
  Length DB
   GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                      US-09-741-873C-3
US-09-741-873C-1
US-10-045-674A-593
US-10-021-698A-1216
US-10-775-972-153
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US-10-767-701-17981
US-10-545-213-2136406
US-60-545-213-6406
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|---------------------|-------------------|-------------------|--------------------|--------------------|--------------------|---------------------|--------------------|---------------------|---------------------|---------------------|---------------------|--------------------|--------------------|-------------------|---------------------|--------------------|---------------------|-------------------|
| 45                  | 44                | 43                | 42                 | 41                 | 40                 | 9                   | 38                 | 37                  | 36                  | 35                  | 34                  | 33                 | 32                 | 31                | 30                  | 29                 | 28                  | 27                |
| 28.2                | 28.2              | 28.2              | 28.2               | 28.2               | 28.2               | 28.2                | 28.4               | 28.4                | 28.6                | 28.6                | 28.6                | 28.8               | 28.8               | 29                | 29                  | 29                 | 29                  | 29.2              |
| 6.2                 | 6.2               | 6.2               | 6.2                | 6.2                | 6.2                | 6.2                 | 6.2                | 6.2                 | 6.3                 | 6.3                 | 6.3                 | 6.3                | 6.3                | 6.4               | 6.4                 | 6.4                | 6.4                 | 6.4               |
| 8206                | 3828              | 3776              | 3416               | 1295               | 610                | 201                 | 394468             | 378                 | 1186                | 749                 | 592                 | 83009              | 959                | 2600              | 1052                | 1002               | 594                 | 757               |
| 6                   | 7                 | 7                 | 6                  | σ                  | σ                  | 7                   | .7                 | σ                   | ۲                   | σ                   | σ                   | σ                  | σ                  | σ                 | σ                   | _                  | 0                   | σ                 |
| US-10-021-698A-3529 | US-60-548-091-38  | US-60-548-091-34  | US-10-100-683-3397 | US-10-100-683-5480 | US-10-767-701-8781 | US-60-548-091-22688 | US-60-548-091-5725 | US-10-417-884A-1059 | PCT-US04-05654-1030 | US-10-767-701-12516 | US-10-767-701-22979 | US-10-417-375A-143 | US-10-767-701-1446 | US-10-451-467A-39 | US-10-767-701-12607 | PCT-US04-05654-859 | US-10-767-701-15041 | US-10-771-241-29  |
| Sequence 3529, Ap   | Sequence 38, Appl | Sequence 34, Appl | Sequence 3397, Ap  | Sequence 5480, Ap  | Sequence 8781, Ap  | Sequence 22688, A   | Sequence 5725, Ap  | Sequence 1059, Ap   | Sequence 1030, Ap   | Sequence 12516, A   | Sequence 22979, A   | Sequence 143, App  | Sequence 1446, Ap  | Sequence 39, Appl | Sequence 12607, A   | Sequence 859, App  | Sequence 15041, A   | Sequence 29, Appl |

## ALIGNMENTS

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Sequence 3, Application:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1997-11-96
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1997-11-05
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-05
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
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PRIOR APPLICATION NUMBER: US 08/187,875
PRIOR APPLICATION NUMBER: US 08/187,875
PRIOR APPLICATION NUMBER: US 08/187,877
PRIOR APPLICATION NUMBER: US 07/347,873
PRIOR APPLI
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Best Local Similarity
Matches 315; Conserv
  NAME/KEY: CDS
LOCATION: (83)..(538)
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CURRENT APPLICATION NUMBER: US/09/741,873C
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR PELICATION NUMBER: US 08/978,878
PRIOR PELICATION NUMBER: US 08/978,878
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PRIOR PELICATION NUMBER: US 08/318,519
PRIOR PELICATION NUMBER: US 08/318,519
PRIOR PELICATION NUMBER: US 08/318,519
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  ; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-741-873C-1
  RESULT 2
US-09-741-873C-1
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   Query Match
Best Local
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  Matches
  Sequence 1, Application US/09741873C GENERAL INFORMATION:
   APPLICANT: Normark, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENITION: Fibronectin Binding Protein As Well As Its Preparation
FILE REFERENCE: 012889-084
   ENGTH: 396
  Local Similarity
   241
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```

```
APPLICANT: ROOKEY, KRISTIN L.

APPLICANT: HOET, RENE

APPLICANT: HOET, RENE

APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.

TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING

TITLE OF INVENTION: LISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY

TITLE OF INVENTION: LIBRARIES

FILE REFERENCE: DYAX/002 CIP2

CURRENT APPLICATION NUMBER: US/10/045,674A

CURRENT APPLICATION NUMBER: US/10/045,674A

FRIOR APPLICATION NUMBER: 096/198,069

PRIOR APPLICATION NUMBER: 09/837,306

PRIOR FILING DATE: 2001-04-17

PRIOR APPLICATION NUMBER: 09/837,306

PRIOR FILING DATE: 2010-04-17

NUMBER OF SEQ ID NOS: 635

SOFTWARE: Patentin Ver. 2.1

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  US-10-045-674A-593
   US-10-045-674A-593
   Best Loc
Matches
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   В
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   В
   Query Match
  Sequence 593, Applic GENERAL INFORMATION:
   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: nucleotide sequence
  APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: WASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
  NAME/KEY: CDS
LOCATION: (1)..(1305)
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995 TYGGYGAYGTYWSYGGYCTKGCTAAYGGYAAYGGWGCYACYGGWGAYTTYGCWGGYTCKA 1054
   140 ттасссетсттеттасссатсавантессаственственавлееватсесствантетс
  815 GYMSYGARGGMGGYGGYMSYGGRÒGYGGYMSYGGYMSYGGYGAYTTYGAYTAYGARAARA 874
  755. CWCCKGTYAAYGCKGGYGGYMSYGGYGGYMGGYMSYGGYGGYMSYGARGGYGGWG
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  TGGCWAAYGCYAAYAARGGSGCYATGACYGARAAYGCYGAYGARAAYGCRCTRCARWSTG

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   ĠĠĊſŢŢĠĠŢĀĀĊĀĀĊĠĊĠĀĊĊĠĊŢĊĀŢĊĀĠŢĀĊŢĀĀ 396
   ggcaaciggrectgeagttgaccagactgeatctaactcctcccccaacgtgactcag
  GGTTTTGGCAACACGCCACGGCTAACCAGTATTAA 456
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; GENERAL INFORMATION:
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  δ
  문
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  문
  RESULT 4
US-10-021-698A-1216/c
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   RESULT 5
   US-10-021-698A-1216
  APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.45EC21
CURRENT APPLICATION NUMBER: US/10/775,972
CURRENT APPLICATION NUMBER: US/10/775,972
CURRENT FILING DATE: 2004-02-10
NUMBER OF SEQ ID NOS: 563
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 153
TENETROL 2007
   Sequence 1216, Application US/10021698A GENERAL INFORMATION:
   Matches 104; Conservative
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Best Local
   SEQ ID NO 1216
  APPLICANT: PANDIT, SUNIL
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: 2976-4044US1
CURRENT APPLICATION NUMBER: US/10/021,698A
CURRENT FILING DATE: 2001-10-22
   NUMBER OF SEQ ID NOS: 6160
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PRIOR FILING DATE: 2000-06-14
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  ACGCTAAAAACTCCGATATTACTGTCGGCCAATAC 354
  VAN EERDEWEGH, PAUL
DUPUIS, JOSEE
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   ALLEN, KRISTINA
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US-10-021-698A-796/c
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   ; ORGANISM: Homo sapiens 
US-10-775-972-154
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CURRENT FILING DATE: 2004-02-10
NUMBER OF SEQ ID NOS: 563
  APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
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APPLICANT: KEITH, TIM
APPLICANT: LITTLE, RANDALL
APPLICANT: VAN EERDEWEGH, PAUL
APPLICANT: DUPUIS, JOSEE
APPLICANT: DEL MASTRO, RICHARD

SIMON,

APPLICANT: ALLEN, KRISTINA
APPLICANT: PANDIT, SUNIL
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY

ö

ILE REFERENCE: 2976-4044US1

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  ; OTHER INFORMATION: Clone ID: US-10-767-701-8827
  APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 63128
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  Sequence 8827, Application US/10767701
GENERAL INFORMATION.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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   NAME/KEY: unsure
LOCATION: (1)..(1099)
OTHER INFORMATION: unsure at
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  76;
  167 GGTGATGATGATGATGATGGT 144
  205 ассаттасссаваесееттатеетаасеесесеатетаеессаееетесееатаатает 264
  287 GÓTGATÓGTGÓTGÁTGATGGTGATGCTGATGGTGATGGTGACGGTGÁTGATGÁTGGT 228
   145
  347
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   Sequence 27, Application US/10788792
GENERAL INFORMATION:
APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Eveleigh, Deepa
APPLICANT: Bigwood, Douglas
TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF I
  밁
   Ş
   US-10-624-149A-1
          FILE REFERENCE: 5152
CURRENT APPLICATION NUMBER: US/10/788,792
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US
  ORGANISM: Equine herpesvirus 1
PUBLICATION INFORMATION:
AUTHORS: Telford, E.A.
AUTHORS: Watson, M.S.
AUTHORS: McBride, K.
  Matches
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US-10-624-149A-1
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  GENERAL INFORMATION:
APPLICANT: Neubauer, Antonie
APPLICANT: Ziegler, Christina
TITLE OF INVENTION: gM-Negative EHV-Mutants without Heterologous
FILE REFERENCE: 1/1372
  CURRENT APPLICATION NUMBER: US/10/624,149A CURRENT FILING DATE: 2003-07-21 PRIOR PELICATION NUMBER: 60/403,282 PRIOR FILING DATE: 2002-08-14 PRIOR APPLICATION NUMBER: DE 10233064 PRIOR FILING DATE: 2002-07-19
  DATABASE ACCESSION NUMBER: NC 0 DATABASE ENTRY DATE: 2000-08-01
  SOFTWARE: PatentIn Version 3.0
  PRIOR APPLICATION NUMBER: DE 10317008 PRIOR FILLING DATE: 2003-04-11 NUMBER OF SEQ ID NOS: 2
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  PAGES: 304-316
DATE: JUL-1992
  AUTHORS: Davison, A.J.
TITLE: The DNA sequence of
JOURNAL: Virology
   VOLUME: 189
  TYPE: DNA
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   ССGАТGTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAA 295
  ATAATGCCACÇATÇGACÇAGTGG 318
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  Application US/10624149A
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   ÇGGTTATGGTAACGGCGCCGATGTAGGCCAGG
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PRIOR FILING DATE: 2003-02-28

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  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-788-792-27
Sequence 6329, Application US/10767795

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei
APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated ITITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53534)B

CURRENT APPLICATION NUMBER: US/10/767,795

CURRENT PILING DATE: 2004-01-30

NUMBER OF SEQ ID NOS: 117596
   Sequence 1287, Application US/10767701 GENERAL INFORMATION:
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SEQ ID NO 1287
  SOFTWARE: PA
  Matches
  Matches
  Query Match
Best Local Similarity
  APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plante and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53535) B
FULL REPERENCE: 38-21 (53535) B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
  NUMBER OF SEQ ID NOS: 254
SOFTWARE: PatentIn version 3.2
  NAME/KEY: unsure
LOCATION: (1)..(883)
OTHER INFORMATION: unsure at
   ORGANISM: Sorghum bicolor FEATURE:
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   112 AGTTCCGGCCCGGACTATGA 131
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   317 GGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGTAATAACGCCGCGCGCTGG
  49;
  59;
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   GGATTTCCATACAGTCTGACCGTGCAGTTGCTCAGTTCGGTCAAAAAGAACGTCGCGCTGG
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   6.8%;
55.7%;
   6.7%;
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; Pred. No. 1.5;
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  ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS13462
US-10-767-701-12486
   RESULT 13
US-10-767-701-12486/c
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   US-10-767-795-6329
  NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 12486
LENGTH: 1203
   Matches
   Query Match
Best Local Similarity
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   SEQ ID NO 6329
LENGTH: 989
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Best Local Similarity
  FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
   TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
  APPLICANT: Kovalic, David APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei
  LENGTH: 989
TYPE: DNA
ORGANISM: Gossypium hirsutum
   TYPE: DNA
ORGANISM: Sorghum bicolor
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OTHER INFORMATION: Clone ID: GOSHI-09MAY01-C1002_1
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  84 CGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGCCCGGACTATGATCAGCTGGTTAC 143
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   TGGTGGTGGTGATGATGGTATCCATAAGCATGGCCACCAAGATATGAACTTGGAAAG
  Zhou, Yihua
Cao, Yongwei
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49.7%;
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Page 6
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
ITILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(5335)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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LENGTH: 656
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: 11064914
US-10-767-701-20611
Search completed: March 17, 2004, 08:25:47 Job time: 70.6301 secs
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; GENERAL INFORMATION:
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; ORGANISM: Sorghum bicolor
; FEATURE:
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  179 A 179
  666 CTGGCGTAGCCGAAGTAGGGGATGACGGCGGTGATGTTCTTGGCGGAGGCCCTCCGGCAG
  546 A 546
  606 GCGTCGÁTCÁTGÁTGÁGGAGCTCCATGAGGTTCTCGTTGGCTGGÁGGGCÁGGTGGGCTGC 547
  119 GCCCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCACTGC 178
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  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-543-407-19

Sequence 19, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Doran, James L.

APPLICANT: Collinson, S. Karen

APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR

TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS

FILE REFERENCE: 920043,406

CURRENT APPLICATION NUMBER: US/09/543,407

KUMBER OF SEQ ID NOS: 59

SOFTWARE: FastSEQ for Windows Version 4.0

TYPE: DNA

TYPE: DNA
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ORGANISM: Artificial Sequence
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Match
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  S US-09-233-642A-56

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24 US-09-543-407-27

25 US-09-543-407-27

26 US-09-543-407-27

27 US-09-741-873B-3

27 US-09-741-873B-1

28 US-09-741-886-172

29 US-09-741-873B-1

20 US-09-741-873B-1

20 US-09-741-873B-1

20 US-09-752-691C-172

20 US-09-753-407-9

20 US-09-753-407-9

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20 US-09-543-407-9

20 US-09-1543-407-9

20 US-09-1543
   US-09-543-407-19
US-08-233-642A-56
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  ALIGNMENTS
  AL SYSTEM FOR HETEROLOGOUS
  PEPTIDE SEQUENCES
   Sequence 19, Appl
Sequence 56, Appl
Sequence 17, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 21, Appl
Sequence 23, Appl
Sequence 21, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
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Sequence 17, Appl
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Sequence 172, Appl
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Sequence 1
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US-08-23.

Sequence 56, Applic.

GENERAL INFORMATION:
APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Doran, James L.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SALMONELLA-
ITITLE OF INVENTION: BASED VACCINES
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: 58
NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
Ceattle
  RESULT 2
US-08-233-642A-56
                                       STREET: 630 Columbia Center, 701 F
STREET: 630 Columbia Center, 701 F
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,642A
PILING DATE: 26-APR-1994
  US-09-543-407-19
  Matches 456;
  Query Match
Best Local
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION
NAME: King, Joshua
   FEATURE:
OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga
OTHER INFORMATION: sequence containing the replacement fragment
OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  Local
  421
  421
   361
   361
  301
  301
   241
  181
  181
   121
  121
  61
   61
  1 ATGAAACTITTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   _
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  gcageccaggerecegataataetactattgaactgactcagaatgetttcagaataat
  Similarity
   AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT
  ccesacricaacerreaecarriarcaeraceerrececraacecrececrrecerecaa
   GGCGTCGTTCCACAATGGGGCGGCGGCGGCAGTAATCATAACGGCGGCGGCAGCAATAGTTCCGGC
   AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGGTGTTGTTACCCCATGAAATGGCACAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  afgaaactitttaaaactgecaccattcecaccaatcctactactrictecccct
  Conservative
   100.0%; Sc.
100.0%; Pr
   US/08/233,642A
  Score 456; DI
Pred. No. 2.1
0; Mismatches
  Version
   456; DB 23;
No. 2.1e-136;
  #1
   456
  456
  Length
  Indels
  o
;-
   Gaps
  300
  420
  420
   360
  360
  300
   240
   240
  180
   180
   120
  120
  60
```

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEI
FILE REFERENCE: 92003.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT TILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTMARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
  RESULT 3
US-09-543-407-1
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; LOCATION: 1...
US-08-233-642A-56
   Sequence 1, Application US/09543407 GENERAL INFORMATION:
   Query Match
Best Local Similarity
   Matches
   REFERENCE/DOCKET NUMBER: 920
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 56:
LENGTH: 456
TYPE: DNA
ORGANISM: Salmonella
  SEQUENCE CHARACTERISTICS:
LENGTH: 456 base pairs
TYPE: nucleic acid
  TOPOLOGY:
  STRANDEDNESS:
  REGISTRATION NUMBER:
   361
  301
   301
  241
   241
  181
  181
   121
   429;
  421
  421
  361
  121
  61
   61
  μ
  μ
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCGCTCTGCGAA
   GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGCC
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTTCTGGCAGTGCTCTGGCT
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCCAATAGTTCCGGC
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   Conservative
  linear
  single
 enteritidis
   90.5%;
94.1%;
   920043.403C3
   0;
  Score 412.8; DB 6;
Pred. No. 2.1e-122;
0; Mismatches 27;
   PEPTIDE SEQUENCES
   Indels
   Length
  456;
   0
   360
  420
  300
  240
   180
   180
  120
  300
   240
   120
  60
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   RESULT 4
US-09-543-407-25
   ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-25
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   US-09-543-407-1
   CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 456
   Sequence 25, Application US/09543407 GENERAL INFORMATION:
  Query Match
Best Local
  Matches 429;
   Query Match
   APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS
  FILE REFERENCE: 920043.406
  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
  Local Similarity
  ocal Similarity
  421
   421
   361
  361
   301
   301
  241
  241
   181
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  121
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 5
   61
  19
  1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
   1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
 GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
                                  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCCAATAGTTCCGGC
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   Conservative
  Conservative
   90.5%;
94.1%;
  84.6%;
  Score 385.6; DB 23;
Pred. No. 1.4e-113;
0; Mismatches 44; I
  <u>.</u>
  Score 412.8; DB 23
Pred. No. 2.1e-122;
D; Mismatches 27;
   DB 23;
   PEPTIDE SEQUENCES
   Indels
  Indels
  Length 456;
   Length
  0
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   Gaps
  Gaps
  420
   180
  120
                                  60
   60
   420
   360
   360
  300
   300
   240
  240
  180
   60
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RESULT 5

US-09-543-407-17

Sequence 17, Application US/09543407

GENERAL INFORMATION:

APPLICANT: White, Aaron P.

APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.

TITLE OF INVENTION: BACTERIAL FIMERIAL SYSTEM FOR
FILE REFERENCE: 920043-406

CCURRENT APPLICATION UNMBER: US/09/543,407

KUNMBER OF SEQ ID NOS: 59

SOPTWARE: FastSEQ for Windows Version 4.0

LENGTH: 456

TYPE: DNA
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   Matches
   Query Match
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  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
  121
  121
   61
  61
  al Similarity
398; Conserv
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   421
   421
  361
  361
                AGGGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTTACCCATGAAATGGCACAT 240
  301
  301
  241
  CCGGACTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCAACTGCAA
  241
  181
  СССВАСТСААССЕТТВАССАТТТАТСАСТАССВТТСССТАДСССТВССТВССТВСТВСТВСТВ
  181
  121
AĞCĞATĞCĞĞTAAATCTĞAAACĞACĞATTAĞĞĞĞAGAGGĞĞTTATGGTAACGGÇĞĞĞT
   GCCGTCGTTCCACAATGGGCCGCCGCGCGTAATCATAACGGCGGCGGCGGCAATAGTTCCCGGC
   121
  61
  ĠĠŦŦŦŤĠĠĊĄĄĊĄĄĊĠĊĊĄĊĠĠĊŦĄĄĊĊĄĠŦĄŦŤĄĄ
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCGCTGGTTAATCAGACCGCATCTGATTCCGAGCGTAATGGTGCGTCAGGTT
   AATAACGCCGGGCTGGTTAATCAGACCGCATCTGATTCCAGGCGTAATGGTGCGTCAGGTT
  ĠĊĊĂĊĠĂŤĊĠĀĊĊĀĠŦĠĠĀĀĊĠĊŦĀĀĀĀĀĊŦĊĊĠĀŦĀŦŦĀĊŦĠŦĊĠĠĊĊĀĀŦĀĊĠĠĊĠĠŦ
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCCGGT
  GTÁGGCCAGGGTGCGGATÁATAGTÁCTATTGAACTGÁCTCAGAATGGTTTCAGAAATAAT
   GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
   CTGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCAGGTTATGGTAACGGCGCCGAT 240
   AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTACCCCATGAAATGGCACAT
  ccedacrcaacerraaccarrrarcaeracerrccerracecrracecrrarearcae 180
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  Conservative
   79.6%;
   Score 363.2; DB 23;
Pred. No. 2.5e-106;
0; Mismatches 58;
  456
   PEPTIDE SEQUENCES
   Indels
   Length 456;
  0,
   Gaps
  180
  120
  120
  300
   420
  360
  360
   240
   120
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RESULT 6
US-09-543-407-11
Sequence 11, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, ABTON P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PERISE FRANCE: 920043.406
CURRENT FILING DATE: 2000-04-05
SCURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER TETEROGRAFIA
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   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-11
   Query Match
Best Local S
Matches 397
   Š
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   В
   8
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   S
  361 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
                                   361
   301
   301
   241
   181 AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTTACCCATGAAATGGCACAT 240
  241
  121
   121
  61
  397;
   61
   1 ATGAAACTTTTAAAAGTGGCAGCAGTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  421
   421
   361
   361
  301
AATAAÓGCÓGÓGCTGGTTAATTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATG
  n. 79.3%; Score 361.6; DB 23; Similarity 87.1%; Pred. No. 8.2e-106; 97; Conservative 0; Mismatches 59; 1
   GTÄGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
  AĞCĞATĞCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   ccddachcaacdrigadcarrrarcagracdgrirccdcriaacdcrigcdcrirdcricigcaa
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  ĠĠĊĠŦĊĠŦŦĊĊĂĊĂĂŤĠĠĠĠĠĠĠĠĠĠĠĠĠŦĂĂŦĊĂŦĂĂĊĠĠĊĠĠĊĠĠĊĀĂŦĂĠŦŦĊĊĠĠĊ
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  ĠĠŦŦŦŦĠĠĊĀĀĊĀĀĊĠĊĊĀĊĠĠĊŦĀĀĊĊĀĠŦĀŦŦĀĀ 456
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGGCGTAATGGTGCGTCAGGTT
   deceacea reacea de la compara 
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT 360
  PEPTIDE SEQUENCES
   Indels
   Length 456;
   0,
   Gaps
  420
  420
   360
   360
  300
   300
   240
  180
   180
  120
   60
   0
   420
  420
  360
  300
  300
```

```
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PER FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
           RESULT 8
US-09-543-407-23
; Sequence 23, Application US/09543407
; GENERAL INFORMATION:
; APPLICANT: White, Aaron P.
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  ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-13
  RESULT 7
US-09-543-407-13
  밁
  S
  Sequence 13, Application GENERAL INFORMATION:
  Matches
  Query Match
Best Local
  APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
   421
   361
   361
   301
   301
   241
   241
   181
   181
   121
   121
  421
   421
   61
  al Similarity
397; Conserv
   61
   _
   _
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCCGGC
   GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   GGCGTCGTTCCACAATGGGGCGGCGGCGGCAATAGTTCCGGC
   CTGGTTACCCGTGTTACCCATGAAATGGCACATGCAAGCGTAATGGTGCGTCAGGTT
   AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATATGATCAG
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   AGCGATGCCCGTAAATCTGAAAACGACCATTACCCCAGAGCGGTTATGGTAACGGCGCCGAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  GCACATGCAÁACAÁCGCCACGCTAACCAGTATTAA 456
  79.3%; ilarity 87.1%; Conservative
  US/09543407
  Score 361.6; DB 23; Pred. No. 8.2e-106; 0; Mismatches 59;
   456
  456
  PEPTIDE
  Indels
  Length
  456;
  ..
..
   360
   300
   240
   240
   180
   120
   60
RESULT 9
US-09-543-407-15
Sequence 15, Application US/09543407
GENERAL INFORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEP
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FastSEQ for Windows Version 4.0
  APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BROTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENVATION OF HETEROLOGOUS PEI
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 23
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  US-09-543-407-23
  Query Match
Best Local Similarity
  Matches
  OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA OTHER INFORMATION: sequence containing the replacement fragment OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
  LENGTH: 456
TYPE: DNA
  ORGANISM: Artificial Sequence FEATURE:
  397;
   181
   421
   421
   361
   361 AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   301
   301
   241
   241
   181
   121
  121
  61
  61
  1 ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCGCTCTGCAA 180
  GGCGTCGTTCCACAATGGGGCGGCGGCGGCGAATAGTTCCGGC
   CATGAAATGGCACATGCAAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC 120
   AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   GCCACCATCGACCAGTGGAACGCTAAAAACTATGATCAGCTGGTTACCCGTGTTGTTACC
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCCT
  Conservative
  79.3%;
  0
  Score 361.6; DB 23;
Pred. No. 8.2e-106;
"" matches 59;
  DB 23;
   PEPTIDE SEQUENCES
  PEPTIDE SEQUENCES
  Indels
  Length
  0,
```

240 180

240

300

300

420

420

360

360

120

60

Gaps

```
APPLICANT: White, Maron P.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
FILE REFERENCE: 920043,406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOPTWARE: FastSEQ for Windows Version 4.0
TYPE: DNA
TYPE: DNA
  ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragment; OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-27
   RESULT 10
US-09-543-407-27
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     Best Local Similarity
  Sequence 27, Application US/09543407
GENERAL INFORMATION:
  US-09-543-407-15
   ORGANISM: Artificial Sequence FEATURE:
  Matches
   Query Match
Best Local
   OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
  LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
  421
   421
   361
  361
  301
   301
   241
  241
  181
   181
  121
  121
  62
   61
  396;
  -
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  Similarity
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   AGCGĂTGCCCGTÀAATCTGÁAACGACCATTACCCAGAGCGGTTATGGTAÁCGGCGCCGÁT
   AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
   GCCGTCGTTCCACAATGGGGCCGCGGGGAATAATCATAACGGCGGCGGCAATAGTTCCGGC
   GÉCGTETATGATEAGETGGTTACCCGTGTTGTTACCCATGAAATGGCACATGCATCCGGC
  atgaaacttttaaaagtgecageattegeageaategtagtttetgecagtgetetget
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAGTCGTAGTTTCTGGCAGTGCTCTGGCT
   Conservative
   Recombinant Salmonella enteritidis 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of Leishmania major.
   78.9%;
86.8%;
   78.9%;
Score 360; DB 23;
Pred. No. 2.7e-105;
  Score 360; DB 23;
Pred. No. 2.7e-105;
0; Mismatches 60;
   456
   PEPTIDE
             Length 456
   Length 456;
  Indels
   SEQUENCES
   0
   Gaps
  420
   420
   360
   300
   240
   120
   240
   180
   120
  60
  60
```

```
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Doran, James L.
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
ITILE OF INVENTION: PRESENTATION OF HETEROLOGOUS PBP
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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   US-09-543-407-21
   RESULT 11
US-09-543-407-21
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  Matches
   Query Match
   Sequence 21, Application US/09543407 GENERAL INFORMATION:
   OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afga OTHER INFORMATION: sequence containing the replacement fragmen OTHER INFORMATION: encoding PT3 from GP63 of Leishmania major.
   Matches
  Local
   395;
   61
  61
   421
  421
  361
  361
   301
   301
  241
  181
  241
   181
   121
   121
  Similarity 86.0
95; Conservative
   61
  61
   396;
CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA 180
  GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCGATAGTTCCGGC 120
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
                                GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  ATGAAA CTTTTAAAA GTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  ш
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
   gécacearegaecaeregaacecraaaaacecegararracreceseceararaces
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCCGATATTACTGTCGGCCAATACGGCGGT
  TATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCATTCAGAAATAAT
  AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
  AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACAT 240
   ccedacticalcerrigagearritateagraceerriceerraleerrigerigeaa
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTTGCGCTTGCTCTGCAA 180
  GGCGTCGTTCCÁCAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC
  GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGC 120
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTTCTGGCAGTGCTCTGGCT
  atgaaactittaaaagtgeeageattegeageaategtagtttetegeagtgetetget
   Conservative
   78.6%;
  0;
  Score 358.4; DB 23; Pred. No. 8.9e-105; 0; Mismatches 61;
  0;
  Mismatches
   456
  60;
   PEPTIDE SEQUENCES
  Indels
   Length 456;
  0
   0
   Сарв
                                120
  60
  60
   420
  420
   360
   360
   300
   120
  240
   180
  0
  6
  60
   0
```

```
APPLICANT: White, Aaron P.
APPLICANT: White, Aaron P.
APPLICANT: Collinson, S. Karen
APPLICANT: Collinson, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 456
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
COLUMN TARGET TO THE PROSENTION OF THE PROPERTY OF THE P
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  ; OTHER INFORMATION: Recombinant Salmonella enteritidis 3b afgA; OTHER INFORMATION: sequence containing the replacement fragmen COTHER INFORMATION: encoding PT3 from GP63 of Leishmania major. US-09-543-407-29
  RESULT 12
US-09-543-407-29
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   Sequence 29, Application US/09543407 GENERAL INFORMATION:
  Query Match 77.9%;
Best Local Similarity 86.2%;
Matches 393; Conservative
  241
  181
  181
   241
   181
   121
   121
  361
   361
   301
   301
   241
  241
  181
   121
   421
  61
  61
  421
  _
   \vdash
  GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT 300
  AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATGGCACAT 240
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCCTAACGCTGCGCTTGCTCTGCAA 180
   GGCGTCGTTCCACAATGGGGCGGCGGCGGCGGTAATCATAACGGCGGCGGCGGCAATAGTTCCGGC
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   ATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   GTAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
  GGCGTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCCGGC
   AGCGATGCCCGTAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
  ATGAMACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT
  ATGAAACTTTTAAAAGTGGCAGCATTCGCAGCAATCGTAGTTTCTGGCAGTGCTCTGGCT 60
   GCACATGCAGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  GTAGGCCAGGGTGCGGATAATTATGATCAGCTGGTTACCCGTGTTGTTACCCATGAAATG
  CGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAA
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTACCCCATGAAATGGCACAT 240
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  PAAATCTGAAACGACCATTACCCAGAGCGGTTATGGTAACGGCGCCGAT
   0
   Score 355.2; DB 23; Pred. No. 9.7e-104; 0; Mismatches 63;
   Indels
   Length 456;
  0
   Gaps
  120
   60
   240
  180
  240
   180
   120
   420
   420
  360
  360
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   RESULT 13
US-08-233-642A-54
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  US-08-233-642A-54
   Sequence 54, Application US/08233642A
GENERAL INFORMATION:
APPLICANT: Kay, William W.
APPLICANT: Collinson, S. Karen
APPLICANT: Clouthier, Sharon C.
   Matches
   Query Match
  ZIP: 98104-7092

ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: FlOppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN PC-DOS/MS-DOS

SOFTWARE: PATENTIN PC-DOS/MS-DOS

SOFTWARE: PATENTIN DATA:

APPLICATION NUMBER: US/08/233,642A

PILING DATE: 26-APR-1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: King, JOShua

REGISTRATION NUMBER: 95,570

REFERENCE/DOCKET NUMBER: 920043.40:

TELECOMMUNICATION INFORMATION:
  TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
TELEX: 3723836 SEEDANBERRY
INFORMATION FOR SEQ ID NO: 54:
   FEATURE:
  MOLECULE TYPE:
   SEQUENCE CHARACTERISTICS:
LENGTH: 361 base pairs
TYPE: nucleic acid
  CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701
  APPLICANT: Doran, James L.
  NAME/KEY:
LOCATION:
   STATE: Washington COUNTRY: U.S.A.
   Local Similarity es 306; Conserv
  STRANDEDNESS:
  CITY: Seattle
   421
   361
  361
   301
                                  124 GACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTGCAAAGC 183
  421
   301
61
   64 GTCGTTCCACAATGGGGCGGCGGCGGTAATCATAACGGCGGCGGCAATAGTTCCGGCCCG 123
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
   GCCACCTATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACATGCAGGCGGT
   GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
   Conservative
   CDS
  linear
  NUMBER: US/08/233,642A
26-APR-1994
  DNA (genomic)
  double
   63.3%;
   BASED VACCINES
58
  METHODS AND COMPOSITIONS FOR SALMONELLA-
   920043.403C3
   0;
   Score 288.6; DB 6;
Pred. No. 3.4e-82;
0; Mismatches 29;
  Version
  Fifth Avenue
  #
   Indels
  Length 361;
   0;
   Gaps
  420
   420
   360
 120
   60
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184

RESULT 14 US-09-543-407-3

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301 364 241

AACGCCGCGCTGGTTAATCAGACCGCATCTGATTC 335 AACGCCGCGCTGGTTAATCAGACCGCATCTGATTC 398 304 181 244

```
Sequence 3, Application US/09543407
GENERAL IMPORMATION:
APPLICANT: White, Aaron P.
APPLICANT: Doran, James L.
APPLICANT: Collineon, S. Karen
APPLICANT: Kay, William W.
TITLE OF INVENTION: BACTERIAL FIMBRIAL SYSTEM FOR
TITLE OF INVENTION: PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES
FILE REFERENCE: 920043.406
CURRENT APPLICATION NUMBER: US/09/543,407
CURRENT FILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 59
SOFTWARE: FASISEQ for Windows Version 4.0
LENGTH: 456
TYPE: DNA
  GGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT
  AATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGTCAGGTT
  GCTACTCTTGATCAGTGGAACGGCAAAAATTCTGAAATGACGGTTAAACAGTTCGGTGGT
  GCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATACGGCGGT
  ĠŦŦĠĠŦĊĀĠĠĠĊŦĊĀĠĀŦĠĀĊĀĠĊŦĊĀĀŦĊĠĀŦĊŦĠĀĊĊĊĀĀĊĠŦĠĠĊŦŤĊĠĠŦĀĀĊĀĠC 300
  GCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAAT
   ACTGATGCCCGTAACTCTGACTTGACTATTACCCAGCATGGCGGCGGTAATGGTGCAGAT
   AGCGATGCCCGTAAATATGATCAGCTGGTTACCCGTGTTGTTACCCCATGAAATGGCACAT
  CCAAATTCTGAGCTGAACATTTACCAGTACGGTGGCGGTAACTCTGCACTTGCTCTGCAA
  CCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCGTTGCTGCAA
   GECGTCGTTCCACAATGGGGCGGCGGCGGCGATAATCATAACGGCGGCGGCAATAGTTCCGGC
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  CURRENT FILING DATE: 1997-11-26

EARLIER APPLICATION NUMBER: SE 8801723-1

EARLIER FILING DATE: 1998-05-06

EARLIER FILING DATE: 1988-05-06

EARLIER FILING DATE: 1989-05-06

EARLIER FILING DATE: 1989-05-04

EARLIER APPLICATION NUMBER: US 07/789,437

EARLIER APPLICATION NUMBER: US 07/789,437

EARLIER APPLICATION NUMBER: US 07/970,846

EARLIER APPLICATION NUMBER: US 07/970,846

EARLIER APPLICATION NUMBER: US 08/187,865

EARLIER FILING DATE: 1992-11-03

EARLIER FILING DATE: 1994-01-28

EARLIER APPLICATION NUMBER: US 08/187,865

EARLIER FILING DATE: 1994-00-5

EARLIER APPLICATION NUMBER: US 08/318,519

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EARLIER APPLICATION NUMBER: US 08/495,959

NUMBER OF SEQ ID NOS: 10

SOPTWARE: PATENTIN DATE: 1995-06-28

SOPTWARE: PATENTIN Ver. 2.0

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ORGANISM: Escherichia coli
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; LOCATION: (83)
US-08-978-878-3
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   Sequence 3, Application US/08978878
GENERAL INFORMATION:
APPLICANT: NORMARK, Staffan
APPLICANT: OLSEN, Arne
TITLE OF INVENTION: FIBRONECTIN BINDING PROTEIN AS WELL
FILE REFERENCE: 012889-081
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  83
   319;
   ш
   n 51.9%;
Similarity 70.0%;
19; Conservative
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   ggcáacegrectecaetre accada creca de creca de consecuencia de c
   GTTGGTCÁGGGCTCAGÁTGACAGCTCAÁTCGATCTGÁCCCÁACGTGGCTTCGGTÁACAGC
  GCTĂCTCTTĠATĊĀĠŦĠĠĀĀĊĠGCĀĀĀĀĀTTĊTGĀĀĀTGĀĊĠĠŦTĀĀĀĊĀĠŦŦĊĠĠŦĠĠŦ
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Similarity

51.9%;

181 121 121

61 61

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Query Match Best Local

TYPE: DNA ORGANISM: E. S-09-543-407-3

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421 421 361 361 301 301 241 241 181

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456

Search completed: March 18, 2004, 02:47:09 Job time: 2925.24 secs

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Minimum
Maximum
  Result
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Maximum Match 100%
Listing first 45 summaries
  Total number of hits satisfying chosen parameters:
   Database
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   Title:
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1, Appli
27, Appl
2643, App
28437, App
217, App
29, Appli
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|----------------------------------------|--------------------|----------------------------------------|-------------------|---------------------|-------------------|--------------------|------------------|--------------------|--------------------|--------------------|---------------------|---------------------|---------------------|--------------------|--------------------|--------------------|
| 44.5                                   | 4 4<br>4 3         | 4 2                                    | 40                | 39                  | 38                | 37                 | 36               | 35                 | 34                 | ω<br>U             | 32                  | 31                  | 30                  | 29                 | 28                 | 27                 |
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| 0.0                                    | ט ט                | σ σ                                    | <b>ν</b> Φ        | 6                   | 6                 | σ                  | σ                | 7                  | 7                  | σ                  | σ                   | σ                   | σ                   | σ                  | 7                  | 7                  |
| US-10-100-683-11419                    | US-10-453-372-1187 | US-10-453-372-1185                     | US-10-773-236-118 | US-10-767-701-12607 | US-10-784-004-232 | US-10-100-683-3854 | US-10-781-469-57 | US-60-545-213-6292 | US-60-545-213-2020 | US-10-767-701-3483 | US-10-767-701-19620 | US-10-767-701-17923 | US-10-767-701-29572 | US-10-767-795-3735 | US-60-545-213-6407 | US-60-545-213-6406 |
| sequence 3499, Ap<br>Sequence 11419, A |                    | Sequence 1185, Ap<br>Sequence 1173, Ap | Sequence 118, App |                     |                   |                    |                  | Sequence 6292, Ap  | Sequence 2020, Ap  | Sequence 3483, Ap  | Sequence 19620, A   | 17923,              | 29572,              | 3735,              |                    | Sequence 6406, Ap  |

## ALIGNMENTS

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APPLICANT: NORMATK, Staffan
APPLICANT: Olsen, Arne
TITLE OF INVENTION: Fibronectin Binding Protein As Well As
FILE REFERENCE: 012889-084
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 0801723-1
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 07/347,189
PRIOR FILING DATE: 1999-05-04
PRIOR APPLICATION NUMBER: US 07/89,437
PRIOR FILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/789,437
PRIOR FILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR PILING DATE: 1994-10-28
PRIOR FILING DATE: 1994-10-28
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SEQ ID NO 3
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113, App 5480, Ap 5480, Ap 3397, Ap 5725, Ap 5725, Ap 22688, A 8781, Ap 8781, Ap 924, App 31417, Ap 31417, Ap 2134, Ap 2134, Ap 2134, Ap

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Sequence

Sequence Sequence

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US-09-741-873C-1
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PRIOR PILING DATE: 1989-05-04
PRIOR PELICATION NUMBER: US 07/789,437
PRIOR PILING DATE: 1991-11-06
PRIOR APPLICATION NUMBER: US 07/970,846
PRIOR PILING DATE: 1992-11-03
PRIOR PILING DATE: 1992-11-03
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/187,865
PRIOR APPLICATION NUMBER: US 08/318,519
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269; Conservative
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US-09-741-873C-1
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   Sequence 1, Applicat: GENERAL INFORMATION:
   APPLICANT: Normark, Staffan APPLICANT: Olsen, Arne TITLE OF INVENTION: Fibronectin Binding Protein As Well As Its Preparation FILE REFERENCE: 012889-084 CURRENT APPLICATION NUMBER: US/09/741,873C CURRENT FILING DATE: 2000-12-22
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  PRIOR APPLICATION NUMBER: SE 8801723-1
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 08/978,878
PRIOR FILING DATE: 1997-11-26
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; ORGANISM: Homo s
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US-10-788-792-27/c
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  Query Match
Best Local Similarity
   SOFTWARE: PatentIn version 3.2 SEQ ID NO 27
   Sequence 27, Application US/10788792 GENERAL INFORMATION:
  APPLICANT: Bayer Pharmaceuticals Corporation
APPLICANT: Eveleigh, Deepa
APPLICANT: Eveleigh, Deepa
APPLICANT: Eveleigh, Deepa
APPLICANT: Bigwood, Douglas
TITLB OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
TILE REFERENCE: 5152
CURRENT FAILURG ANTE: 2004-02-27
ERIOR APPLICATION NUMBER: US 60/450,655
PRIOR APPLICATION NUMBER: US 60/450,655
PRIOR FILING DATE: 2003-02-28
NUMBER OF SEQ ID NOS: 254
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   181 GTTGGTCAGGGCTCAGATGACAGCTCAATCGATCTGACCCAACGTGGCTTCGGTAACAGC
TGCAACTCGCTGGCTCTCTTCTCCAAGACTTGGGACTCCAGGTTGG 583
   GGCTTTGGTAACAACGCGACCGCTCATCAGTACTAA
   GGTTTTGGCAACAACGCCACGGCTAACCAGTATTAA 456
  GGCAACGGTGCTGCAGTTGACCAGACTGCATCTAACTCCTCCGTCAACGTGACTCAGGTT 360
   Conservative
   sapiens
  6.8%;
55.7%;
   Score 30.8; DB Pred. No. 1.1; 0; Mismatches
   0;
   DB 6;
   47;
  Length 1575;
   Indels
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   Gaps
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   376
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RESULT 4
US-10-100-683-643
; Sequence 643, Application US/10100683
; GENERAL INFORMATION:
APPLICANT: Rosen, et al.
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS900
CURRENT FILLING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR PILLING DATE: 1997-03-07
PRIOR FILLING DATE: 1997-03-07
PRIOR FILLING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR FILLING DATE: 1997-05-23
PRIOR FILLING DATE: 1997-05-23
PRIOR FILLING DATE: 1997-08-22
PRIOR FILLING DATE: 1997-08-25
PRIOR FILLING DATE: 1997-08-25
PRIOR APPLICATION NUMBER: US 60/043,580
PRIOR APPLICATION NUMBER: US 60/047,599
PRIOR APPLICATION NUMBER: US 60/047,599
PRIOR APPLICATION NUMBER: US 60/047,599
PRIOR APPLICATION NUMBER: US 60/047,599
PRIOR APPLICATION NUMBER: US 60/047,599
PRIOR APPLICATION NUMBER: US 60/047,599
PRIOR APPLICATION NUMBER: US 60/047,599
PRIOR APPLICATION NUMBER: US 60/047,599
PRIOR APPLICATION NUMBER: US 60/047,599
PRIOR APPLICATION NUMBER: US 60/043,314
```

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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Ott
TITLE OF INVENTION: Plants and Uses Thereof For I
FILE REFERENCE: 38-21(53535)8
CURRENT APPLICATION UNMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 28437
  US-10-771-241-117/c
; Sequence 117, Application US/10771241
; GENERAL INFORMATION:
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  밁
  밁
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   ; OTHER INFORMATION: Clone ID: 7551688 US-10-767-701-28437
   US-10-767-701-28437; Application (1984)
  RESULT 5
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   ई
  US-10-100-683-643
  Matches
   Query Match
Best Local Similarity
   GENERAL INFORMATION:
  Matches
  SEQ ID NO 643
   Query Match
APPLICANT: Zyskind, Judith
APPLICANT: Forsyth, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED
TITLE OF INVENTION: ESCHERICHIA COLI
   Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 13468 SOFTWARE: PatentIn Ver. 2.0
  PRIOR APPLICATION NUMBER: US 60/047,632
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,892
PRIOR FILING DATE: 1997-08-22
   TYPE: DNA
ORGANISM: Sorghum bicolor
   TYPE: DNA ORGANISM: Homo sapiens
  FEATURE:
   ENGTH: 300
  ENGTH: 848
  Local
  183
  118 GGCCCGGACTCAACGTTGAGCATTTATCAGTACGGTTCCGCTAACGCTGCGCTTGCTCTG
   238 CATGCAGGCCAGGGTGCGGATAATAGTACTATTGAACTGA 277
  61
  74 AATGGGGCGGCGGTAATCATAACGGCGGCGCAATAGTTCCGGCCCGG 124
  60;
  79;
   Similarity
   GTAAGGGCGGCGGTTATGGCGGCGGCGGCGGTTACGGTGGCAACCGGG
   AAGAAGGCGGTTACGAAGCCGGTGGTTACGGTGGCGGCGGCGGCGGTTACGGCGGTCCCC 182
  ACTGGGTCCCTGGGGGTGGATATTGCTTATATTAGACTTA 160
  AGAAGTAACCCATTTAACTAAAACCAGCTGGTTGGCCCCACTCAGATTTATCAAAGGGTT 120
  ĠĠĊAĊĠAGĊAĊŦĀĊŦGŤAĀĠAGCŤGGŤĊĀĠŤGAATGTGGTTGCAGCATĠGCĊŤŤTGGGCA
   Conservative
  Conservative
   Application US/10767701
   6.7%;
   6.4%;
   Score 29.4; DB Pred. No. 1.5; 0; Mismatches
  0;
   0
  Score 30.4; DB 6; Pred. No. 1.1; 0; Mismatches 81

    See File Wrapper or PALM

  DB 6;
   51;
  81;
   Other Molecules Associated With
                    FOR
  Length 300;
   Length 848;
   Indels
  Indels
                    PROLIFERATION
  0,
                    H
  60
   0
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  US-10-771-241-29
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  ; TYPE: DNA
; ORGANISM: E.
US-10-771-241-117
   US-10-771-241-29
  NUMBER OF SEQ ID NOS: 485
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 29
LENGTH: 757
   Sequence 29, Application US/10771241 GENERAL INFORMATION:
   Query Match
  Matches
   Query Match
Best Local Similarity
   SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 117
   FILE REFERENCE: ELITRA.001C1
CURRENT APPLICATION NUMBER: US/10/771,241
CURRENT FILING DATE: 2004-02-03
  PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
  APPLICANT: Foreyth, R. Allyn
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED
TITLE OF INVENTION: ESCHERICHIA COLI
  APPLICANT: Zyskind, Judith APPLICANT: Forsyth, R. Al
   FILE REFERENCE: ELITRA.001C1
CURRENT APPLICATION NUMBER: US/10/771,241
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
  NUMBER OF SEQ ID NOS:
   TYPE: DNA
ORGANISM: E. Coli
FEATURE:
  OTHER INFORMATION: n = A, T, C or
   NAME/KEY: misc_feature LOCATION: (1)...(757)
   ENGTH:
   Local
                                      324
   295 AATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGATATTACTGTCGGCCAATAC
   415 CA 416
  120 GGCACCGACTATCCCCCAGCAGGATAGTCATAAAGAATCCACCTCCATCTTTACCTGGCAT
   355 GGCGGTAATAACGCCGCCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGT 414
  295 AATAATGCCACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATAC 354
   60 GA 59
   64;
   Similarity
.Ω
                                      GGCACCGACTATCCCCAGCAGGATAGTCATAAAGAATCCACCTCCATCTTTACCTGGCAT
   GGCGGTAATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCAGCGTAATGGTGCGT 414
     416
  Coli
  Conservative
   Conservative
   6.4%;
52.5%;
   52.5%;
   Score 29.2; DI
Pred. No. 2.8;
0; Mismatches
   Score 29.2; DB
Pred. No. 1.6;
0; Mismatches
   0;
   멂
  DB 6;
   58;
   6
  FOR PROLIFERATION
   Length 757;
  Length 249;
   Indels
   0
   0,
   Gaps
   Gaps
   323
  354
  61
   0
```

US-10-048-770C-3/c

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384

GA 385

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TITLE OF INVENTION: ENZYMES
FILE REFERENCE: PF-1507 PCT
CURRENT APPLICATION NUMBER: PCT/US04/04280
CURRENT FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: US 60/447,246
PRIOR FILING DATE: 2003-02-12
PRIOR PPLICATION NUMBER: US 60/449,087
PRIOR PILING DATE: 2003-02-21
PRIOR PILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: US 60/450,622
PRIOR PILING DATE: 2003-02-26
PRIOR APPLICATION NUMBER: US 60/456,704
PRIOR APPLICATION NUMBER: US 60/463,194
PRIOR PILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: US 60/463,194
PRIOR APPLICATION NUMBER: US 60/469,358
PRIOR APPLICATION NUMBER: US 60/469,358
PRIOR APPLICATION NUMBER: US 60/469,358
PRIOR APPLICATION NUMBER: US 60/469,358
PRIOR APPLICATION NUMBER: US 60/469,358
PRIOR APPLICATION NUMBER: US 60/469,358
PRIOR PILING DATE: 2003-04-15
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   PCT-US04-04280-78/c
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   US-10-048-770C-3
  APPLICANT:
  APPLICANT:
   Matches
   Query Match
Best Local :
  SOFTWARE: PatentIn version 3.1 SEQ ID NO 3
   Sequence 3, Application US/10048770C
GENERAL INFORMATION:
APPLICANT: NEW BIOTECHNIC, S.A.
APPLICANT: UNIVERSIDAD DE SEVILLA
   PPLICANT:
   PPLICANT:
   CURRENT APPLICATION NUMBER: US/10/048,770C CURRENT FILING DATE: 2002-01-31 PRIOR APPLICATION NUMBER: PCT/ES00/00292 PRIOR FILING DATE: 2000-07-28
   LENGTH: 1046
TYPE: DNA
ORGANISM: Trichoderma harzianum
   NUMBER OF SEQ ID NOS: 8
   TITLE OF INVENTION: ANTI-FUNGAL COMPOSITIONS AND METHOD FOR CONTROLLING FUNGI
  TI INCYTE CORPORATION; KABLE, Amy E.;
TYUE, Henry; BAUGHN, Mariah R.;
TT TRIBOULEY, Catherine M.; RING, Huijun Z.;
TT TRAN, Uyen K.; EMERLING, Brooke E.;
ST: RAMKUMAR, Jayalaxmi; HAFALIA, April J.A.;
NT: SWARNAKAR, Anita; LEE Soo Yeun;
NT: CHAWLA, Narinder K.; GIETZEN, Kimberly J.;
NT: MARQUIS, Joseph P.; ELLIOTT, Vicki S.;
NT: MARQUIS, Joseph P.; ELLIOTT, Vicki S.;
NT: MARQUIS, Joseph P.; BLLIOTT, Vicki S.;
NT: MARQUIS, Jonathan T.; NAIDU, Sangeeta;
NT: HAWKLNS, Phillip R.; JIN, Pei;
   INFORMATION:
  640 GGCCTGGAACGTTTGAGTGGTGCCACCAGACGTGACC 604
  277 АСТСАGAATGGTTTCAGAAATAATGCCACCATCGACC 313
  217 GITGITĀCCÇAŢGAAAŢĢĢÇACĀŢĢÇAĢĢÇÇAĢĢGŢGCĢĢĀTAĀTĀGŢACTAITĢAACŢG 276
  700
   760 GCAAACGTTGGTGAŤATCĊATĊĀĀŢĠĀĠĠŤTĊĊGCŤĀĀĀGĀCĠGŤĊTĠACCGŤŤĀĊGĀĠŤ
  157
   6.4%;
1 Similarity 49.0%;
77; Conservation
   CAGAGCÂAACTTTTGCTGGCCGÀTGCTGGCCGGGATTTGGAAGAGATTGGCTCCGGCGTT 641
  GCTAACGCTGCGCTTGCTCTGCAAAGCGATGCCCGTAAATATGATCAGCTGGTTACCCGT 216
  Application PC/TUS0404280
   Conservative
NUMBER: US 60/475,532
  0;
   Score 29; DB 6; Length 1046; Pred. No. 3.9;
   Mismatches
   80;
  Indels
   °,
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  ; NAME/KEY: misc_feature
; LOCATION: (1)...(83009)
; OTHER INFORMATION: n = A,T,C or G
US-10-417-375A-143
   US-10-417-375A-143/c
: Sequence 143, Application US/10417375A
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  8
  TITLE OF INVENTION: Novel Therapeutic Targets in Cancer FILE REFERENCE: 529452001600 CURRENT APPLICATION NUMBER: US/10/417,375A CURRENT FILING DATE: 2003-04-15 NUMBER OF SEQ ID NOS: 176 SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 143
   Matches
  Query Match
Best Local :
   PCT-US04-04280-78
  Sequence 143, App
GENERAL INFORMATI
  Best Local Similarity
Matches 69; Conserv
  APPLICANT: David W. Morris APPLICANT: Marc Malandro
   Query Match
Best Local (
   SOFTWARE: PI
SEQ ID NO 78
  LENGTH: 83
  ORGANISM: Mus musculus
  FEATURE:
  PRIOR FILING DATE: 2003-06-02
PRIOR APPLICATION NUMBER: US 60/476,278
PRIOR FILING DATE: 2003-06-04
PRIOR APPLICATION NUMBER: US 60/483,395
PRIOR FILING DATE: 2003-06-27
NUMBER OF SEQ ID NOS: 78
  OTHER INFORMATION: Incyte ID No: 7517280CB1
   ORGANISM: Homo sapiens FEATURE:
   LENGTH: 3816
TYPE: DNA
  NAME/KEY: misc_feature
                 13936
   13996
   14056
   401
  341 CTGTCGGCCAATACGGCGGTAATAACGCCGCGCTGGTTAATCAGACCGCATCTGATTCCA
   281
  2125 GTGCĊAĠĠĊĊACTĠTĠ 2110
  2185
  2245 GGCCATGACAAAGGTATGAGGAAAGAGCATAGCTGCACCCTTCCTCATGCCCTGAAGCTG 2186
   78;
  178 саладосдатдососдтвалататод Садостод тасосд тотта составалатод са
  GAATAATGAGACCTCAGATGGATTACAGGCACGATGCCAC 13897
  Similarity
  GCGTAATGGTGCGTCAGGTTGGTTTTGGCAACAACGCCAC 440
  CTTTCAAGTÁCACTTAAGTTÁÁTGCTTCAATGAAATACAAGCÁGGCACCTATTACTTCTÁ 13937
  AGĀĀTĀTTĀAAĀGAĀTGCATAATATČCTCAĀĀAĀGAACATTGACTĀGTĀTTCCTTTĀTTC 13997
   адалгадттерадалаталгассяссятся десадта в поставлявающей в заправодения деста на применения в поставлявающей в поставлява
  CATGCAGGCCAGGGTG 253
  CACAGTGTTGCCCTGGAACATGACTCCATGCACATCAGTCTCTGTGCCCAGGCCGAGCAG 2126
   PERL
   6.3%;
ilarity 48.8%;
Conservative
   Conservative
  Program
   50.7%;
   ,
,
   Score 28.8;
Pred. No. 38
   ٥,
  Score 28.8;
Pred. No. 8.
  Mismatches
   Mismatches
  38,
   DB 6;
  DB 1;
  82;
   67;
  Length 83009;
   Indels
   Length 3816;
   Indels
   0
   0;
  Gaps
   Gaps
  400
   237
  0
  0,
```

RESULT

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  PCT-US04-05654-1030
  ; OTHER INFORMATION: Predicted polypeptide sequence is orthologous to PCT-US04-05654-1030
  Best Loc
Matches
   Query Match
   SEQ ID NO 1030
   GENERAL INFORMATI
   equence 5480,
  CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR FILING DATE: 1997-03-07
   NUMBER OF SEQ ID NOS: 2950
SOFTWARE: PatentIn version 3.2
  PRIOR APPLICATION NUMBER: 10/374,780 PRIOR FILING DATE: 2003-02-25 PRIOR APPLICATION NUMBER: 10/675,852 PRIOR FILING DATE: 2003-09-30
   equence 5480, Application US/10100683
  ILE REFERENCE: PS900
  10-100-683-5480/c
  CURRENT APPLICATION NUMBER: PCT/US04/05654
   RPPLICANT: Kumimoto, Roderick W
APPLICANT: Pilgrim, Marsha L
TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 PCT
  PPLICANT: Rosen, et al.
TILE OF INVENTION: Human Secreted Proteins
   TYPE: DNA
ORGANISM: Zea mays
FEATURE:
  APPLICANT:
   PPLICANT
   PPLICANT
   PPLICANT:
  PPLICANT:
  PPLICANT:
  ENGTH:
  Local
   APPLICATION NUMBER: US 60/043,576 FILING DATE: 1997-04-11 APPLICATION NUMBER: US 60/047,601 FILING DATE: 1997-05-23 APPLICATION NUMBER: US 60/056,845 FILING DATE: 1997-08-22
                        APPLICATION NUMBER: US 60/043,580 FILING DATE: 1997-04-11
  606 CAGGGACTGCTCCAGCGGCCGGCGGCGGCGGCGGCGGCGGCGGCGGTGGTGGCCG
   104 GCGGCAATAGTTCCGGCCCGGAC 126
   44 стесслегостесствесствет ссислате в в стесствет в ст
  1 Similarity
49; Conserv
  1186
  GCTGCTACAACTGCGGCCAGGCC 688
   Creelman, Robert A
Ratcliffe, Oliver
Adam, Luc J
   Riechmann, Jose
Jiang, Cai-Zhong
   Yu, Guo-Liang
Broun, Pierre E
  Gutterson, Neal
  Century, Karen
  неаго, Jacqueline E
Haake, Volker
  Conservative
   Application PC/TUS0405654
NUMBER: US 60/047,599
   l III, Arnold N
a, Omaira
  e, James
  Bradley K
   T. Lynne
   Peter
  6.3%;
  ; Score 28.6; D; Pred. No. 5.7; 0; Mismatches
   DB 1;
  34;
   Length 1186;
  Indels
  0
  Gaps
  0
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RESULT 13
US-10-100-683-3397/c
  В
   8
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  ; ORGANISM: Homo sapiens US-10-100-683-5480
Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 13468
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3397
TENTIN: 3416
   Sequence 3397, Appli GENERAL INFORMATION:
  SOFTWARE: Pat
SEQ ID NO 5480
  Matches
  Query Match
Best Local
   PRIOR FILING DATE: 1997-08-22
  PRIOR APPLICATION NUMBER: US 60/040,162 PRIOR FILING DATE: 1997-03-07
   CURRENT APPLICATION NUMBER: US/10/100,683
CURRENT FILING DATE: 2002-03-19
   PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/056,664
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/043,314
PRIOR APPLICATION NUMBER: US 60/047,632
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: US 60/047,632
PRIOR FILING DATE: 1997-05-23
  TITLE OF INVENTION: Human Secreted Proteins
   Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 13468
  PRIOR
   ENGTH:
   Local
   APPLICATION NUMBER: US
  FILING DATE: 1997-08-22
APPLICATION NUMBER: US 60/043,314
   APPLICATION NUMBER: US 60/056,845 FILING DATE: 1997-08-22
  FILING DATE: 1997-05-23
  APPLICATION NUMBER: US 60/047,601
   APPLICATION NUMBER: US 60/043,576 FILING DATE: 1997-04-11
  APPLICATION NUMBER: US 60/047,632
  FILING DATE:
  APPLICATION NUMBER: US 60/056,664
   APPLICATION NUMBER: US 60/047,599
  APPLICATION NUMBER: US 60/043,580
  FILING DATE:
  APPLICATION NUMBER: US 60/056,892 FILING DATE: 1997-08-22
  FILING DATE:
   DNA
   362 ATAACGCCGCGCTGGTTAATCAGACCG 388
   302
   242 CAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATG 301
  l Similarity 49.773; Conservative
   1295
  PatentIn Ver.
  ACAGCATCAATCAGCTCATCACTATGTGCACCCAGCAGGCACCCGGCCAGAAGGAGTGTG 648
   ccaccarcaaccagragaacacraaaaaacrccgararracrgrcggccaaracggcggra 361
  ATAACGCCCTGCGGGAATTGGAGACGG 621
  Application US/10100683
   PS900
   et al
  1997-04-11
   1997-04-11
  1997-05
   1997-05-23
   1997-04-11
   6.3%;
   60/056,892
  Score 28.6; DB Pred. No. 5.9; 0; Mismatches
  0

    See File Wrapper or PALM.

  See
   DB 6;
  74;
  File Wrapper or PALM
   Length 1295;
  Indels
  ٠,
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; ORGANISM: Homo sapiens US-10-100-683-3397

TYPE: DNA

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RESULT 15
US-60-548-091-5725
; Sequence 5725, Application US/60548091
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: STROKE, METHODS OF DETECTION AND USES THEREOF
ULE REFERENCE: CL001506
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   RESULT 14
US-10-021-698A-3529/c
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   APPLICANT: SIMON, JASON
APPLICANT: ALLEN, KRISTINA
APPLICANT: PANDIT, SUNIL
TITLE OF INVENTION: NUCLECTIDE AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: 2976-4044US1
CURRENT, APPLICATION NUMBER: US/10/021,698A
CURRENT, FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/211,749
PRIOR FILING DATE: 2000-06-14
NUMBER OF SEQ ID NOS: 6160
SOFTWARE: Patentin 2.1
SEQ ID NO 3529
   δ
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   뭐
  Matches
  Query Match
   -10-021-698A-3529
   GENERAL
   Ouery Match 6.3%; Score 28.6; DE Best Local Similarity 49.7%; Pred. No. 9.5; Matches 73; Conservative 0; Mismatches
  TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
  OTHER INFORMATION: a, t, c or
   NAME/KEY: modified_base
LOCATION: (401)
   APPLICANT: KEITH,
  ENGTH: 8206
   Local
  4054 ATAACGCCCTGCGGAATTGGAGACGG 4028
  4114 ACAGCATCAATCAGCTCATCACTATGTGCACCCAGCAGGCACCCGGCCAGAAGGAGTGTG 4055
  4174 CGGACCCTGCTGCCCTAACCTCAAGAGTCAGCTGGCTGCAGCTGCCAGGGCAGTAACTG
  362 АТААССССССССТССТВАТСАСАССС 388
   302 CCACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATACGGCGGTA 361
  242 CAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATG
  641
   362
   701
   302 CCACCATCGACCAGTGGAACGCTAAAAACTCCGGATATTACTGTCGGCCAATACGGCGGTA 361
   761 CGGACCCTGCTGCCCTAACCTCAAGAGTCAGCTGGCTGCAGCTGCCAGGGCAGTAACTG 702
  242 CAGGCCAGGGTGCGGATAATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATG
   6.3%;
Similarity 49.7%;
  ATAACGCCGCGCTGGTTAATCAGACCG 388
  ACÁGCATCAATCAGCTCATCACTATGTGCACCCAGCAGGCACCCGGCCAGAAGGAGTGTG 642
  ĀTĀĀĊĠĊĊCTĠĊĠĠĠAATTGĠĀĠĀĊĠĠ 615
   LITTLE, RANDALL
VAN BERDEWEGH, PAUL
DUPUIS, JOSEE
  DEL MASTRO, RICHARD
  Conservative
   Application US/10021698A
   MIT
   Score 28.6; DI
Pred. No. 15;
0; Mismatches
   0;
  DB 6;
   74;
   DB 6;
   74;
  Length 8206;
   Indels
   Length 3416;
   Indels
   ٥,
   0;
   Gaps
   Gaps
  4115
  301
  301
   0
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  US-60-548-091-5725
   Query Match
Best Local S
Matches 53
   CURRENT APPLICATION NUMBER: US/60/548,091
CURRENT FILING DATE: 2004-02-27
NUMBER OF SEQ ID NOS: 24433
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5725
LENGTH: 394468
   NAME/KEY: misc_feature
LOCATION: (1)...(394468)
OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
  TYPE: DNA ORGANISM: Homo sapiens FEATURE:
208367 ÁGCCTAATAACTCCAGGTCTATAATCCTTCAAGA 208400
  208307 ATATTACAACTCTAATGCCCATAATTTGTCTTGCAGATATTACCACCATTGAGTTGCTGA 208366
                               320 ACGCTAAAAACTCCGATATTACTGTCGGCCAATA 353
  260
  Similarity
   ATAGTACTATTGAACTGACTCAGAATGGTTTCAGAAATAATGCCACCATCGACCAGTGGA 319
  Conservative
   56.4%;
  0;
  Score 28.4; DB 7;
Pred. No. 1.1e+02;
0; Mismatches 41,
  41;
  Length 394468,
  Indels
  0;
```

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